Title

Plant Spellcheckers: Molecular Basis of PPR-mediated RNA Editing and a Model for Retrograde Communication

Author

DIAZ, MICHAEL FRANCISCO

Publication Date

2019

UNIVERSITY OF CALIFORNIA,
IRVINE

Plant Spellcheckers: Molecular Basis of PPR-mediated RNA Editing and a Model for Retrograde Communication

DISSERTATION

submitted in partial satisfaction of the requirements
for the degree of

DOCTOR OF PHILOSOPHY

in Biological Sciences

by

Michael Diaz

Dissertation Committee:
Professor R. Michael Mulligan, Chair
Professor Grant MacGregor
Professor Brandon Gaut

2019

Dedication

To my Wife—
Thank you for your patience and support. My success
would not be possible without you.

To my Parents—
Thank you for letting me be curious.

TABLE OF CONTENTS

List of Figures

Chapter 3

Chapter 4

Supplementary Figures

Chapter 5

Supplementary Figures

List of Tables

Chapter 3

Chapter 4

Supplementary Tables

Chapter 5

Supplementary Tables

Acknowledgements

Thank you to Dr. Michael Mulligan for taking a chance on me as a doctoral student and cultivating my growth as a scientist. Thank you for accommodating my growing family—we have valued your flexibility. Most importantly, thank you for being a colleague instead of a boss—the intellectual exchanges over the years have been intense, thought-provoking, and inspiring.

Thank you to my committee members, past and present, for supporting and improving my work. Special thanks to Dr. Grant MacGregor for having high standards—we are all better for it.

Thank you Dr. Michael Hayes for mentoring my PhD work early on. Amid all the stresses and unknowns for your future, you still took the time to train me. Thanks for all the non-science discussions—it reminded me that there was more to life than what was waiting for me at the bench.

Thank you Dr. Aparna Sreenivasan for being the original source of inspiration and helping my dream to be a scientist become a reality. You made it exciting to study science. You made it exciting to be a researcher. You created opportunities that I never thought were possible. Many others have benefited from your investment in me over the years since my time at CSU Monterey Bay. I have mentored several students and peers and, in my efforts, I try to be as effective as you were. You invested a tremendous amount of time to my success and I will always be indebted to you.

Thank you Dr. William Head for setting a high bar for academic achievement. Your expectations forced me to push beyond what I thought was possible and it has served me well. Thank you for your leadership in the Undergraduate Research Opportunity Center (UROC)—my success would not have been possible without it.

Thank you Dr. Jeffery Tomberlin and Dr. Micah Flores for making my first foray into research a memorable one. Amid sweltering Texas heat, countless insects, and the unforgettable smell of decomposition, I got the buzz for research and have never looked back. Thank you for the memories—I will carry them with me for the rest of my life.

Thank you to the Faculty at Chaffey Community College for not giving up on me. I was hopeless on paper, but you saw something worth investing in. Thank you for the many second chances.

NSF Graduate Research Fellowship Program, NIH-MBRS Program, UC President's Dissertation Year Fellowship for funding my research.

Lastly, thank you to friends and family for not letting me give up—it has been a trial, but we made it.

Curriculum Vitae

Michael Diaz

EDUCATION

Doctor of Philosophy Developmental and Cell Biology University of California, Irvine, Irvine, CA	Conferred Spring 2019
Master of Science Developmental and Cell Biology University of California, Irvine, Irvine, CA	Conferred Spring 2016
Bachelor of Science Biology California State University, Monterey Bay, Seaside, CA	Conferred Fall 2012

RESEARCH EXPERIENCE

Graduate Researcher University of California, Irvine Department of Developmental and Cell Biology, Irvine, CA *Principal Investigator, R. Michael Mulligan*	April 2014 – June 2019
Graduate Researcher University of California, Irvine Cellular and Molecular Biosciences Program, Irvine, CA *Principal Investigators, David Fruman, Melissa Lodoen, Manuella Raffatellu*	June 2013 - April 2014
Undergraduate Researcher University of California, Santa Cruz Microbiology and Environmental Toxicology Department, Santa Cruz, CA *Principal Investigator, Karen Ottemann*	July 2012 - January 2012
Undergraduate Researcher California State University, Monterey Bay Science and Environmental Policy Department, Seaside, CA *Principal Investigator, Aparna Sreenivasan*	August 2011 - January 2012
Undergraduate Researcher University of Dayton Biology Department, Dayton, OH *Principal Investigator, Mark Eric Benbow*	May 2011 - August 2011

Undergraduate Researcher United States Department of Agriculture, Salinas, CA *Principal Investigator, Beiquan Mou*	January 2011 - May 2011
Undergraduate Researcher Texas A&M University Entomology Department, College Station, TX *Principal Investigator, Jeffery K. Tomberlin*	May 2010 - August 2010

FELLOWSHIPS, GRANTS, AWARDS, HONORS, & SCHOLARHSIPS

Undergraduate Research Opportunities Program Grant *Mentees: Kolton Peck, April Taniguchi*	January 2018
William D. Redfield Award for Outstanding Molecular Biology Research	June 2015
Diverse Educational Community and Doctoral Experience (DECADE) Travel Award	January 2015
Gordon Research Conference Carl Storm Underrepresented Minority Fellowship	January 2015
National Science Foundation’s Graduate Research Fellowship	April 2013
Francisco J. Ayala/ School of Medicine Dean’s Fellowship Award	April 2013
National Institutes of Health MBRS-IMSD Research Fellowship	April 2013
First Place, TriBeta National Honor Society Johnson C. Johnson Award for Excellence in Student Research for Poster Presentation	April 2012
Second Place, American Academy for the Advancement of Science Emerging Researchers National Conference for Poster Presentation	February 2012
Washington University, St. Louis, MO, Genomics Education Partnership Scholarship	Spring 2012
First Place, North American Forensic Entomology Association Conference for Oral Presentation	July 2011

ORAL PRESENTATIONS

Diaz M., Hayes M, Bentolila S and R. Michael Mulligan. RNA Spellcheckers: Characterizing the RNA Editing Complex in Plants. Dept. of Developmental and Cell Biology Research in Progress Seminar. April 7, 2016.

Diaz M., Hayes M, Dang K, and R. Michael Mulligan. Molecular Mechanisms of RNA editing in Plants. Dept. of Developmental and Cell Biology Research in Progress Seminar. April 22, 2015.

Diaz M., Behnsen J., Raffatellu M. The *fhuE* Receptor Confers a Competitive Advantage to *Salmonella* in the Inflamed Gut. Cellular and Molecular Biosciences Mini-symposium, Irvine, CA, March 21, 2014.

Diaz M., Gov L., Lodoen M. Investigating the Role of ASC in MAPK Activation in *Toxoplasma gondii* Human Monocytes. Cellular and Molecular Biosciences Mini-symposium, Irvine, CA, December 13, 2013.

Diaz M., Lomon S., Fruman D. Pharmacogenetic Dissection of the mTOR Pathway in Mature B Cells. 2013 Minority Science Program Symposium, Irvine, CA, September 24, 2013.

Diaz M., J. Tomberlin, M. Flores, 2010. Pupal Size Throughout Dispersal of the Secondary Screwworm *Cochliomyia macellaria* (Diptera: Calliphoridae): Implications for Forensic Entomology. 2011 North American Forensic Entomology Association Conference, College Station, Texas, July 20, 2011.

POSTER PRESENTATIONS

Diaz MF, Hayes M, Bentolila S, R. Michael Mulligan. Gordon Research Conference. RNA Editing: Biology and Mechanisms of RNA and DNA Modification, Ventura, CA, Mar. 12-17, 2017.

Hayes M, Dang K, Diaz MF, Mulligan RM. Gordon Research Conference. Chloroplast Biotechnology, Ventura, CA, Jan. 18-23, 2015. The DYW Deaminase Domain of Pentatricopeptide Repeat Proteins Has Key Characteristics of an Editing Deaminase.

Diaz M., Sreenivasan A, Benbow ME. TriBeta National Convention, San Juan, PR, May 14-20, 2012.

Diaz M., Sreenivasan A, Benbow ME. TriBeta Regional Convention, Seaside, CA, April 7, 2012.

Diaz M., Sreenivasan A, Benbow ME. Emerging Researchers National, Atlanta, GA, Feb. 23-25, 2012.

Diaz M., M. Flores, J. Tomberlin. 2010 Society for the Advancement of Chicano/ Native Americans in Science (SACNAS) National Conference, Anaheim, CA, Sept. 30 – Oct. 3, 2010.

OTHER RESEARCH CONTRIBUTIONS

Benbow ME, Lewis A, Pechal J, Blair T, Berg Maureen, Diaz MF, Tomberlin JK, Crippen TL, Tarone A. 2012. American Academy of Forensic Sciences (AAFS) 64th Annual Scientific Meeting, Atlanta, GA, Feb. 20-25, 2012.

Flores, M., A.M. Tarone, M. Diaz, and J.K. Tomberlin. 2011. Entomological Society of America Conference, Reno, NV, Nov. 13-16, 2011.

Masood, N, Mou B, Diaz M., Bi J. 2011. Entomological Society of America Conference, Reno, NV, Nov. 13-16, 2011.

TEACHING EXPERIENCE & TRAINING

Teaching Assistant, BIO 93 DNA to Organisms University of California, Irvine	Fall 2017
Teaching Assistant, BIO 93 DNA to Organisms University of California, Irvine	Fall 2015
Teaching Assistant, BIO 361-01 Eukaryotic Molecular Biology California State University, Monterey Bay	Fall 2012
Teaching Assistant Training, Genomics Education Partnership Washington University, St Louis, Missouri	Spring 2012
Teaching Assistant, BIO 395-02 Special Topics in Biology California State University, Monterey Bay	Spring 2012 - Fall 2012

LEADERSHIP & SERVICE

Volunteer Scientist Educator National Council for Science Education Scientist in the Classroom Initiative	Spring 2017
Council Representative, School of Biological Sciences Diverse Educational Community and Doctoral Experience Program	March 2014 – March 2016

University of California, Irvine	
Co-organizer and Mentor DECADE-PUMP (Peer Undergraduate Mentoring Program) University of California, Irvine	March 2014 – March 2015
Co-organizer Biology-based Python Computer Programming Course California State University, Monterey Bay	January 2013
Mentor Peer-to-Peer Mentoring Program California State University, Monterey Bay	January 2012 – December 2012
Mentor, Recruitment in Science Education California State University, Monterey Bay and Marina High School	October 2012 - December 2012
Organizer & Facilitator Research Skills Workshop: Engaging in a Journal Club California State University, Monterey Bay	January 2012
Mentor Recruitment in Science Education Mentorship Workshops California State University, Monterey Bay	October 2011 and June 2012
Mentor Preparation for Summer Research Workshops California State University, Monterey Bay	April 2011 - May 2011

PUBLICATIONS

Diaz M, Hayes ML, Bentolila S, Mulligan RM. A Protein with an Unusually Short PPR Domain, MEF8, affects editing at over 60 *Arabidopsis* mitochondrial C targets of RNA Editing. 2017. The Plant Journal 92(4): 638-649.

Hayes ML, Dang K, Diaz M, Mulligan RM. A Conserved Glutamate Residue in the C-terminal Deaminase Domain of Pentatricopeptide Repeat Proteins Is Required for RNA Editing Activity. 2015. Journal of Biological Chemistry 290(16): 10136-10142.

Abstract of the Dissertation

Plant Spellcheckers: Molecular Basis of PPR-mediated RNA Editing and a Model for Retrograde Communication

By

Michael Francisco Diaz
Doctor of Philosophy in Biological Sciences

University of California, Irvine,

Professor R. Michael Mulligan

RNA editing in plants converts cytidines to uridines (C-to-U) in chloroplast and mitochondrial transcripts. Pentatricopeptide repeat (PPR) protein family members have been shown to be required for editing, and possess key characteristics of editing deaminases found in other organisms. PPRs have an N-terminal RNA binding domain responsible for RNA recognition and a C-terminal DYW domain that has deaminase-like characteristics.

The role of several features of the DYW domain was investigated. The DYW domain includes the HXE motif that provides a glutamate residue that is catalytically required. Glutamate to alanine substitution ablated editing, and establishes a key characteristic of the DYW domain that is required for editing. In addition, a highly conserved PG box was identified between the N- and C-terminal domains that was required for editing in PPRs that lacked a DYW domain, and the PG box may be required for protein-protein interactions to recruit a deaminase in *trans*. These observations led to the development of the *cis* and *trans*-editing models for RNA editing that posits that the deaminase may be provided in *cis* from a single PPR or in *trans* in PPRs that lack a DYW domain. PPRs, such as MEF8, which have a short RNA binding domain and an intact deaminase domain, were identified as candidates for a *trans*-deaminases. RNAseq analysis was performed on *mef8* null mutants and catalytically ablated variants to examine the role of MEF8 in mitochondrial editing. Sixty editing sites were affected, and suggests that MEF8 may participate as a *trans*-editing deaminase by providing deaminase capability for a large number of editing sites.

The role of reactive oxygen species (ROS) during editing dysfunction was investigated to examine the potential mechanisms of sensing and signaling oxidative distress. *LPA66* mutant plants fail to edit a photosystem II polypeptide and exhibit a strong phenotype. Mutant plants produced elevated levels of ROS, and transcriptomic analysis revealed higher expression of ROS reactive network genes and PPR or editing related genes. Lipidomics analysis of the mutant indicated highly elevated levels of oxylipins including arabidoside A and G and phytoprostanes. Possible signaling mechanisms through oxylipins and jasmonic acid pathways are discussed.

Chapter 1

Introduction

Eukaryotic life is dependent on elegantly organized cellular compartments called organelles. In plant cells, mitochondria and chloroplasts are core organelles that produce energy through respiration and photosynthesis—without these processes, life on earth would cease to exist. Central to organelle function is the expression of both nuclear and organelle genes, with the lion's share residing in the nuclear genome. For example, in *Arabidopsis thaliana*, approximately 7-12% (2,000-3,500) of all protein coding genes in the genome are targeted to the chloroplast . Among this bevy of chloroplast-targeted proteins, pentatricopeptide repeat (PPR) proteins represent the largest family, with 114 genes characterized to date. An additional 382 PPRs are mitochondrial-targeted, making the sum total between the chloroplast and mitochondria 496 genes. Pentatricopeptide repeat proteins are broadly involved in RNA metabolism in the mitochondria and chloroplast, of which RNA editing is the most enigmatic.

RNA editing in plant organelles causes post-transcriptional cytidine-to-uridine (C-to-U) changes in transcripts [2]. In flowering plants, chloroplast transcriptomes have approximately 35 C-to-U editing sites [3], and over 600 Cs are edited in *Arabidopsis* mitochondria [4,5]. In general, editing results in non-synonymous amino acid substitutions that convert aberrant codons to the evolutionarily conserved sequences [6]. The primary role of RNA editing in higher plant organelles appears to be a genetic correction mechanism required for the functional expression of the organelle genomes [7].

Structure and Function of PPR Proteins

In *Arabidopsis*, the majority of PPR proteins (~283) are described as P-type which are typically composed of about 10 to 20 tandem repeats of a 35 amino acid motif known as the P repeat (**Figure 1.1 A, P-type**). Through computational and biochemical analysis, a PPR code has been developed that predicts modular RNA sequence recognition by conserved residues in each PPR repeat [8–10]. Furthermore, structural analyses have demonstrated that PPR proteins form superhelical structures with residues that bind RNA on the inner surface of the helix (**Figure 1.2**) [11–13]. These structural analyses confirmed the general features of the PPR–RNA complex predicted by the PPR code, including modular binding and the detailed participation of polar amino acid side chains at residues 5 and 35 of each P motif in nucleotide recognition (**Figure 1.1 B**), and underscore their well-defined roles in RNA processing such as RNA stabilization, translation

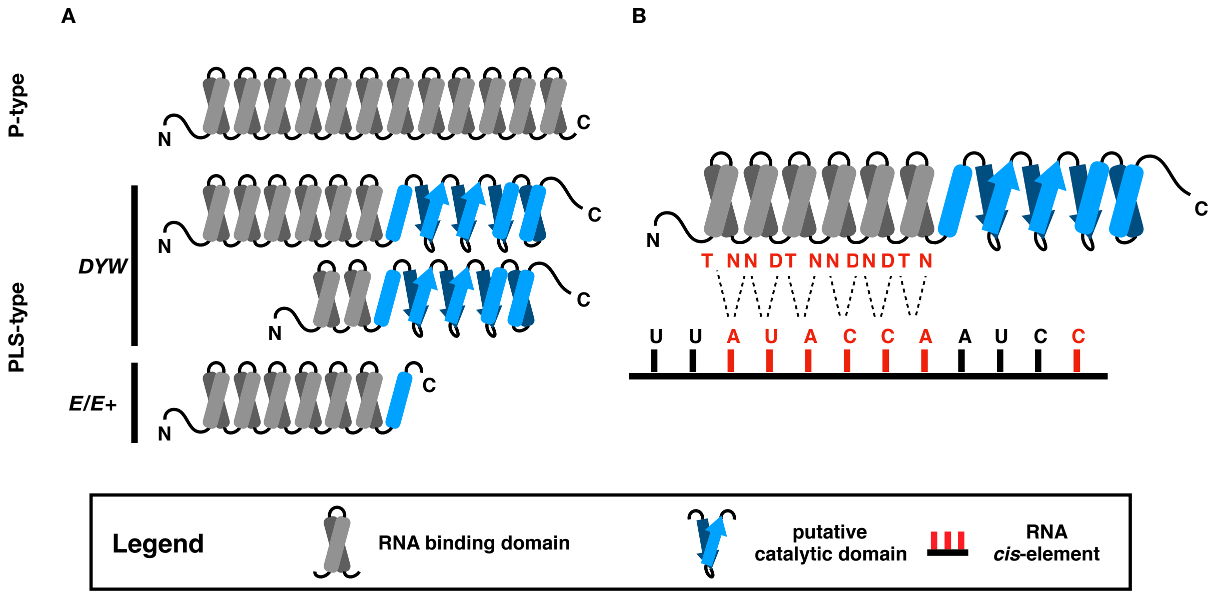


Figure 1.1. Cartoon representation of PPR proteins structure and RNA recognition. **A**) P-type PPRs are involved in RNA stabilization, translation activation/repression, and *trans*-splicing. PLS-type PPRs are exclusively involved in RNA editing. **B)** RNA recognition by PPRs requires polar/charged amino acids in the 5' and 35' amino acid position of tandem repeats in the RNA binding domain. Two amino acids interact with one nucleotide in the *cis*-element of a target RNA via hydrogen bonding.

activation/repression, and trans-splicing[2]. These PPRs have been thoroughly described elsewhere [2]. The remaining 213 PPRs are involved in the enigmatic process of RNA editing, and investigating their form and function, and regulation are the focus of my dissertation research.

Editing PPR Proteins are members of the PLS subfamily

The N-terminal repeat region of PPR proteins contain the characteristic 35 amino acid P repeat as well as long (L) and short (S) variants [14]. The PPR code has been extended to this PLS subfamily [9,10], predicting recognition of RNA sequences that is similar to the code developed for the P subfamily [15]. Amino acid residues located in each PLS repeat interact with specific nucleotides within the *cis*-element to provide site specificity for RNA editing (**Figure 1.1 B** and **Figure 1.2**) [8–10,16]. The PLS subfamily of

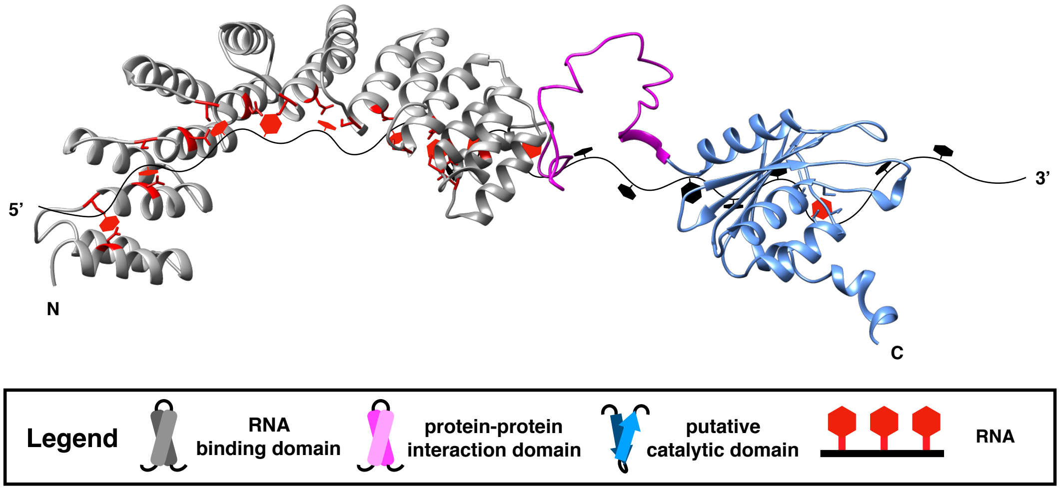


Figure 1.2. Predictive model of PLS-type PPR. The predicted structure of PLS-type PPR was created using the solved structure of a synthetic cytidine binding PPR tract (PDB: 4WSL) and concatenating it to an asymmetric unit (i.e. monomer) of the solved dimeric structure of *Bacillus subtilis* cytidine deaminase (PDB: 1JTK). The *ab initio* domain assembly (AIDA) server was used to concatenate the amino sequences of the two solved structures. During the energy minimization simulation, AIDA constrains the final model by keeping the separate domains rigid while allowing the linking region to be flexible. A cartoon RNA molecule was woven through the structure. In the RNA binding domain, the red hexagons represent nucleic acids bound by the PPR tract. In the putative catalytic domain, the red hexagon represents the edited cytidine. The pink region represents a protein-protein interaction domain (referred to as PG box in **Chapter 3**)thought be involved in the formation of high molecular weight editing complexes.

PPR proteins also includes characteristic C-terminal domains known as the E/E+ and DYW deaminase domains (**Figure 1.1 A**), which have recently been elaborated [14,17]. While the E/E+ domain contains degenerate PPR repeats [17] whose complete function remains unclear, it does not appear to contribute to RNA binding [16]. The E/E+ domain is, however, involved in protein-protein interactions that contribute to the formation of high molecular weight RNA editing complexes [18,19].

The DYW Deaminase Domain of PPRs Has Key Features of Editing Deaminases

The DYW deaminase domain (hereafter, DYW domain) is so called for the last three amino acids found in a majority of editing PPRs—aspartic (D), tyrosine (Y), and tryptophan (W). The DYW domain has key features of editing deaminases that include

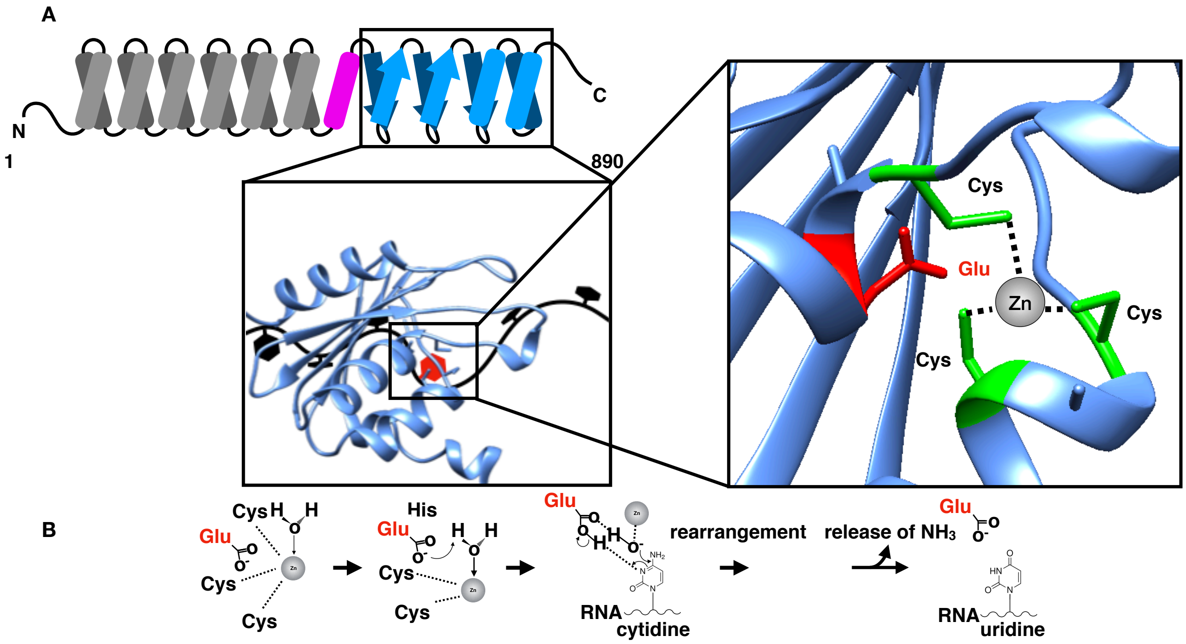


Figure 1.3. DYW-type PPRs maintain a highly conserved glutamate residue found in other cytidine deaminases. **A**) Close up representation of the putative active site of PPRs. In this example, three cysteines (green) coordinate an active site zinc ion (grey). The active site glutamate (red) is critical for editing in other deaminases. **B**) The glutamate residue participates in a proton shuttling mechanism. First, the zinc ion binds water. The glutamate residue abstracts a proton from the zinc-water complex to produce a zinc-hydroxide that attacks the cytidine residue. After a subsequent rearrangement and loss of ammonia, a uridine remains in place of the cytidine.

canonical zinc binding motifs (HXE, CXXC, where X is any amino acid), the presence of a zinc prosthetic group, and a conserved catalytic glutamate residue of the HXE motif [20]. The conserved glutamate residue found in the DYW domain of PPRs is catalytically involved in the deamination mechanism of bacterial cytidine deaminase. This conserved glutamate residue is a key characteristic expected for an editing deaminase (**Figure 1.3**) [21–24]. While PPRs appear to have key features of deaminases, it remained unknown whether these features bestowed biochemical function. **In chapter 3**, we approached this question experimentally by studying the behavior of several transgenes *in planta*, overexpressed in plants with null alleles of PPRs, rendering the native gene non-functional. By overexpressing various transgenes in a knockout background, we were able to study the behavior of PPRs with truncations that remove the DYW domain entirely. In addition, we were able to study the function of the key glutamate residue directly, by substituting this residue with a non-polar, and therefore non-functional alanine residue, (**Figure 1.3 B**) enabling us to address whether the deaminase features retained by PPRs were critical for RNA editing.

Evolution of Pentatricopeptide Repeat Proteins and RNA Editing in Plants

While PPRs are found in all eukaryotes, the expansion of PPRs in plants is the most striking, with upwards of 500 genes present in *Arabidopsis*. With few exceptions, members of each clade of plant evolution have PPRs and exhibit RNA editing [17,25,26]. Numbers of PPRs vary, but editing site number and number of PPR genes show strong correlation, starting with basal angiosperms, and marching on through higher plants, with losses exhibited over time [27]. As to why RNA editing in plants emerged is a matter of some debate, but it appears it does not provide an easily explained positive selective advantage and instead is likely a case of neutral evolution [25,28,29]. In addressing how RNA editing has expanded in plants, limited evidence points to retrotransposition events increasing PPR number. Most of the PPRs found in the moss *Physcomitrella patens*—one of the oldest land plants—contain introns, and vestiges of these introns are observed in the 5’ region of intron-less PPRs of higher angiosperms [30]. Therefore, it is posited that reversed transcribed cDNA, reintegrated into the genome through homologous recombination, resulted in preferential loss of the 3’ end, where reverse transcription starts, and truncations on the 5’ end, where reverse transcription terminates [30,31]. This hypothesis helps explain the diversity of PPRs present in plants.

While many editing PPRs contain an N-terminal RNA binding domain and C-terminal DYW domain (**Figure 1.1 A, 1.2**, **1.3 A**), several PPRs have a truncated C-terminal DYW domain or reduced N-terminal RNA binding domains [21,32,33]. Several of these variants, specifically those without a deaminase domain, can complement editing activity, which is confusing, since the deaminase domain is thought to be responsible for editing activity [34,35]. If the DYW domain is critical for RNA editing, then only two possible explanations can resolve this conundrum: a yet to be described non-PPR deaminase is responsible for the editing activity observed in plants, or PPRs can interact with one another to support editing activity. Researchers have not identified any other genes targeted to the chloroplast and mitochondria with domain architecture that would support a deaminase-like reaction [14]. In addition, a non-PPR deaminase would be an unlikely scenario, given that insertional mutagenesis of a PPR gene typically disrupts editing at one or a few sites in chloroplasts and mitochondria, with dozens of published examples, with a list that keeps growing [2,36]. A likely scenario is that a PPR that lacks a deaminase domain must interact with another PPR with a functional deaminase domain in order to support RNA editing activity. In **Chapter 3**, we investigate a highly conserved region between the N-terminal RNA binding domain and C-terminal DYW domain, which we hypothesize supports PPR-PPR interactions. We refer to this region as the PG box in **Chapter 3**.

We have posited that a PPR lacking a DYW domain could not support editing activity alone and that it would require a DYW domain supplied in *trans*, as opposed to cis-editing where the PPR encodes an RNA binding domain and DYW domain in one polypeptide (**Figure 4**). Indeed, one published example highlights this possibility. Chlororespiratory reduction 4 (CRR4) is a PPR that lacks a deaminase domain, but maintains 11 RNA binding motifs capable of recognizing chloroplast transcript NADH-dehydrogenase complex 1 (*ndhD*-1). On the other hand, DYW1 is a PPR that lacks a N-terminal RNA binding domain but has retained a functional DYW domain. A chimeric version of these two genes was able to complement editing of *ndhD-1* in a *crr4 dyw1* double mutant [37]. Surprisingly, DYW1 was not responsible for editing more RNA editing

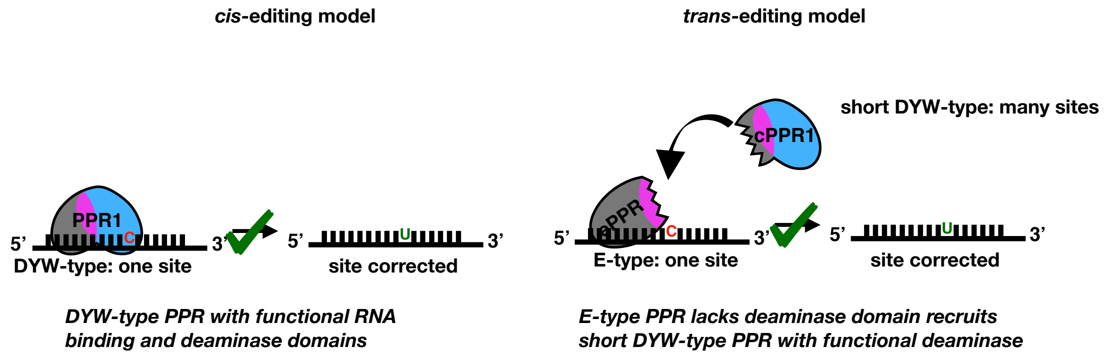


Figure 1.4. A *cis*- and *trans*-editing Model for RNA Editing in Plants. In the *cis*-editing model, a PPR contains the PLS RNA binding repeat domains and DYW deaminase domain in the same polypeptide. In the *trans*-editing model, an E-type PPR that lacks a functional deaminase domain, interacts with the DYW containing PPR to edit a site. In our model, we use a short DYW-type PPR that has reduced RNA binding capacity as the data in **Chapter 4** supports this model, however we believe this model may extend to PPRs involved in the *cis*-editing model as well.

sites in the chloroplast in insertional mutants of *dyw1*. Given that DYW1 has a degenerate RNA binding domain, we expected more promiscuous editing activity or rather editing of more sites that are recognized by E-type PPRs, which lack a DYW domain. We revisited this possibility by investigating a related PPR, mitochondrial editing factor 8 (MEF8) in **Chapter 4**. The mitochondria is well-suited to study the *trans*-editing model since MEF8 is structurally related to DYW1, with an unusually small PLS repeat domain—too small to effectively act in editing site recognition. In addition, approximately 110 editing PPRs are targeted to the mitochondria, of which only 43 contain a DYW domain. The remaining are E-type PPRs with varying PLS repeats number, and therefore varying RNA binding capacity. It follows then, to edit all 600 sites of the mitochondria, either each DYW-type PPR must edit $\geq$ 6 editing sites, or E-type PPRs interact with DYW-type PPRs to supply the site specificity and editing activity in *trans*. Several insertional mutants of mitochondria-targeted PPRs show defects in as few as one site [36], making the six editing sites for every DYW-type PPR hypothesis untenable. Instead, *trans*-editing among PPRs is a more likely scenario, and evidence from **Chapter 3** and **Chapter 4** supports this model.

Non-PPR Proteins are Required for RNA Editing in Higher Plants

While members of the pentatricopeptide repeat protein family are thought to participate directly in C-to-U catalysis, several genes have been identified that are posited as indirectly participating in catalysis (**Figure 1.5 A**). These genes include the RNA Editing Interacting Protein/Multiple Organellar RNA Editing Factor (RIP/MORF) family [5,38,39], the Organelle RNA Recognition Motif containing protein (ORRM) family [40–42], the

Organelle Zinc finger editing factor (OZ) family [43], tetrapyrrole biosynthetic protein protoporphyrinogen IX oxidase (PPOI) [44], and the PPR-like protein NUWA [34,35]. Since PPR proteins are the only genes with conserved deaminase-like domains, these additional genes are posited as functioning as a scaffold for C-to-U catalysis, mediated by protein-protein interaction domains as well as non-specific RNA binding domains [7] (**Figure 1.5 B**). The diversity and complexity of RNA editing genes warrants further investigation to identify additional RNA editing genes, as well as understanding how C-to-U catalysis and editing complex formation is regulated.

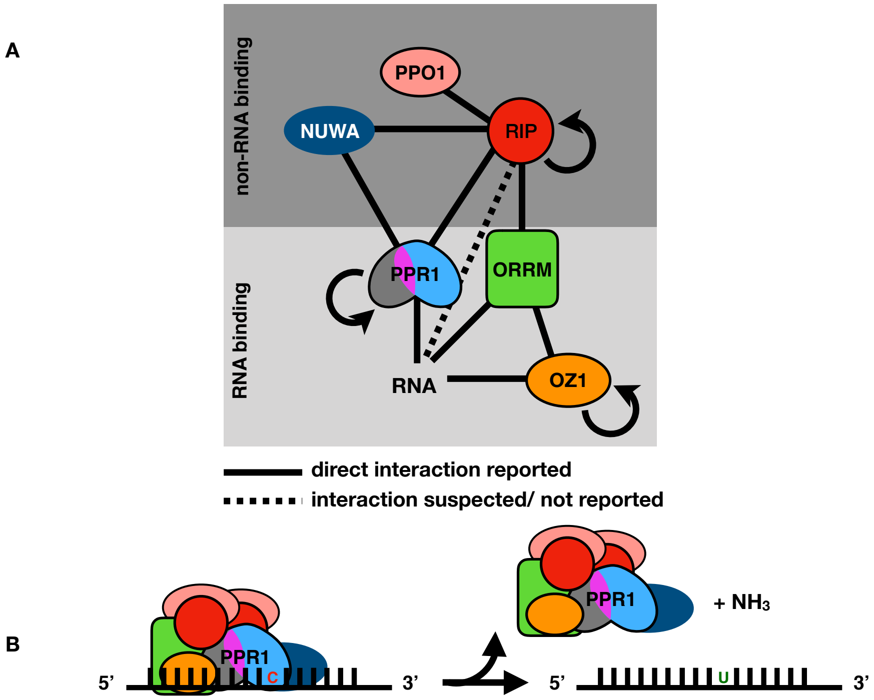


Figure 1.5. Proposed model for RNA editing complex in plants. **A**) RNA editing involves several non-RNA binding and RNA binding proteins. PPO1, NUWA, and RIPs are non-RNA binding proteins. Both NUWA and PPOI form interactions with RIP family proteins. RIP can form homodimers. PPRs, ORRMs and OZs are RNA binding proteins. OZs and ORRMs interact with each other and with RNA. PPRs interact with RNA as well as non-RNA binding proteins NUWA and RIPs. In addition, PPRs and OZs form homodimers **B**) Proposed model of RNA editing complex including PPRs and non-PPR editing factors.

Role of PPRs in Electron Transport Machinery Maturation and Their Regulation Via Reactive Oxygen Species

A majority of RNA editing events in plant mitochondria and chloroplasts occur in transcripts that encode polypeptides in the electron transport chain (ETC) (**Table 5.1**). This is mostly likely by chance, given the majority of genes retained by both the mitochondria and chloroplasts are involved in ETC. Organelle ETC genes are mostly membrane bound and it is thought the hydrophobicity of these proteins made targeting and import into the organelle difficult [45]. Hence, these genes were maintained by the organelle. By consequence, disruption of electron transport is expected to be a common consequence of RNA editing dysfunction and a possible convergence point for regulation. For example, Photosystem II is a potent producer of singlet oxygen ($^1O_2$) and superoxide anion ($O_2 \bullet^{-}$), and hydrogen peroxide (H_2O_2) is mainly produced around photosystem I. In contrast, $O_2 \bullet^{-}$ is the main reactive oxygen species (ROS) in mitochondria under normal metabolic conditions, and effectively processed to non-reactive products by organelle ROS network proteins [46,47]. However, when electron transport is disrupted, upstream redox centers may become highly reduced and result in high levels of ROS production. Moderate levels of ROS production can be managed by stress acclimation and signal transduction, but higher levels may significantly overwhelm metabolic scavenging mechanisms, and ROS can be cytotoxic and lead to programmed cell death [48].

Reactive oxygen species have been extensively documented as retrograde signaling molecules in plants outside of RNA editing dysfunction[49–55]—retrograde signals originate in a subcellular compartment outside the nucleus and drive gene expression changes in the nucleus. ROS are unlikely candidates for signaling molecules during RNA editing dysfunction because ROS are rapidly detoxified in the chloroplast and mitochondria, and would not be expected to move through the cell even over short distances [48]. However, it is important to note that ROS molecules can move out of, or between, organelles via aquaporins or stromules [56,57]. Instead, ROS acting on other molecules is a more likely source for retrograde signaling molecules. Therefore, we hypothesize lipid peroxidation is increased in editing mutants, which would result in production of lipid-derived signaling molecules. Indeed, ROS generation in chloroplast provokes the formation of potent lipid-derived retrograde signaling molecules [58,59]. We expect the identity of these signals depends on what compartment is affected by RNA editing dysfunction, since ROS production can be site-specific [50,52,58,60]. ROS production and upregulation of ROS network genes has been documented in PPR mutants, but this was contextualized as mitigating oxidative stress due to loss of editing or RNA stability [61–66], rather than addressing the possibility that ROS or other retrograde signaling molecules can mitigate RNA editing dysfunction directly. So, is there a nuclear response to help mitigate RNA editing dysfunction? Several publications have demonstrated mutations in PPRs affect the abscisic acid (ABA) response, yet these investigations focus on global plant physiological responses and how disruption of PPRs impact abiotic and biotic responses [62–69], and not how ABA influences RNA editing in the cases where editing PPRs were studied [62,65,67,69]. A growing body of research has demonstrated how oxylipins and cardiolipins, oxygenated lipids from the chloroplast and mitochondria, respectively, play important roles in retrograde signaling from the organelles, and that free-radical catalyzed as well as enzyme-catalyzed lipid oxygenation occurs during abiotic and biotic stress [70,71]. Therefore, we hypothesized an early messenger of a retrograde signaling cascade would be an oxylipin, as is the case in several abiotic and biotic stress responses [48,50,52,54,58,70,72]. We investigate this possibility in **Chapter 5**.

Since the discovery of the RNA editing in plants in 1989 [6] and the identification of the first PPR [73], our understanding of RNA editing has seen tremendous gains in large part due to the introduction of next-generation sequencing technologies and high-throughput reverse genetic screens. What many researchers could have not foreseen, is that RNA editing is exceedingly complex, and we would barely be scratching the surface thirty years later. Several hundred PPR proteins are expected to be involved in RNA editing, many of which are yet to be characterized [17]. Our lab and others have observed highly conserved regions within PPR proteins, which we hypothesize bestow biochemical function to the proteins. Investigating these regions is the primary focus of **Chapter 3** and **Chapter 4**. Some of these highly conserved regions are suspected in supporting protein-protein interactions. We investigated this hypothesis in **Chapter 3** and **Chapter 4**. Simultaneously, several labs have identified numerous non-PPR editing factors, which has profoundly changed our understanding of RNA editing in plants. What was once thought to be an enigmatic reaction carried out solely by PPRs, now involves proteins from at least 4 different gene families (**Figure 1.5**). As the number of PPRs and non-PPRs involved in RNA editing continues to grow, it begs the question whether this process is regulated—it is difficult to imagine hundreds of gene constitutively expressed to carry out RNA editing, when the expression patterns of most of the edited RNAs are dynamic. Several organelle processes are regulated by nuclear-encoded genes with organelle-derived retrograde signaling molecules mediating communication between the organelles and nucleus. One of the most common signals are lipid-derived signals called oxylipins and cardiolipins in the case of the chloroplast and mitochondria, respectively. We investigate the involvement of lipid-based retrograde signals during RNA editing dysfunction in **Chapter 5**.

Chapter 2: Materials and Methods

Chapters 3, 4, and 5 represent three separate publications. Therefore, the methods for each publication will be organized as separate sections to reflect the methods specific to each publication.

Materials and Methods for Chapter 3

Plant Materials

Arabidopsis T-DNA lines SALK_078415C (*cref7-1*), SALK_120902C (*otp84-2*), and SALK_142061C (*otp84-3*) were obtained from the *Arabidopsis* Biological Resource Center. Seeds for *Arabidopsis* ecotype Columbia (Col-0) were purchased from Lehle seeds (Round Rock, TX) and were used for the wild type line.

Transgenic plant lines were produced by introducing the following genes: OTP84 (At3g57430); *OTP84-trcDYW* (OTP84 truncated after residue F770), *OTP84trcPG* (OTP84 truncated before the PG box after residue K754); *OTP84-E824A* (E to A substitution at residue 824); *CREF7* (At5g66520), and *CREF7-E554A* (E to A substitution at residue 554).

Gene Cloning and Plant Transformation

Gene sequences from *OTP84*, *OTP84trcPG* (M1-K754), and *OTP84trcDYW* (M1-F770) were amplified by PCR to introduce 5' *BamH*I and 3' *Sal*I restriction sites. Sequences for *CREF7* were amplified with flanking *Bgl*II and *Sal*I restriction sites. Mutations were introduced by amplification with primers that altered codon E824 of *OTP84* and E554 of *CREF7* to alanine codons. All gene fragments were cloned into pCHF1 using *BamH*I and *Sal*I restriction sites [21]. Binary vectors were electroporated into

Agrobacterium strain ASE [74], and plants were transformed by floral dip [75]. Seedlings were selected using 100 mg/L Gentamicin.

RNA Editing Analysis Through Bulk Sequencing

Total RNA was isolated from green leaves using RiboZol from AMRESCO (Solon, OH). The GoScript Reverse Transcription System (Madison, WI) was used with Random Hexamers from ThermoFisher (Waltham, MA) to create a cDNA pool. Gene specific primers were used to amplify sequences including editing sites from the cDNA templates with DreamTaq Green DNA Polymerase from ThermoFisher. Bulk sequencing of RT-PCR products was carried out at the University of California, Berkeley DNA Sequencing Facility. Peak heights were measured from electropherograms using BioEdit V7.0.9.0 to estimate the extent of RNA editing in RNA templates isolated from leaves.

Poisoned Primer Extension Editing Analysis

Poisoned primer extension (PPE) assays were performed as previously described [76] with one modification. Purified PCR products were treated with FastAP from Thermo Scientific and incubated for 10 min at 37°C followed by 5 min at 75°C. This is similar to the ExoSAP-IT step of the PPE assay from the Hanson lab [76]. The addition of the FastAP step consistently reduced read-through to less than 3%. Oligonucleotide primers contained a 5’ hexachlorofluorescein tag from Eurofins (Ebersberg, Germany). Vent DNA polymerase and acyNTPs from NEB (Ipswich, MA) were utilized for chain termination reactions. Primer extension products were separated by electrophoresis on 12% polyacrylamide gels with 6 M urea. Gels were covered in plastic wrap and immediately scanned using a Typhoon Trio imager from GE Healthcare (Little Chalfont, United

Kingdom). Percent conversion was calculated from the intensity of bands measured from a gel image using GELQUANT.NET V1.8.2.

Mass Spectrometry

The DYW domain from *ELI1* (At4g37380: D478-W632) was amplified by PCR to add flanking *BamH*I and *Sal*I restriction sites. A single nucleotide mutation (GAG to GCG) was introduced using a PCR primer to create the E566A mutation. The *ELI1-E566A* gene was cloned into pET28a using *BamH*I and *Sal*I restriction sites and introduced into *E. coli* strain Rosetta 2 (DE3) pLysS from Novazymes (Bagsvaerd, Denmark). Recombinant ELI1-E566A was expressed as previously described [21] and purified. Native protein samples were dialyzed in 20 mM ammonium acetate prior to mass spectrometry. Denatured protein samples were treated with 50% acetonitrile and 1% formic acid prior to mass spectrometry. Protein samples were ionized with an ESI voltage of 3.6 kV, a cone voltage of 40 V, and a desolvation temperature of 120°C. Mass determinations were made with a Waters QTOF2 mass spectrometer.

Materials and Methods for Chapter 4

Plant Materials and Growth Conditions

The T-DNA insertion line for *mef8*, SALK-106391C, was obtained from the *Arabidopsis* Biological Resource Center through TAIR and was confirmed as homozygous by PCR. Wild type Columbia-0 ecotype seeds were obtained from Lehle Seeds (Round Rock, TX) and were used as the wild type reference line. Plants were grown at 70% relative humidity with a 16-hour light period at 22^{o}C and an 8-hour dark period at 18^{o}C. Transgenic plants were prepared by introduction of the following genes into the *mef8* T-DNA insertion line: *MEF8* (AT2G25580), *MEF8-E549A* (*MEF8* with a glutamate to alanine substitution in the HXE motif at amino acid position 549).

Gene Cloning and Plant Transformation

MEF8 was amplified with High-Fidelity Phusion PCR from ThermoFisher, and 5' *BglI*I and 3' *Sal*I restriction sites were introduced into each of these amplicons by primer design. The *MEF8-E549A* mutant gene was generated using a mutagenic primer method (Sarkar and Sommer, 1990) where the glutamate codon at position 549 was altered to an alanine codon. A list of primers is provided in **Table S6**. Amplicons were cloned into the binary vector, pCHF1, using the *BamH*I and *Sal*I restriction sites, and electroporated into *Agrobacterium* strain ASE. Plants were transformed with these vectors by the floral dip method [75]. Transgenic progeny were selected on PhytoAgar from bioWORLD (Dublin, OH) supplemented with 1/2 strength Murashige and Skoog salts and 100 mg/L gentamicin from Sigma-Aldrich (St. Louis, MO). Plants transformed with the mutated version of *MEF8* (HXA) are referred to HXA transgenic plants, while plants transformed with the wild-type version of *MEF8* (HXE) are referred to HXE transgenic plants.

RNA Editing Analysis Through STS-PCRseq

Total RNA was isolated from 200 mg of green leaf tissue of 4-5 week old plants. Leaf tissue was pulverized on dry ice and homogenized with Ribozol from AMRESCO, and RNA was isolated according to the manufacturer's instructions. RNA was further purified with the PureLink RNA Mini Kit from Ambion by Life Technologies (Carlsbad, CA). The purified RNA was treated with Turbo DNase from Ambion by Life Technologies. Duplicate RNA samples were prepared from three plant lines for RNA seq as previously described [5]. The plant lines included wild type (Col-0) plants, *mef8* (SALK-106391C), and *mef8* plants complemented with the *MEF8-E549A* construct.

Editing site conversion for mitochondrial and chloroplast editing sites were determined as previously described [5]. Briefly, the RNAs from samples analyzed in this study, *mef8* mutant, wild-type, and transgenic plant, were reverse transcribed using organelle gene specific primers. After quantification, all the RT-PCR amplicons from one sample were mixed in equimolar ratio; the mix of cDNAs was then sheared by sonication and used as a template for the preparation of an Illumina True seq DNA library. Seventy-nine libraries, including 6 libraries obtained from the samples in this study, were pooled in one sequencing lane of an Illumina HiSeq 2500 instrument. Data processing including read quality control, read trimming and alignment, and determination of editing sites by using a likelihood ratio test were performed as described previously [5].

Statistical Tests Used to Identify Changes of Editing Extent in the mef8 Mutant vs. Wildtype, and in the Transgenic vs. the mef8 Mutant

The significance of a difference in editing extent between a wild-type sample and a mutant sample for a certain site was achieved by a chi-square test with one degree of freedom using the number of edited and unedited reads found in each sample at that particular site. For a site to be declared significantly different, the 4 pairwise tests (mef8-1 vs. wt-1, *mef8-1* vs. wt-2, *mef8-2* vs. wt-1, *mef8*-2 vs. wt-2) had to fulfill the significance threshold requirement. Because of repetitive testing, we chose a nominal error rate of $P < 1.6e-6$ to achieve the desired family error rate of $P < 1e-3$ when analyzing 612 sites (36 plastid sites + 576 mitochondrial sites). In addition to this condition, the variation in editing extent, of mef8, defined as: (% editing of the wt - % editing of *mef8*)/% editing of the wt, had to be either ≥ 0.1 (decrease of editing in the mef8 mutant) or ≤ - 0.1 (increase of editing extent in the mef8 mutant) for all the 4 pairwise comparisons. The same *modus operandi* was followed to test for significant difference of editing extent between the transgenic plant and the mutant plant, substituting in the test the wild-type by the transgenic plant.

RNA Editing Analysis Through Bulk Sanger Sequencing

Additional assays for editing site conversion were performed using Sanger sequence analysis of bulk PCR products. cDNA was prepared with random hexamers using the GoScript Reverse Transcription System from Promega (Madison, WI), and amplification of cDNA was confirmed with a RT minus control. For bulk sequence analysis, DreamTaq Green DNA polymerase from ThermoFisher was used to generate amplicons with previously published gene specific primers [5] for the following mitochondria genes: *nad5*, *nad6*, *ccmFN1*, *atp4*, *ccmFc*, *cox2*, *nad5*-intron, *matR*, and *mttB*. Amplicons were gel purified and sequenced by Sanger sequencing at Retrogen, Inc. (San Diego, CA). Editing site conversion was calculated by T and C peak heights measured from electropherograms using BioEdit v7.2.5 software. Error bars show the standard deviation (SD) of the samples.

Materials and Methods for Chapter 5

Plants Materials

Arabidopsis T-DNA lines SALK_039955 (*lpa66*), SALK_139995 (*dot4-2*), were obtained from the *Arabidopsis* Biological Resource Center and bred to homozygosity. Seeds for *Arabidopsis* ecotype Columbia (Col-0) were purchased from Lehle seeds and were used for the wild type line. Insertional mutagenesis was confirmed by PCR using gene specific primers and left border T-DNA primers as designed by the Salk Institute.

While both editing mutants have obvious phenotypes, we confirmed the loss of editing by RT-PCR as previously described [77]. For all experiments, seeds were vernalized at 4°C for 3 days in the dark to synchronize germination on 1/2 murashige and skoog agar plates, and transferred into an *Arabidopsis* growth chamber for two weeks at 80-100μmol/m^2/s with 16h day/ 8h night light cycle. At two weeks, seedlings were transplanted into ProMix PGX soilless mix and supplemented with MiracleGro 24:8:16 (N:P:K). Plants were sub-irrigated with fertilizer supplemented water as needed until harvesting.

Histochemical Staining for O_2^- and H_2O_2 using Nitroblue Tetrazolium and H_2DCFDA

The nitroblue tetrazolium (NBT) assay was performed as previously described . Briefly, fully expanded 4-5 week old leaves were detached prior to reproductive growth. Leaves were detached using a scalpel and immediately submerged, abaxial side up, in 0.1% NBT/ 10mM Sodium Azide/ 10 mM K-Phos pH 6.4 in 6 well plates. Samples were incubated for three hours at room temperature under ambient lighting (i.e. <10 μmol m^{-2} s^{-1}) as measured by a LiCOR 6400 portable photosynthesis system PAR meter (Lincoln, Nebraska). Leaves were cleared using a fixer solution containing 3:1:1 (ethanol:acetic acid:glycerol) overnight or until leaves were devoid of chlorophyll. Samples were imaged using UVP Analytik-Jena ChemStudio Plus Imager (Upland, CA). Experiments were performed using biological triplicates. ImageJ [78] was to used analyze images. Images were converted to 16-bit grayscale and scaled when converting. Duplicate images were used to create a binary version, and MaxEntropy threshold setting was used to select formazan precipitate areas, and separately for total leaf area. Threshold sliders were adjusted as needed. Default pixel intensities were used—black = 0 and white = 255. Formazan area, as determined by thresholding, was redirected to original 8-bit grayscale non-binary image to determine pixel area density and results are reported as percent NBT reduction (formazan area/total leaf area).

The H_2DCFDA assay was performed as previously described [79]. Briefly, 100 mg of tissue was frozen in liquid nitrogen and ground using a pre-chilled mortar and pestle. The powder was immediately resuspended in 10mM Tris-HCl buffer, pH 7.3 and centrifuged twice at 15,000 RCF for 5 minutes at 4°C, and each time, supernatant was removed and placed in a fresh pre-chilled microfuge tube. Final supernatants were split into two tubes—one for fluorescence detection and the other for protein quantification. Protein concentration from each sample was measured using the Bradford Reagent. Samples were transferred in 96 well plates and run as biological triplicates with technical triplicates to account for plate effects during spectrophotometric readings. One-hundred mM H_2DCFDA from Thermo Fisher Scientific Invitrogen (Waltham, MA) was pre-diluted in anhydrous DMSO from Thermo Fisher Scientific Invitrogen and added to each well to a final concentration of 10uM and 0.1% DMSO. Because H_2DCFDA is not specific for H_2O_2 and is instead a general indicator of oxidative stress [80], a control treatment using 300U/mL of Millipore Sigma Catalase from bovine liver (St. Louis, MO) was added to editing mutant samples as a positive control for H_2O_2 since it converts H_2O_2 into water and oxygen. Plates were shaken on a rotary plate shaker at 700 rpm for 1 minute at room temperature. Measurements were taken on a BioTek Synergy HT plate reader with moderate shaking for 15s prior to timepoint measurements every 5 minutes for 30 minutes. Measurements were expressed as RFU per ug protein as determined by the Bradford Assay.

Differential Expression Transcriptome Analysis

RNA-Seq –Library Preparation with polyA selection, HiSeq Sequencing, and Data Analysis RNA library preparations, sequencing reactions, and bioinformatics analysis were conducted at GENEWIZ, LLC. (South Plainfield, NJ, USA) as a fee-for-service. RNA samples received were quantified using Qubit 2.0 Fluorometer from Life Technologies (Carlsbad, CA) and RNA integrity was checked with 4200 TapeStation from Agilent Technologies (Palo Alto, CA).

RNA sequencing library preparation used the NEBNext Ultra RNA Library Prep Kit for Illumina followed by manufacturer's instructions. Briefly, mRNA were first enriched with Oligo-d(T) beads. Enriched mRNAs were fragmented for 15 minutes at 94 °C. First strand and second strand cDNA were subsequently synthesized. cDNA fragments were end repaired and adenylated at 3' ends, and universal adapters were ligated to cDNA fragments, followed by index addition and library enrichment by PCR with limited cycles.

The sequencing library was validated on the Agilent TapeStation, and quantified by using Qubit 2.0 Fluorometer as well as by quantitative PCR using KAPA Biosystems technology (Wilmington, MA). The sequencing libraries were clustered on a single lane of a flowcell. After clustering, the flowcell was loaded on the Illumina HiSeq instrument according to manufacturer's instructions. The samples were sequenced using a 2x150 Paired End (PE) configuration. Image analysis and base calling were conducted by the HiSeq Control Software (HCS). Raw sequence data (.bcl files) generated from Illumina HiSeq was converted into fastq files and de-multiplexed using Illumina's bcl2fastq 2.17 software. One mis-match was allowed for index sequence identification.

After investigating the quality of the raw data, sequence reads were trimmed to remove possible adapter sequences and nucleotides with poor quality using Trimmomatic v.0.36. The trimmed reads were mapped to the *Arabidopsis thaliana* TAIR10 reference genome available on ENSEMBL using the STAR aligner v.2.5.2b. The STAR aligner uses a splice aligner that detects splice junctions and incorporates them to help align the entire read sequences. BAM files were generated as a result of this step. Unique gene hit counts were calculated by using feature Counts from the Subread package v.1.5.2. Only unique reads that fell within exon regions were counted.

After extraction of gene hit counts, the gene hit counts table was used for downstream differential expression analysis. Using DESeq2, a comparison of gene expression between the groups of samples was performed. The Wald test was used to generate p-values and Log2 fold changes. Genes with adjusted p-values < 0.05 and absolute log2 fold changes > 1 were called as differentially expressed genes for each comparison. A PCA analysis was performed using the "plotPCA" function within the DESeq2 R package. The plot shows the samples in a 2D plane spanned by their first two principal components. The top 500 genes, selected by highest row variance, were used to generate the plot. To estimate the expression levels of alternatively spliced transcripts, the splice variant hit counts were extracted from the RNA-seq reads mapped to the genome. Differentially spliced genes were identified for groups with more than one sample by testing for significant differences in read counts on exons (and junctions) of the genes using DEXSeq. For groups with only one sample, the exon hit count tables were provided. The results of the splice variant expression analysis are included as a .html file.

Glycerolipid Lipidomics Analysis of lpa66 RNA Editing Mutant

Approximately 25mg dry mass of *Arabidopsis* leaves were harvested and immediately immersed in 3 ml 75ºC-preheated isopropanol with 0.01% butylated hydroxytoluene (BHT) from Millipore Sigma (Waltham, MA) for 15 min, to eliminate the activity of phospholipase D. 50 ml (25 x 150 mm) glass tubes with a Teflon-lined screw cap were used to prevent leaching from tubes. 1.5 ml chloroform and 0.6 ml water were added to isopropanol extract, vortexed, then agitated at room temperature for 1 hour. With a Pasteur pipette, lipid extracts were transferred to fresh glass tubes with Teflon-lined screw-caps. 4 ml of chloroform/methanol (2:1) with 0.01% BHT were added to each sample and shaken for 30 min on a rotary shaker at room temperature. This extraction was repeated four times for every sample, at which point the leaves were devoid of chlorophyll. One ml 1 M KCl was added to the combined extract, vortexed, centrifuged, and the upper phase was discarded. Two ml of water was added to combined extract, vortexed, centrifuged, and again the upper phase was discarded. Combined extract was evaporated under a stream of nitrogen and stored at -80^{o}C until analysis. Extracted leaves were dried at 105°C in an oven overnight and weighed with a microscale from Mettler-Toledo (Melbourne, Australia).

Total lipid extracts were analyzed by tandem mass spectrometry (MSMS) which include an API 4000 and a Q-TRAP by Applied Biosystems (Waltham, MA). Samples were introduced into the MSMS by electrospray ionization. Samples are not pre-separated. Instead, two types of scans were used to obtain polar lipid profiles: precursor and neutral loss. Samples are continuously introduced by continuous infusion in solvent into the ESI source, where lipid molecular ions are produced from the lipid molecules. PC, lysoPC, PS, PE and lysoPE are analyzed as singly-charged positive $[M+H]^+$ ions, MGDG, DGDG, PG, PI, PA and PS are analyzed as singly-charged $[M+NH4]^+$ ions, and lysoPG as negative $[M-H]^-$ ions. Ions enter the MSMS in the gas phase. More details on the methods used can be found at **https://www.k-state.edu/lipid/analytical_laboratory/lipid_profiling/index.html**.

Chapter 3: A Conserved Glutamate Residue in the C-terminal Deaminase Domain of Pentatricopeptide Repeat Proteins is Required for RNA Editing Activity

Abstract

Many transcripts expressed from plant organelle genomes are modified by C-to-U RNA editing. Nuclear encoded Pentatricopeptide Repeat (PPR) proteins include an RNA binding domain that provides site specificity. In addition, many PPR proteins include a C-terminal DYW domain with characteristic zinc binding motifs (CXXC, HXE) and has recently been shown to bind zinc ions. The glutamate residue of the HXE motif is catalytically required in the reaction catalyzed by cytidine deaminase. In this work, we examine the activity of the DYW domain through truncation or mutagenesis of the HXE motif. OTP84 is required for editing three chloroplast sites, and transgenes expressing OTP84 with C-terminal truncations were capable of editing only one of the three cognate sites at high efficiency. These results suggest that the deaminase domain of OTP84 is required for editing two of the sites, but another deaminase is able to supply the deamination activity for the third site. *OTP84* and *CREF7* transgenes were mutagenized to replace the glutamate residue of the HXE motif, and transgenic plants expressing *OTP84-E824A* and *CREF7-E554A* were unable to efficiently edit the cognate editing sites for these genes. In addition, plants expressing *CREF7-E554A* exhibited substantially reduced capacity to edit a non-cognate site, *rpoA* C200. These results indicate that the DYW domains of PPR proteins are involved in editing their cognate editing sites, and in some cases may participate in editing additional sites in the chloroplast.

Introduction

RNA editing takes place in most land plant chloroplasts and mitochondria [6,81]. In flowering plants, the transcripts of chloroplasts and mitochondria are modified post-transcriptionally by C-to-U editing with about 35 C-to-U editing events in chloroplasts, and hundreds of editing sites in the mitochondria [4]. Editing in higher plants and in Physcomitrella patens is known to require nuclear proteins [38,39,82–84].

Pentatricopeptide Repeat (PPR) genes have been shown to be required for RNA editing [2], and form a large family of protein-coding genes in higher plants with over 400 members in *Arabidopsis* [14]. The known editing factors are members of the PLS subfamily of PPR proteins, which are composed of characteristic P, L (long), and S (short) repeats [85]. Amino acid residues located in specific locations within the repeats have been shown to specify the base recognized in the cis-element [8–10], and the PLS repeat domain interacts with specific nucleotides within the cis-element to provide site specificity for RNA editing [8,16].

The PLS subfamily of PPR proteins also includes characteristic C-terminal domains known as the E, E+ and DYW domains [14]. Bioinformatics analysis identified characteristic structural motifs present in part of the E, the entire E+, and most of the DYW domains that place the protein in the deaminase superfamily [20]. This region has been identified as the “DYW family of nucleic acid deaminases” (PFam 14432) [86], and is referred to as the “DYW domain” in this work. There is mounting evidence that supports the role of the DYW domain as the catalytic component of the editing reaction. This region has canonical zinc binding motifs (HXE, CXXC) [21,22,87], which are conserved in deaminases that act on nucleotides, RNA, and DNA [20,88–93]. The DYW domain has recently been shown to bind zinc ions [21,22]. In addition, mutagenesis of the zinc binding motifs has been shown to interfere with editing in transgenic plants [22] and through transient expression in protoplasts [24]. The glutamate residue of the HXE motif has been shown to be directly involved in the *E. coli* cytidine deaminase mechanism through deprotonation of the substrate water molecule and transfer of the proton to the product ammonia [88]. Thus, the requirement of this conserved glutamate residue is a key characteristic expected for an editing deaminase.

The editing of the ndhD C2 site in *Arabidopsis* chloroplasts requires two PPR proteins, *CRR4* and *DYW1* [37]. *CRR4* lacks the entire DYW domain but has a canonical PLS repeat region and is apparently required for editing as a site specificity factor [73]. DYW1 has an intact DYW domain; however, the N-terminal PLS-like region is small and composed of degenerate repeats. Furthermore, DYW1 has canonical zinc binding motifs, and has been shown to bind zinc ions [21,22] . Mutagenesis of the zinc binding motifs and the catalytic glutamate residue of DYW1 ablated that ability to edit the ndhD site [22]. Thus, the editing of the ndhD site requires both CRR4 and DYW1, and the functions of site recognition and deamination appear to be separated into two proteins in this case.

Many PPR proteins that are required for editing lack a DYW domain. In addition, there are several examples in which the DYW domain is present in a PPR, but may be eliminated by truncation and still support editing of the cognate sites [21,32,33]. Finally, PPR genes have been shown to undergo truncation in evolution [21], indicating that the DYW domain is dispensable in an evolutionary context. Thus, the role of the DYW domain in these editing reactions has remained elusive.

In this work, we have investigated the role of the DYW domain of two PPR proteins, OTP84 and CREF7. In contrast to DYW1 and CRR4, both of these PPR proteins have canonical PLS repeat regions and an intact DYW domain. In this work, we examine the function of the DYW domain by gene truncation and mutagenesis of the catalytic glutamate residue and show that the DYW domain is required for editing the cognate editing sites.

Results

Plants Expressing Truncated OTP84 Edit One of Three Cognate Sites

Previous studies have examined the role of the DYW domain by expression of truncated variants, and in several examples, these experiments have demonstrated that the DYW domain was not required for editing of the cognate sites [21,32,94,95]. Since OTP84 has three editing site targets, the role of the DYW domain was examined on these editing sites.

The *OTP84* gene has an intact DYW domain (**Figure 3.1**) and is required for editing of *ndhF* C290, *psbZ* C50, and *ndhB* C1481 [96]. Two truncated variants of *OTP84* were each prepared and tested for editing activity in three independent transgenic plants (**Figure 3.1**). Truncation immediately C-terminal to the PG box eliminated most of the DYW domain (*OTP84trcDYW*) and truncation immediately N-terminal of the PG box eliminated all of the PG box and downstream DYW domain (*OTP84trcPG*). The truncated variants were introduced into an *OPT84* knockout background (*otp84*) [96]. The effects of *OTP84* truncation are shown in **Figure 3.2**. Expression of the *OTP84trcDYW* transgene did not restore editing of *ndhF* and *psbZ* transcripts to wild type levels (**Figure 3.2 A** and

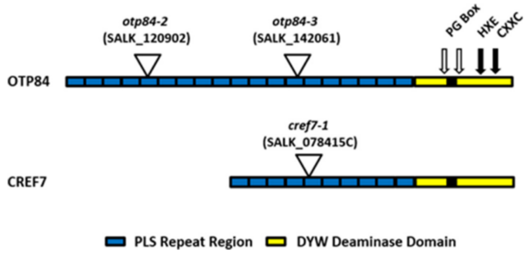


FIGURE 3.1 PPR domain architecture for OTP84 and CREF7. Repeats in the PLS region are indicated by *rectangles*. Features in the DYW deaminase domain include the PG box, which is indicated as the *solid black rectangle*, and the *open arrows* indicate the position of truncations in OTP84. The positions of the zinc binding and catalytic glutamate residues (HXE, CXXC) are indicated with *solid arrows*. The location of T-DNA insertions is shown at the point of the *triangle*.

3.2 B, respectively), suggesting that the DYW domain is required for editing these two cognate editing sites. In contrast, the editing of *ndhB* C1481 remained at wild type levels in transgenic plants expressing *OTP84trcDYW* (**Figure 3.1 C**), which suggests that editing of the *ndhB* site does not require the *OTP84* DYW domain. Truncations that eliminate the PG box (*OTP84trcPG*) resulted in highly reduced editing for all three sites. This result is consistent with earlier studies performed with *ELI1* that indicated that the PG box is critical for editing a site in *ndhB* transcripts [21]. Although OTP84 is required for editing three sites, transgenes lacking a large portion of the DYW domain were capable of restoring editing to wild type levels in *ndhB* transcripts, suggesting the participation of an unknown DYW deaminase(s) for that site.

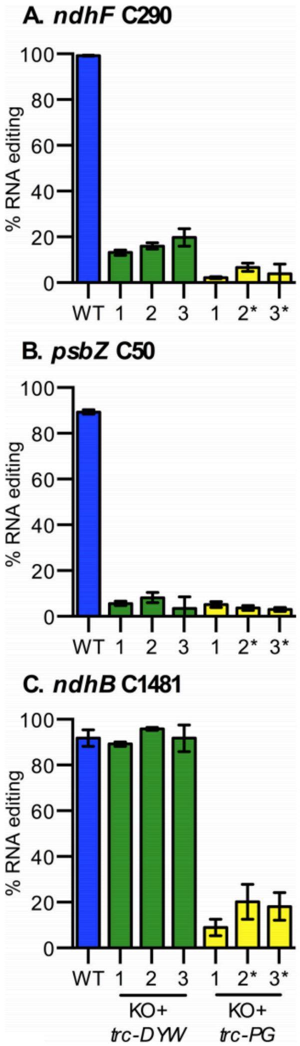


FIGURE 3.2 truncation shows differential effects on the editing of three cognate sites. *A–C* show the response of editing *ndhF* C290, *psbZ* C50, and *ndhB* C1481, respectively. Truncation of the DYW domain (*OTP84trcDYW*) resulted in a large decrease in editing of the *ndhF* and *psbZ* sites, but the *ndhB*

Mutagenesis of the HXE Motif of OTP84 Decreases Editing of the Three Cognate Sites

The HXE motif of OTP84 was mutagenized to HXA to produce *OTP84-E824A*, which was introduced into *otp84-3* and into the wild type Col-0 background. The conversion of the *ndhF*, *psbZ*, and *ndhB* editing sites is represented in **Figure 3.3**. Each editing site was converted at 90% or greater in the wild type plants and remained unedited in *otp84-3*. Complementation of *otp84-3* with a wild type transgene restored editing to ~90% or greater. In contrast, the *OTP84-E824A* transgene was unable to restore editing of the three editing sites to wild type levels

(**Figure 3.3**). Plants expressing *OTP84-E824A* did not edit the *ndhF* and *psbZ* sites. In contrast, 23% of transcripts were edited at *ndhB* C1481 in plants expressing *OTP84-E824A*. Since the *OTP84-E824A* transgene was unable to restore editing to the cognate sites, the mutant transgene might act in a dominant negative manner to suppress editing in wild type plants by formation of inactive editing complexes. Therefore, we tested whether expression of the *OTP84-E824A* transgene could disrupt editing in wild type plants. In three independent transgenic lines, the mutant transgene did not reduce editing levels in the wild type background and therefore did not act in a dominant negative manner over the native gene (**Figure 3.3**).

Mutagenesis of the HXE Motif of CREF7 Decreases Editing of the Cognate Site

The *CREF7* gene has an intact DYW domain (**Figure 3.1**) and a single cognate editing site, *ndhB* C1255 [97]. Transgenes for wild type *CREF7* and a mutant variant with the HXE motif changed to HXA (*CREF7-E554A*) were introduced into a *CREF7* knockout line (*cref7-1*); in addition, the *CREF7-E554A* transgene was introduced into wild type plants. Transgenic plants were analyzed for editing of the cognate site (**Figure 3.4**). The *ndhB* C1255 site was 100% edited in wild type plants, but remained unedited in *cref7-1* plants. Editing of *ndhB* C1255 in *cref7-1* plants expressing the *CREF7-E554A* transgene was approximately 10% based on Sanger sequencing. In contrast, plants with wild type background expressing *CREF7-E554A* edited *ndhB* transcripts at wild type levels, and the transgene did not behave in a dominant negative manner. These results demonstrate that the E554 plays a crucial role in the activity of CREF7 in editing *ndhB* transcripts.

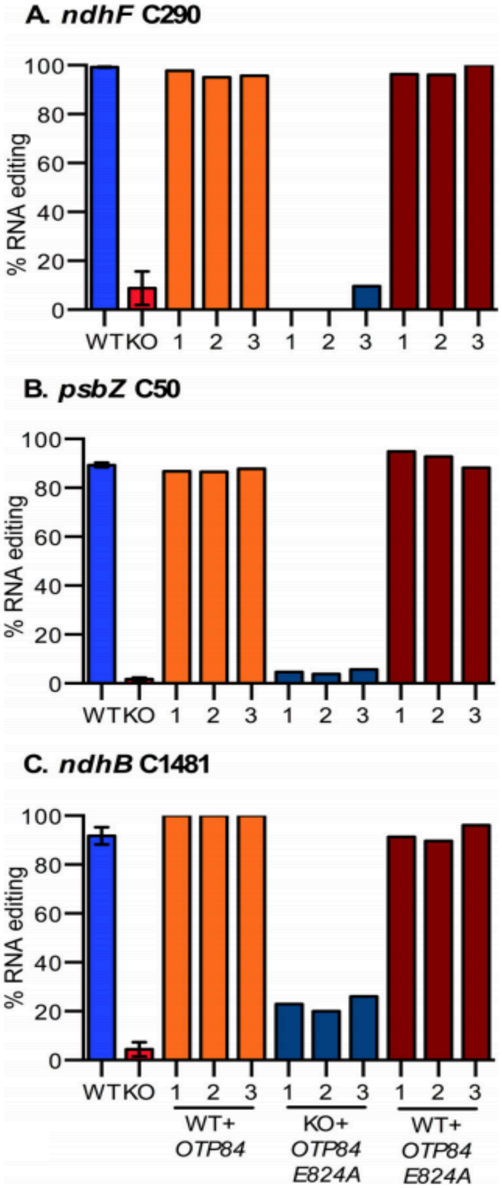


FIGURE 3.3 **OTP84-E824A does not restore editing to wild type levels in *OTP84* knock-out plants.** *A–C* show the response of editing *ndhF* C290, *psbZ* C50, and *ndhB* C1481, respectively. Wild type *OTP84* complemented the knock-out phenotype in the *OTP84* knock-out line; however, *OTP84-E824A* did not increase editing of the *ndhF* or *psbZ* editing sites. Editing of the *ndhB* editing site was significantly greater (23%) over the level observed in the knock-out line (5%). A single leaf sample was analyzed from three independent wild type (*WT*) and *otp84-3* knock-out (*KO*) plants. A single leaf sample was analyzed from each of three independent integration events for these backgrounds and transgenes: wild type plants with *OTP84* transgene (WT + *OTP84*); *otp84-3* with *OTP84E824A* (KO + *OTP84 E824A*); and wild type expressing *OTP84E824A* (WT + *OTP84 E824A*). *Error bars* show the S.D. of the three leaf samples from three independent plants in the case of WT and KO.

Expression of CREF7-E554A Reduces Editing of rpoA C200, a Non-Cognate Site

Editing site conversion was determined for the 34 major chloroplast editing sites in plants expressing *OPT84-E824A* and *CREF7-E554A* in their respective gene knockout backgrounds (data not shown). In several instances, small changes in editing site conversion were detected at non-cognate editing sites.

The strongest effect of the mutant transgene was observed on *rpoA* C200 editing in plants expressing *CREF7-E554A* (**Figure 3.5**). The *rpoA* editing site is about 70% converted in wild type Col-0 plants, the *cref7-1* plants, and in *cref7-1* plants complemented with the wild type *CREF7* gene. The *CREF7-E554A* transgene had no detectable effect when expressed in wild type plants; however, in *cref7-1* plants, the E554A substitution caused a 25% reduction of *rpoA* editing to about 45%. Thus, expression of *CREF7-E554A* caused a significant reduction of *rpoA* editing, suggesting that CREF7 may participate in editing *rpoA* transcripts.

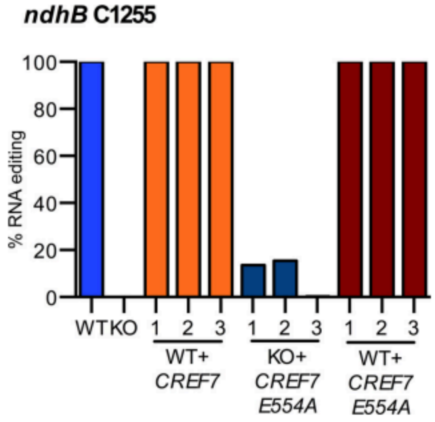


FIGURE 3.4 **CREF7-E554A does not restore editing in *CREF7* knock-out plants.** Wild type *CREF7* complemented the knock-out phenotype when expressed in the *CREF7* knock-out line; however, *CREF7-E554A* only increased editing of *ndhB* C1255 to about 10%. A single leaf sample was analyzed from three independent wild type (*WT*) and *cref7-1* knock-out (*KO*) plants. A single leaf sample was analyzed from each of three independent integration events for these backgrounds and transgenes: wild type plants with *CREF7* transgene (WT + *CREF7*); *cref7* with *CREF7-E554A* (KO + *CREF7-E554A*); and wild type expressing *CREF7-E554A* (WT + *CREF7-E554A*).

The HXA Mutation of the DYW Deaminase Domain Maintains Zinc Binding

Mutagenesis may cause a protein to lose function because of improper folding, or through a direct effect on catalysis. Previous investigations of the structure and function of *E. coli* cytidine deaminase used circular dichroism and zinc stoichiometry to demonstrate that the polypeptide with the E-to-A substitution retained native structure [98]. The ELI1 DYW domain was selected for zinc analysis to determine whether the DYW deaminase domain was able to fold into a native structure. An E-to-A mutation was introduced at position 566 in the ELI1 DYW domain [21]. The recombinant protein was expressed in *E. coli*, purified, and analyzed by mass spectrometry as previously described [21]. The purified recombinant ELI1-E566A protein had a native mass of 19,519 amu, and the denatured protein had a mass of 19,395 amu. The mass difference of 124 amu is consistent with the native DYW domain binding two zinc molecules of 65.4 amu and the loss of several protons from the cysteine ligands that are predicted to coordinate the zinc atoms [21]. This result demonstrates that the ELI1-E566A mutant DYW domain binds two zinc ions, and retains native structure.

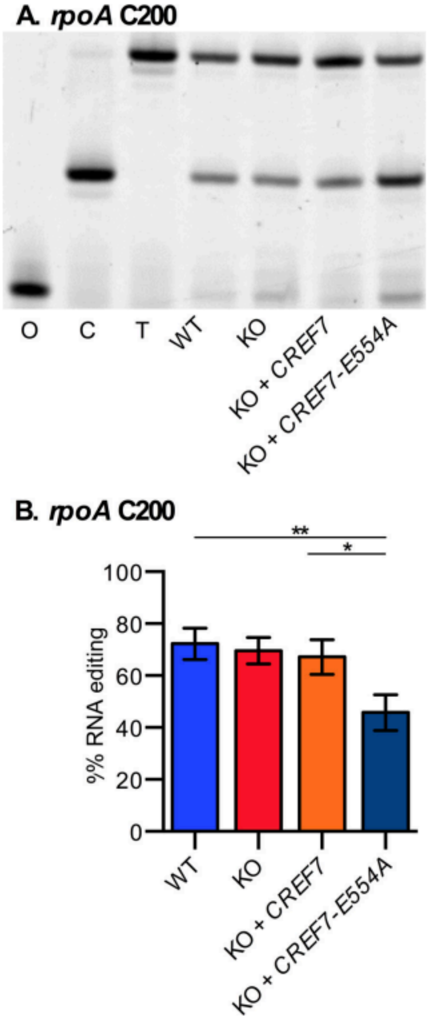


FIGURE 3.5 The *CREF7-E554A* mutation decreases editing of *rpoA*, a non-cognate editing site. *A*, poisoned primer extension assay was used to determine *rpoA* editing site conversion. Control lanes show oligonucleotide (*O*), unedited template (*C*), and edited template (*T*). *B*, editing of *rpoA* was about 70% in wild type and knock-out plants. Expression of *CREF7-E554A* in the CREF7 knock-out line resulted in a decrease in *rpoA* editing to about 45%. Three leaf samples were analyzed from wild type plants (*WT*) and *cref7-1* knock-out (*KO*) plants. A single leaf sample was analyzed from each of three independent integration events for these backgrounds and transgenes: wild type plants with *CREF7* transgene (WT + *CREF7*); and *cref7* with *CREF7-E554A* (KO + *CREF7-E554A*). For statistical analysis, the Student's *t* test was performed with significance indicated as * and ** for >0.05 and >0.005 at the 0.05 level, respectively. *Error bars* show the S.D. of the three leaf samples from three independent plants.

Discussion

The enzyme responsible for RNA editing in plants has been controversial. Early biochemical analyses indicated that the enzymatic reaction was probably a deamination reaction [99,100], and *in vitro* editing assays established that the reaction occurred through a cytidine deamination mechanism [101–103]. After discovery of the role of PPR proteins in RNA processing reactions in plant organelles [14], deaminase-like zinc binding motifs were recognized in the DYW domain [87]. More recently, the DYW domain was shown to bind zinc as a prosthetic group [21,22], further supporting the hypothesis that the DYW deaminase functions as the deaminase in plant editing. Mutagenesis of amino acid residues in the zinc binding motifs and of the catalytic glutamate (HXE, CXXC) of DYW1 resulted in the loss of the ability to edit *ndhD* C2 in transgenic plants [22]. Thus, the DYW domain possesses several features that would be expected for an editing deaminase.

In this work, we explored the role of the glutamate residue of the HXE motif in full-length PPR proteins that have a canonical PLS repeat region and an intact DYW domain. Mutation of the putative catalytic glutamate residue caused a dramatic decrease in the editing of the cognate sites for OTP84 and CREF7. The requirement of the glutamate residue of the HXE domain and zinc binding by the DYW domain are two key features that are expected for an editing deaminase. They strongly support the hypothesis that the DYW domain provides the catalytic activity for the editing reaction.

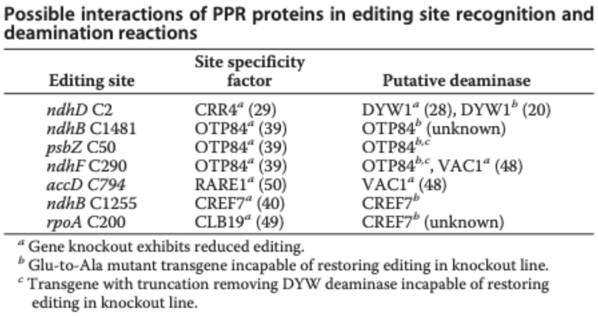
There are several examples in which the DYW deaminase is dispensable for complementation of a knockout mutant phenotype [21,32,33,104]. The truncation of *OTP84* had markedly different effects on the three editing site targets. The *OTP84trcDYW* transgene restored editing of *ndhB* C1481 to wild type levels, and this site responded similarly to previously characterized editing sites for ELI1, CRR22, CRR28, OTP82, and MEF11[21,32,33,104]. Editing of the *psbZ* and *ndhF* sites was highly reduced in the presence of the *OTP84trcDYW* transgene, although the *ndhF* site may have been somewhat higher than gene knockout levels. The *ndhF* C290 editing site is also affected by disruption of the PPR gene, VAC1, which results in a partial loss of editing of the *ndhF* site [105]. The DYW domain of VAC1 might participate with *OTP84trcDYW* to incompletely edit the *ndhF* C290 site. These results suggest that a set of editing sites can share a single specificity factor, but might rely on different deaminases *in trans* to complete the editing reaction.

Editing was highly reduced at the three cognate sites of OTP84 in plants expressing the *OTP84-E824A* transgene. The editing of the *psbZ* and *ndhF* sites was near gene knockout levels, and the OTP84-E554A protein may form non-functional editing complexes for these sites. The editing of the *ndhB* C1481 site responded somewhat differently, and editing of the *ndhB* site increased well above knockout levels to about 23%. The *ndhB* site also responded differently from the other two cognate sites in plants expressing *OTP84trcDYW*, and the increase in *ndhB* editing might result from the participation of other deaminases in the editing of this site.

Expression of *CREF7-E554A* substantially decreased editing of *rpoA* C200, a cognate editing site for CLB19 [106]. Since CLB19 is truncated at the end of the E domain and lacks an intact DYW domain [106], it could recruit a deaminase domain from another PPR protein. The reduction in editing of a non-cognate site suggests that CREF7 may participate as a deaminase in *rpoA* C200 editing. Since editing of *rpoA* C200 is not reduced in the CREF7 knockout line (**Figure 3.5**), there may be other DYW deaminases that participate in *rpoA* editing.

Nineteen PPR proteins have been shown to be required for editing in *Arabidopsis* chloroplasts. Four of these PPRs (CLB19, CRR4, CRR21, and OTP80) have truncated DYW domains [94,96,106], and could not function in cytidine deamination. A complex network of PPR proteins could be involved in RNA editing. The PLS repeat domain may be sufficient for specifying an editing site; however, one or more deaminases could be recruited *in trans* as enzymatic components. **Table 3.1** summarizes the relationships between several chloroplast editing sites, site specificity factors, and possible PPR proteins involved in the deamination reaction. PPR proteins that lack complete DYW domains may acquire the activity from other proteins as in the case of CRR4 and DYW1. Based on these results, OTP84 acts as a site specificity factor for three cognate sites and participates as a deaminase along with other PPR proteins in the editing of these sites. CREF7 appears to function as both a specificity factor and deaminase in the editing of its cognate site, but also contributes to rpoA editing with the CLB19 as a specificity factor. VAC1 is a PPR protein with a DYW domain, and the gene knockout results in a strong lethal phenotype and partial editing of *ndhF* C290 (a cognate site of OTP84) and accD C794 (a cognate site of RARE1) [105]. Since the VAC1 knockout exhibits partial editing, VAC1 is not essential for each site. If other PPR proteins participate in these editing reactions, these proteins have partial redundancy. The partial reduction in editing of *rpoA* C200 by the *CREF7-E554A* mutant suggests that CREF7 is partially redundant with other deaminases in rpoA editing. Expression of catalytically deficient PPR transgenes by mutation of the HXE motif has

TABLE 3.1



Possible interactions of PPR proteins in editing site recognition and deamination reactions

Editing site	Site specificity factor	Putative deaminase
ndhD C2	CRR4[a] (29)	DYW1[a] (28), DYW1[b] (20)
ndhB C1481	OTP84[a] (39)	OTP84[b] (unknown)
psbZ C50	OTP84[a] (39)	OTP84[b,c]
ndhF C290	OTP84[a] (39)	OTP84[b,c], VAC1[a] (48)
accD C794	RARE1[a] (50)	VAC1[a] (48)
ndhB C1255	CREF7[a] (40)	CREF7[b]
rpoA C200	CLB19[a] (49)	CREF7[b] (unknown)

[a] Gene knockout exhibits reduced editing.
[b] Glu-to-Ala mutant transgene incapable of restoring editing in knockout line.
[c] Transgene with truncation removing DYW deaminase incapable of restoring editing in knockout line.

proven to be a powerful way to distinguish the DYW deaminase function for a PPR protein from the site specificity role. Our results provide direct support for the model that PPR proteins have dual and separable functions as site specificity factors and as deaminases [10,21,104].

Statement of contribution

This chapter is already published. I helped generate plant materials for this study along with co-authors MH and KD as well as performing RNA editing analysis, specifically for figure 3, 4, and 5. I helped write the manuscript with MM and MH.

Reference*: Hayes ML, Dang K, Diaz M, Mulligan RM. A Conserved Glutamate Residue in the C-terminal Deaminase Domain of Pentatricopeptide Repeat Proteins Is Required for RNA Editing Activity. 2015. Journal of Biological Chemistry* 290(16): 10136-10142.

Chapter 4. A Protein With an Unusually Short PPR Domain, MEF8, Affects Editing at Over 60 Arabidopsis Mitochondria C Targets of RNA Editing

Abstract

An RNA-seq approach was used to investigate the role of a PLS-subfamily pentatricopeptide repeat protein, Mitochondrial Editing Factor 8 (MEF8), on editing in *Arabidopsis* mitochondria and plastids. MEF8 has an intact DYW domain, but possesses an unusually short PLS repeat region of only five repeats. The MEF8 null allele (*mef8*) line exhibited reduced editing at 38 mitochondrial editing sites and increased editing at 24 sites; therefore, the absence of MEF8 affects 11% of the mitochondrial editome. Notably, 60% of the matR transcripts' sites showed a decrease of editing extent in the mef8 mutant. An E549A substitution in the MEF8 protein replaced the putatively catalytic glutamate of the HXE motif in the DYW domain. Complementation with *MEF8-E549A* failed to restore editing at the main target sites but was able to restore editing at the *matR* transcript; it also decreased the editing extent of most of the C targets exhibiting an increase of editing extent in the *mef8* mutant plant. Thus, MEF8 has two antagonistic effects on mitochondrial editing: stimulatory, which requires a catalytic glutamate for most of the targets except for the *matR* transcript, and inhibitory, for which glutamate is dispensable.

Introduction

RNA editing in plant organelles causes post-transcriptional C-to-U changes in transcripts [2]. In flowering plants, chloroplast transcriptomes have approximately 35 C-to-U editing sites [3], and over 600 Cs are edited in *Arabidopsis* mitochondria [4,5]. In general, editing results in non-synonymous amino acid substitutions that convert aberrant codons to the evolutionarily conserved sequences [6]. The primary role of RNA editing in higher plant organelles appears to be a genetic correction mechanism required for the functional expression of the organelle genomes[7]. Multiple proteins are required for RNA editing in higher plants. Among them are members of the pentatricopeptide repeat (PPR) protein family [7], the RNA Editing Interacting Protein/Multiple Organellar RNA Editing Factor (RIP/MORF) family [5,38,39], the Organelle RNA Recognition Motif containing protein (ORRM) family [40], and the Organelle Zinc finger editing factor (OZ) family [43].

Pentatricopeptide repeat proteins are typically composed of about 10 to 20 tandem repeats of a 35 amino acid motif known as the P repeat. Through computational and biochemical analysis, a PPR code has been developed that predicts modular RNA sequence recognition by conserved residues in each repeat [8–10]. Furthermore, structural analyses have demonstrated that PPR proteins form superhelical structures with residues that bind RNA on the inner surface of the helix [11–13]. These structural analyses confirmed the general features of the PPR–RNA complex predicted by the PPR code, including modular binding and the detailed participation of polar amino acid side chains at residues 5 and 35 of each P motif in nucleotide recognition.

Pentatricopeptide repeat proteins have well-defined roles in RNA processing, including but not limited to, RNA editing. Specifically, members of PLS subfamily are the best characterized RNA editing factors. The N-terminal repeat region of these proteins contain the characteristic 35 amino acid P repeat as well as long (L) and short (S) variants [14]. The PPR code has been extended to this PLS subfamily [9,10], predicting recognition of RNA sequences that is similar to the code developed for the P subfamily [15]. The PLS subfamily of PPR proteins also includes characteristic C-terminal domains known as the E and DYW domains [14,17]. While the E domain contains two degenerate PPR repeats [17] whose function remains unclear, it does not appear to contribute to RNA binding [16]. The E domain is, however, involved in PPR-RIP/MORF interactions and therefore the formation of high molecular weight RNA editing complexes [18,19]. The DYW domain has key features of editing deaminases. These features include canonical zinc binding motifs (HXE, CXXC), the presence of a zinc prosthetic group, and a conserved catalytic glutamate residue of the HXE motif [20]. The conserved glutamate residue is catalytically involved in the deamination mechanism of bacterial cytidine deaminase. Requirement of this conserved glutamate residue is a key characteristic expected for an editing deaminase [21–24].

The function of the DYW domain in the editing reaction remains controversial because several observations defy a simple role for the DYW domain as the editing deaminase. First, in *Arabidopsis*, there is considerable diversity in the protein architecture of the PLS subfamily—intact DYW domains are present in about 40% of these proteins, while the remaining members have a C-terminus that includes the E domain but completely lack the deaminase-like features of the DYW domain [17]. Second, of the 20 PPR proteins characterized as chloroplast editing factors, 6 (30%) are E type and lack the DYW domain, while the remaining 14 include a DYW domain. Third, several investigators have reported on truncated PPR genes that maintain the PG box [21,94], eliminate the deaminase features of DYW domain, and ultimately lead to genes that are fully functional in editing in a null background. Fourth, the DYW domain is unstable in evolution. Truncation of the DYW domain occurred in a chloroplast PPR gene, OTP82, in the lineage to the *Brassicaceae* [107]. In addition, MEF3 experienced a similar truncation of the DYW domain [108]. Thus, the DYW domain is dispensable based on experimental and evolutionary observations, and the remainder of the PPR gene is sufficient to supply gene function for RNA editing.

Our labs and others have posited a resolution of these observations. We propose the recruitment of a deaminase that acts *in trans* to supply the deamination activity in an editing complex [23,104,109]. In this model, the N-terminal PLS repeat domain functions in RNA binding and sequence recognition to provide editing site specificity. The catalytic activity could be provided by the C-terminal DYW domain *in cis* by the same protein, or *in trans* by another protein recruited to an editing complex [7]. This model assumes PPR proteins could participate with distinct and potentially separable functions of site specificity and deamination, which was partially demonstrated in the editing of *ndhD* C2 by CRR4 and DYW1 [37] in *Arabidopsis* chloroplasts. CRR4, an E-type PLS PPR lacking a C-terminal DYW domain, acts as an editing site recognition factor, while DYW1, a DYW domain PPR with a degenerate PLS repeat domain, has key features of an editing deaminase [22,37].

In this work, we have performed a detailed analysis of the role of MEF8 in mitochondrial editing in *Arabidopsis*. MEF8 was selected for this analysis because it has an unusually small PLS repeat domain composed of five repeats, and the domain may be too small to effectively act in editing site recognition. MEF8 was previously shown to affect editing of two mitochondrial editing sites in *Arabidopsis* [110]. In this report, we utilize strand- and transcript-specific PCR-seq (STS PCR-seq) [5], to comprehensively analyze editing in the *Arabidopsis* mitochondrial and chloroplast transcriptomes and show that *mef8* T-DNA insertional mutant plants (hereafter, *mef8* mutant) exhibit decreased editing at 38 mitochondrial editing sites, including the two previously discovered sites, and increased editing at 24 mitochondrial sites. In the overwhelming majority of cases, the MEF8 mutant phenotype is characterized by a partial loss in editing; in contrast, T-DNA insertion into most PPR genes required for RNA editing in plastids or in mitochondria results in a complete loss of editing activity at a small number of sites. Mutagenesis of the glutamate residue in the conserved HXE motif, which is proposed to be catalytically required for deamination activity, recapitulates the partial losses in editing activity observed in mef8 mutant plants except for the defective sites on the matR transcript. The glutamate residue in the HXE motif is dispensable for the inhibitory effect of MEF8 on mitochondrial editing—the majority of sites showing an increase in the mef8 mutant plant experience a decrease of editing extent in the transgenic lines transformed with the mutated MEF8 (HXA). Thus, MEF8 participates in the editing of approximately 11% of the mitochondrial editing sites. Based on the requirement for glutamate in the HXE motif and the direction of the effect on editing extent, MEF8 appears to participate in three different ways in mitochondrial editing: stimulatory on its main targets and glutamate-dependent, stimulatory and glutamate-independent on the matR transcript, and inhibitory and glutamate-independent.

Results

MEF8 Mutation Causes Both Mitochondrial Decrease and Increase of Editing Extent

We used a next-generation sequencing based methodology named STS-PCRseq to survey the editome in the *mef8* mutant and the wild-type plants [5]. Two biological replicates were assayed per genotype. The statistical test to declare the presence of an editing site has been outlined previously [5,41] and resulted in the identification of 612 editing sites, among which 576 are mitochondrial and 36 are plastid (**Table S-4.1**). The insertion of the T-DNA in the mef8 mutant is located upstream of the PPRs and results in a null allele, as no detectable level of MEF8 expression was observed by qRT-PCR in the *mef8* mutant (**Figure S-4.1**).

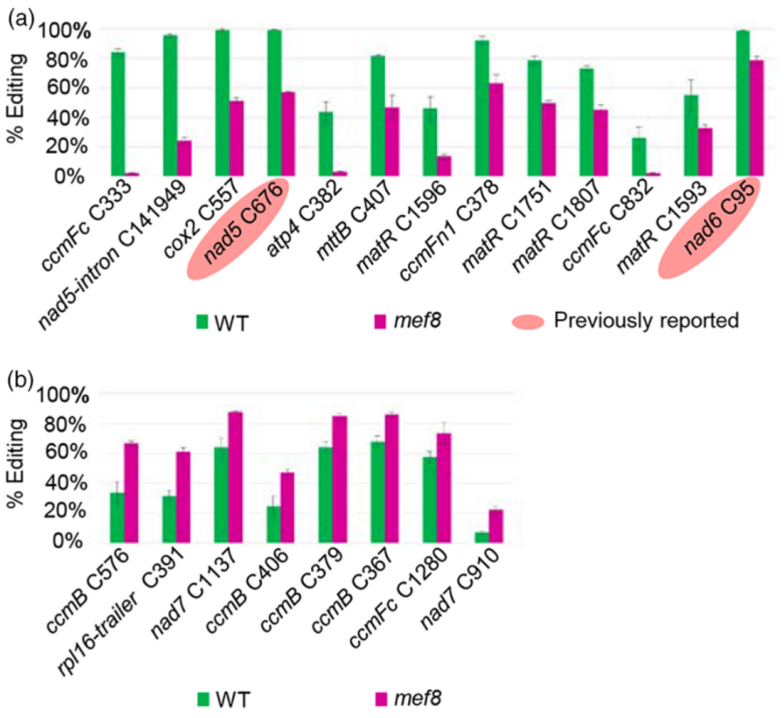


FIGURE 4.1 *mef8* mutation causes mitochondrial editing changes.
(a) Editing sites exhibited a significant decrease of editing extent in the *mef8* mutant. The difference in editing extent of the 13 sites shown is ≥20% between the wild-type and the mutant.
(b) Editing sites exhibited a significant increase of editing extent in the *mef8* mutant. The difference of editing extent of the eight sites shown is ≥15% between the wild-type and the mutant. Values represent mean ± standard deviation (SD). Both sites in (a) and (b) are presented according to the difference between the wild-type (WT) and *mef8* from the highest to the lowest.

Thirty-eight mitochondrial sites, or 7% of all the mitochondrial sites surveyed, exhibited a significant reduction of editing extent in the mef8 mutant plant when compared to the wild-type plant (cf experimental procedures for an explanation of the statistical tests, **Figure 4.1 A**, **Table S-4.2**). Surprisingly, 24 sites, or 4% of all the mitochondrial surveyed, showed a significant increase of editing extent in the mef8 mutant plant (**Figure 4.1 B**, **Table S-4.3**). Combining both of these categories, 62 mitochondrial sites, or 11% of all the sites surveyed. experienced a significant variation of their editing extent in the mef8 mutant plant. Examination of the sites whose editing extent is decreased in the mef8 mutant plant reveals an enrichment in sites belonging to the matR transcript. Among the 13 sites showing the most pronounced decrease of editing extent in the mef8 mutant, 4 sites belong to the matR transcript (**Figure 4.1 A**). That observation prompted us to focus our attention on the effect of MEF8 mutation specifically on the editing extent of the sites found on the matR transcript. Seven of the 11 sites of the matR transcript have their editing extents significantly reduced in the mef8 mutant plant (**Figure 4.2 A**). The reduction of editing extent is not constant along the matR transcript, as it shows three peaks at position 1596, 1751, and 1807, and is not significant towards the extremities of the transcript (**Figure 4.2 B**).

To examine how MEF8 affects editing, we analyzed the distribution of the affected C targets on different transcripts by calculating the percentage of affected edited sites per transcript in the mef8 mutant plant. This distribution was reported according to which complex the affected transcript belongs (**Figure S-4.2 A**). Examination of **Figure S-4.2 A** shows that even though there is variation within a complex, the average of the percentage of affected sites/complex is quite similar to the overall average of ca. 10%. *MatR* stands out as the only noticeable outlier with around 60% of its sites affected in the *mef8* mutant. MEF8 mutation affects the editing extent of sites distributed on 23 transcripts (**Figure S-4.2 A**). We also divided the sites that show editing changes upon MEF8 mutation into two subgroups: the group that experiences reduced editing, and the group that exhibits increased editing in the mef8 mutant (**Figure S-4.2 B, S-4.2 C)**. The reduction of editing extent is rather evenly distributed and occurs on 19 transcripts, while an increase of editing is restricted to 9 transcripts (**Figure S-4.2 B, S-4.2 C)**. The majority of transcripts affected by the *mef8* T-DNA insertional mutation experienced either a reduction of editing extent of all their sites like *matR* or an increase of editing extent of all their sites like *ccmB*.

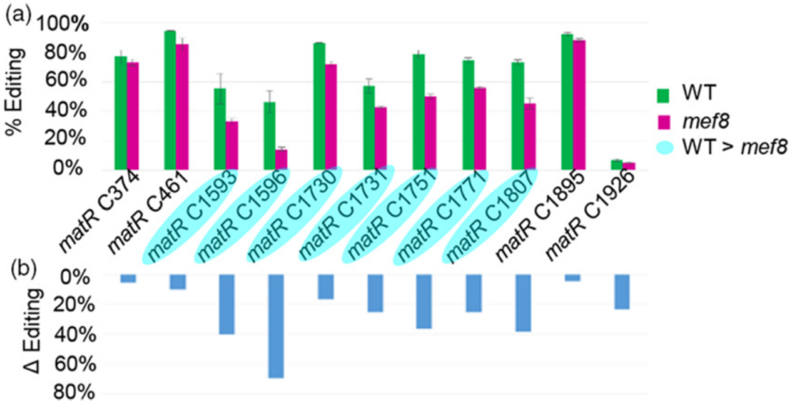


FIGURE 4.2 A T-DNA insertional mutation in *MEF8* decreases the editing extent of the majority of sites in the *matR* transcript.
(a) Editing extent of wild-type (WT) and *mef8* mutant in the *matR* transcript. Marked in a blue background are the sites showing a significant decrease in the *mef8* mutant.
(b) Variation in editing extent (Δ editing) along the *matR* transcript. Δ editing: (% editing of WT − % editing of *mef8*)/% editing of WT. Values represent mean ± standard deviation (SD).

Only 5 transcripts, *ccmFc*, *nad2*, *nad4*, *nad7*, and *rpl16* possess both sites experiencing either a reduction or an increase of editing extent in the mef8 mutant.

Although MEF8 is predicted to be targeted to the mitochondrion by both TargetP [111] and Predotar [112] and that most of the editing variation in the *mef8* mutant occur in the mitochondrial editome, we found 3 plastid sites with a significant change of editing extent in the *mef8* mutant plant (**Figure S-4.3**). It is likely that this effect is indirectly caused by altered mitochondrial function, as these sites tend to show significant variation in other mitochondrial mutants, *accD* C1568 and *ndhD* C2 in *orrm4* [41], rpoC1-488 in *rip3-2* [5].

A Mutated MEF8 is Able to Complement Only a Quarter of the Defective Editing Sites

We transformed the *mef8* mutant with a construct expressing a mutated version of the MEF8 protein under the control of a 35S promoter. The mutation replaced the putatively catalytic glutamate of the HXE motif found in the DYW domain by an alanine (HXE HXA), hence the transgenic plant will be referred as HXA in what follows. We analyzed two independent transgenic events. The level of expression of the transgene in the transformed mutants was around six times higher than the wild-type gene (**Figure S-4.1**). Among the 38 mitochondrial defective sites that show a reduction of editing extent in the mef8 mutant, only ten sites, or about a quarter, exhibit a significant increase of the editing extent in at least one HXA transgenic plant (**Table S-4.2**). The HXA mutation has no effect on the majority of the sites with reduced editing in the mef8 mutant, in particular *ccmFc* C333, the main target of MEF8 (**Figure 4.3**). The editing extent at *ccmFc* C333

FIGURE 4.3

remains at 3% (HXA) transgenic plants, the same value as in the *mef8* mutant (**Table S-4.2**, **Figure 4.3**). In contrast, all seven sites with reduced editing on the matR transcript are partially or fully complemented by the mutated MEF8 (HXA) (**Table S-4.2**, **Figure S-4.4**). Three sites, *nad5*-intron C141949, *cox2* C557, and *nad5* C676, show a significant reduction of their editing extent in the HXA transgenic plants when compared to the *mef8* mutant plant (**Table S-4.2**, **Figure 4.3**). As a positive control for the ability to complement the decreased editing in the *mef8* mutant, we transformed this mutant with the wild-type MEF8. In each case, the wildtype MEF8 gene partially or fully restored editing extent in the *mef8* mutant (**Figure 4.3**).

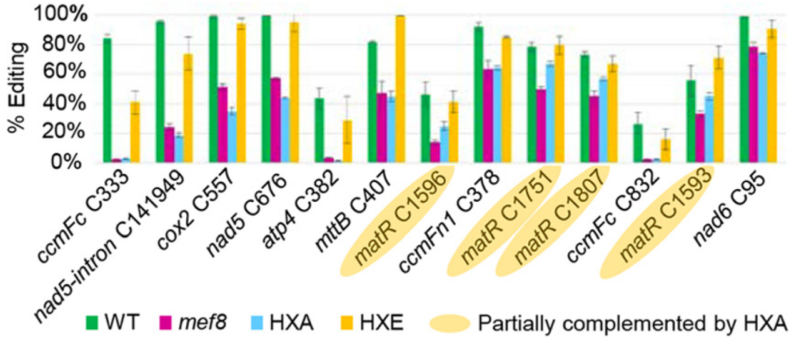


Figure 3. A mutated MEF8 (HXA) is unable to complement the majority of the defective editing sites in the *mef8* mutant.
Editing extents of the 13 sites exhibiting the most pronounced decrease of editing extent in the *mef8* mutant, are given for the wild-type (WT), the *mef8* mutant, the HXA transgenic plants and the HXE transgenic plants. HXA plants were obtained by transforming the *mef8* mutant with a mutated version of MEF8 in which the putatively catalytic glutamate of the HXE motif is replaced by HXA. HXE transgenic plants were obtained by transforming the *mef8* mutant with a wild-type version of MEF8. Values represent mean ± standard deviation (SD). Editing extent for WT, *mef8* and HXA are calculated from the STS-PCR-seq and are based on two biological replicates. Editing extent for transgenic plants transformed with the wild-type MEF8 is estimated from Sanger bulk sequencing from three biological replicates.

Two-thirds of the Editing Sites Showing an Increase of Editing Extent in the mef8 Mutant Are Complemented by the Mutated MEF8

The behavior of the 24 sites whose editing extent was significantly increased in the *mef8* mutant was analyzed in the HXA transgenic plants. Thirteen of these sites (54%) showed a significant reduction of their editing extent in both HXA transgenic plants, while sixteen sites (67%) exhibited a significant reduction in at least one HXA transgenic plant (**Table S-4.3**, **Figure 4.4**). Contrary to what was observed with the sites with decreased editing on the matR transcript, which were all complemented by the overexpression of the mutated MEF8 (HXA), the effect of the complementation on these sites depends on the transcript considered. All the sites on rpl16 exhibit a significant reduction of their editing extent in the HXA transgenics, while some sites on *ccmB*, and none of the sites on *nad3* are complemented by the mutated MEF8 (HXA) (**Table S-4.3**).

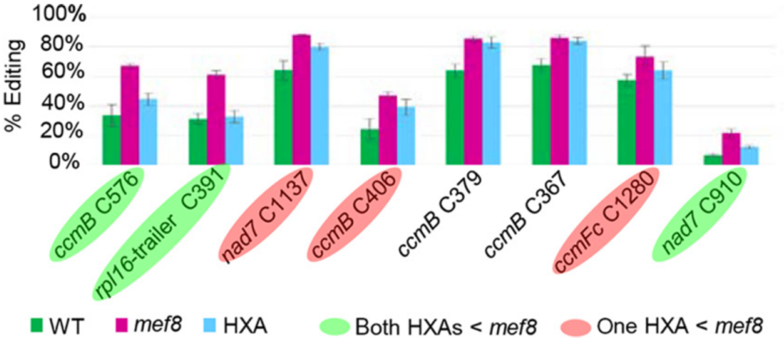


FIGURE 4.4 A mutated MEF8 (HXA) is able to reduce the editing extent of the majority of the editing sites showing an increase in the *mef8* mutant. Editing extents of eight sites exhibiting a significant increase of editing extent in the *mef8* mutant vs. wild-type (≥15%) are given for the wild-type (WT), the *mef8* mutant and the HXA transgenic plants. HXA plants were obtained by transforming the *mef8* mutant with a mutated version of MEF8 in which the putatively catalytic glutamate of the HXE motif is replaced by HXA. Values represent mean ± standard deviation (SD).

Overexpression of a Mutated MEF8 Reduces the Editing Extent at Many Sites

Another striking observation is the number of mitochondrial sites whose editing extent is significantly reduced in the HXA transgenic plants when compared to the *mef8* T-DNA insertional mutant. This is an important observation because overexpression of a catalytically non-functional MEF8 (HXA) could result in the formation of editing complexes with a non-functional DYW domain and a reduction of the extent of editing. The editing extent of 72 sites is reduced in at least one HXA transgenic plant; among those, 16 showed a significant increase in the *mef8* T-DNA insertional mutant plant when compared to the wild-type, while 56 were invariant in the *mef8* T-DNA insertional mutant plant (**Table S-4.4**, **Figure S-4.5**). The reduction of editing extent in the HXA transgenic plant occurs mostly on transcripts belonging to the complex I and ribosomal proteins (**Figure S-4.5**). For instance, *rps3*, *rps4* and *rps7* possess several sites whose editing extent is significantly reduced in the HXA transgenic plant, while the difference in editing extent at those sites between the mutant and the wild-type was not significant (**Table S-4.4**, **Figure S-4.5**). At these sites, overexpressing the mutated MEF8 HXA causes a reduction of editing extent which is more pronounced than the one observed in the wild-type. As an illustration, if we consider *rps3* C603, the average editing extent in the wild-type is 83% vs. 89% for the *mef8* mutant; however, the editing extent drops to 73% in the HXA plants (**Table S-4.4**).

In contrast, overexpression of the mutated MEF8 HXA does not have the same impact on the number of sites whose editing extent is significantly increased in the HXA transgenic plants. Sixteen sites show an increase of editing extent in at least one HXA plant; among these sites, 10 showed a significant decrease in the *mef8* mutant plant when compared to the wild-type, while only 6 were invariant in the *mef8* mutant plant (**Table S-4.5**). If the impact of overexpressing the mutated MEF8 HXA on increasing the editing extent of certain sites was the same as the effect on decreasing the editing extent of other sites, we would have expected 35 sites (according to the ratio 56/16 x 10) with an increase of editing extent in the HXA transgenic while invariant in the *mef8* mutant.

The Steady State Level of Mitochondrial Transcripts is Similarly Increased in Both the mef8 Mutant and the HXA Transgenic Plants Compared to the Wild-type Plants

Because RNA editing extent and transcript abundance have been correlated before [113], we analyzed the level of expression of seven mitochondrial genes by qRTPCR assay. The choice of the mitochondrial genes assayed reflected the different classes of transcript in relation to the effect of the MEF8 mutation on their editing extent. *CcmB* transcripts experienced an increase of editing extent only at 10% of its sites, while *matR*, *nad5*, and *rps3* exhibited only a decrease of editing extent on some of their sites (**Figure S-4.2**). None of the sites on *rps4* showed a significant variation of editing extent in the *mef8* mutant, whereas *ccmFc* and *rpl16* possess sites that showed either a reduction or an increase of editing extent in the *mef8* mutant (**Figure S-4.2**). In addition, *nad5*, *rps3*, and *rps4* were selected because they contain a high number of sites that showed a decrease of editing extent in the MEF8 HXA transgenic plants while invariant in the *mef8* mutant plant (**Figure S-4.5**).

We tested two pairs of primers per gene to ascertain the validity of the qRT-PCR assay. The first result is the good agreement between each set of primer pairs for all the mitochondrial genes assayed (**Figure S-4.6**). The second noticeable result is the overall increase of transcript abundance, both in the *mef8* mutant and HXA transgenic plants when compared to the wild-type plant. The level of MEF8 expression in the transgenic plant was significantly higher than in the wild-type plant for all the genes measured, while

2 genes, *ccmFc* and *nad5,* showed a level of expression significantly higher in the *mef8* mutant than in the wild-type plant (**Figure S-4.6**). Given the results of this experiment, it is unclear how the effect of the *mef8* mutation on the transcript abundance can explain the different outputs on the editing extent. The overall increase of transcript abundance is not correlated with editing extent, because the variation in transcript abundance is entirely in one direction, increasing, while the variation in editing extent both increases and decreases. As an illustration, the increase in transcript abundance in the *mef8* mutant vs. the wild-type plant is similar in the *ccmB* and *matR* transcripts (1.5-2X, **Figure S-4.6**); however, the variation in editing extent is in opposite direction (**Figures 4.1 B, 4.2 A**).

Discussion

Based on the analysis of the mitochondrial editome in the *mef8* mutant and in the HXA transgenic plants, we propose that MEF8 acts on editing through three processes that can be defined depending on the requirement of the glutamate in HXE and the effect of MEF8 on editing—either an increase or a decrease of editing extent.

MEF8 Requires E in HXE to Positively Control the Editing Extent of Its Main Targets

The use of STS-PCRseq allowed the survey of 576 mitochondrial sites and the identification of many mitochondrial sites whose editing is impaired in the *mef8* mutant. Two of these sites have been previously reported [110]. The larger number of MEF8 targets identified in this report comes from the power of the STS-PCRseq, a methodology which is much more sensitive than bulk-sequencing of RT-PCR products [5]. Secondly, our screen covers more sites than the 369 annotated editing sites probed in the original report [110]. Among the 38 defective sites showing an impaired editing in the *mef8* T-DNA insertional mutant, the mutated *MEF8* (HXA) could not complement about 75% of these sites. In particular, the main targets, or the six sites with the most pronounced reduction of editing extent in the *mef8* mutant, did not show any recovery in the HXA transgenic plants.

There is mounting evidence that the DYW domain acts as the catalytic component of the editing reaction. This region contains signature motifs of known cytidine deaminase active sites, HXE and CXXCH [87]. Mutagenesis of these conserved residues, in particular the glutamate residue, have prevented RNA editing from occurring in transgenic plants [22,23], a finding that is also observed by transient expression in protoplasts [24]. Our results further support an active role of the glutamate residue in the HXE motif as being crucial for the editing reaction; the majority of the defective sites in the mef8 mutant, with the exception of the sites on the matR transcript, require the presence of the HXE in the DYW domain of MEF8 to be complemented in the transgenic plants. A faulty expression of the transgene cannot be the reason for a lack of complementation by the mutated MEF8 (HXA), as the level of expression of the transgene is around 6 times higher in the transformed mef8 plant than in the wild-type plant. The residual extent detected in the mef8 mutant for some targets of MEF8 –*cox2* C557 is edited on 50% of the transcripts in the mef8 mutant (**Figure 4.1 A**)– suggesting that other editing factors are able to contribute to their editing extent by supplying a functional DYW domain, as was proposed in the previous report describing MEF8 [110].

The Recognition by MEF8 of Its Main Targets Likely Involves Binding to Other Trans Factors

The recognition of MEF8 for its main target is site-specific; the C at position 333 on *ccmFc* is drastically reduced in the *mef8* mutant, while the next C one nucleotide away at position 334 is fully edited (**Table S-4.1**). This site specificity is true for all the sites whose editing extent could not be rescued by the mutated MEF8. Recent co-crystallization studies determined that the succession of PPR repeats form a solenoid like structure that wraps around single-stranded RNA [13,114]. The recognition between the PPR protein and its RNA ligand involves a one-to-one relationship between a ribonucleotide and a repeat, in which the identity of two amino acids at certain position in the repeat is critical for RNA recognition [8–10]. The specificity recognition between MEF8 and its main targets is puzzling, as this protein has a short track of 5 consecutive repeats which is not long enough to convey a tight specificity. Moreover, the identity of the amino acids at the two critical positions of the repeats does not fit the recognition code. Nevertheless, the alignment of the sequences around the target C for editing reveals some conserved nucleotides, suggesting that MEF8 might still recognize and bind its RNA targets (**Figure 4.5**).

MEF8, with its short track of PPR repeats, belong to a small subfamily of PPR-DYW proteins. One of its members, DYW1, contains only a plastid target sequence and a DYW domain without any PPR motif. Editing of *ndhD* C2 is completely obliterated in the *dyw1* mutant, phenocopying the editing defect of the *crr4* mutant [37,82]. CRR4 is a PPR-PLS protein lacking a DYW domain that recognizes and binds to the sequence surrounding the *ndhD* C2 site [73]. CRR4 and DYW1 were shown to interact *in planta* by bimolecular fluorescence complementation [37]. Furthermore, a functional chimeric *CRR4-DYW1* protein was able to complement the *ccr4 dyw1* double mutant, suggesting that DYW1 by interaction with CRR4, provides *in trans* the essential function carried by its DYW domain [37].

In this report, MEF8-HXA plants are shown to experience reduced editing at a large number of sites relative to the mef8 null mutation (**Figure 4.4**, **Table S-4.4**). This observation suggests that MEF8-HXA may act in a partial dominant negative manner to interfere with the formation of functional editosomes through the incorporation of a catalytically incompetent DYW. Thus, the CRR4/DYW1 model may extend to MEF8, which could interact with other PPR-PLS recognition factors lacking the DYW domain. Unfortunately, the limited knowledge of mitochondrial editing factors does not allow us to further test this hypothesis. None of the recognition factors for the main targets of MEF8 (the nine sites in **Figure 4.1 A** excluding the sites on the matR transcript) has been identified.

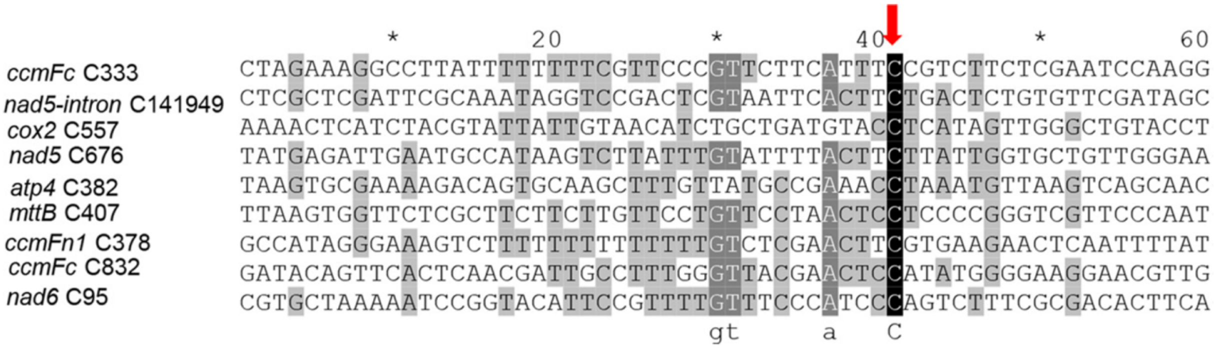


FIGURE 4.5 Sequences upstream of the target C for editing by an HXE-containing MEF8 contain conserved nucleotides.
Forty nucleotides upstream of the target C (indicated by a red arrow) and 20 nucleotides downstream were aligned using T-Coffee software version_11.00. The alignment was displayed using GeneDoc with the conserved residue shading mode defaults (100%: white letter in black background, 80%: white letter in grey background, 60%: black letter in grey background). The alignment was restricted to the sequences for which the difference in editing extent of the targeted C between the wild-type and the *mef8* mutant was at least 20%. The sites belonging to *matR* were excluded from this alignment because they are partially complemented by a mutated MEF8 (HXA), while the sites aligned in this figure are not.

An alternative hypothesis is that binding to the RNA target and to other recognition factors is not exclusive. MEF8 could somehow use a hybrid approach to recognize its targets by binding to the RNA, like normal recognition *trans* factors, but also to the *trans* factors themselves, as DYW1 binds with CRR4.

The Glutamate in HXE is Dispensable for the Editing Function of MEF8 on the Sites Located on the matR Transcript

All the defective sites located on the matR transcript were either partially or fully complemented by the mutated MEF8, thus supporting that the glutamate residue in HXE is not required for this particular role of MEF8. The partial complementation of certain sites might be due to an inadequate level of expression of the transgene. Full complementation could possibly have been obtained in transgenic lines with higher expression of the mutated MEF8, since the mutated protein likely has less activity than wild-type MEF8. The effect of MEF8 on the editing of the matR transcript is reminiscent of what was reported for ORRM4, a mitochondrial editing factor that broadly affects mitochondrial RNA editing [41]. All the known editing sites on the *rpl5* transcript exhibited a reduction of editing extent in the *orrm4* mutant. However, the reduction of editing extent caused by ORRM4 mutation was still site-specific, as it was not constant along the *rpl5* transcript. Northern blots showed that the abundance of the *rpl5* transcript was not affected in the *orrm4* mutant, thus strengthening the hypothesis of a site-specific effect [41]. This particular role of MEF8 in editing, positively controlling editing extent independently of the glutamate residue, is not restricted to the *matR* transcript. Two of the sites on the *rpl5* transcript at position 35 and 47 and the *ccmC* C270 site were complemented by the mutated *MEF8* (**Table S-4.2**). The mechanism by which MEF8 exerts its effect on *matR* editing is unclear. Because an earlier study has shown that a change in transcript abundance could have a pleiotropic effect on editing [113], we checked the steady state level of some mitochondrial transcripts, including *matR*, by qRT-PCR. Our data show a general increase of transcript abundance in the mef8 mutant irrespective of the direction of the variation of editing extent, increase or decrease. Therefore, a change in transcript abundance for the *matR* transcript in the *mef8* mutant cannot explain the effect of the MEF8 mutation on the editing extent of this transcript. It is still possible that the MEF8 mutation could affect the turnover of the *matR* transcript, and thus, pleiotropically reduce the editing extent of its sites. Increasing the turnover of *matR* transcript might kinetically prevent the editing machinery from carrying out its role.

The MEF8 Protein Plays an Inhibitory Role on Mitochondrial Editing

A T-DNA insertional mutation in MEF8 resulted in increased editing at 4% of the mitochondrial sites when compared to the wild-type. This effect is not negligible, as the editing extent of *ccmB* C576 almost doubles, increasing from 34% in the wild-type to 67% in the *mef8* mutant (**Figure 4.1 B**). This event might not have functional significance, since the editing at that position does not change the encoded amino acid (F→F, 192) . However, some of the targets for the inhibitory role of MEF8 are non-silent sites, upon which editing changes the encoded amino-acid, for instance *ccmB* C379 (P→S, 127). The inhibitory action of MEF8 maintains the editing of *ccmB* C379 at around 60% in the wild-type (**Figure 4.1 B**).

The accepted dogma in the plant organelle RNA editing field posits that RNA editing is a corrective mechanism, allowing the production of functional proteins by restoring the presence of conserved amino-acids [6,81]. In other editing systems, both edited and unedited transcripts are translated, giving rise to proteins with different biological properties [115,116]. The occurrence of partial RNA editing in plant mitochondria [117,118] raises the possibility that editing could generate protein polymorphisms. By probing them with antibodies specific to each form, both unedited and edited RPS12 proteins have been shown to be present in maize and petunia mitochondria [119,120]. Furthermore, both unedited and edited RPS12 proteins were found in the petunia mitochondrial ribosome fraction; thus, both versions of the RPS12 protein could be assembled into ribosomes [119]. While there is no evidence of useful protein polymorphism created by translation of incompletely edited transcripts, only a few proteins encoded by partially edited transcripts have been analyzed to date. The inhibitory function of MEF8 on mitochondrial RNA editing maintains a certain amount of unedited transcripts; further analysis would be needed to determine whether any of the proteins thus encoded are relevant to mitochondrial function. We have recently reported the identification of ORRM5, which has also a marked inhibitory effect on mitochondrial editing. The absence of ORRM5 results in an increase of editing extent in 14% of the mitochondrial sites surveyed, while only 3% of the mitochondrial sites show a decrease of editing extent [42].

The Inhibitory Role of MEF8 Does Not Need the Glutamate in HXE for the Majority of Its Targets

Forty-three mitochondrial sites, or 8% of the whole mitochondrial editome surveyed, show a decrease of mitochondrial editing extent in both HXA transgenic plants when compared to the *mef8* mutant plant. The size of this population reaches 72 sites, or 12% of the whole mitochondrial editome, when the decrease of editing extent affects at least one HXA transgenic plant (**Figure S-4.5**). Approximately 75% of the sites exhibiting an increase of editing extent in the *mef8* T-DNA insertional mutant were complemented by the mutated MEF8 (HXA). A full complementation was observed for the all the sites on the *rpl16* transcript, while only one site was partially complemented on the *ccmB* transcript (**Table S-4.3**).

All the sites on *nad3* that exhibited an increase of editing extent in the mef8 mutant failed to show a significant decrease in the HXA transgenic plants (**Table S-4.3**). The simplest explanation is the glutamate in HXE motif of MEF8 is required to restore the editing extent to the wild-type level. However, examination of the level of editing extent in the *mef8* TDNA insertional mutant of the sites complemented by the mutated MEF8 (HXA) indicates that most of them are edited at a low-to-medium level in wild-type (**Table S-4.3**). Conversely, the sites not complemented by the mutated *MEF8* (HXA) are edited at a high level in wildtype. Therefore, the failure of the mutated *MEF8* (HXA) to complement some

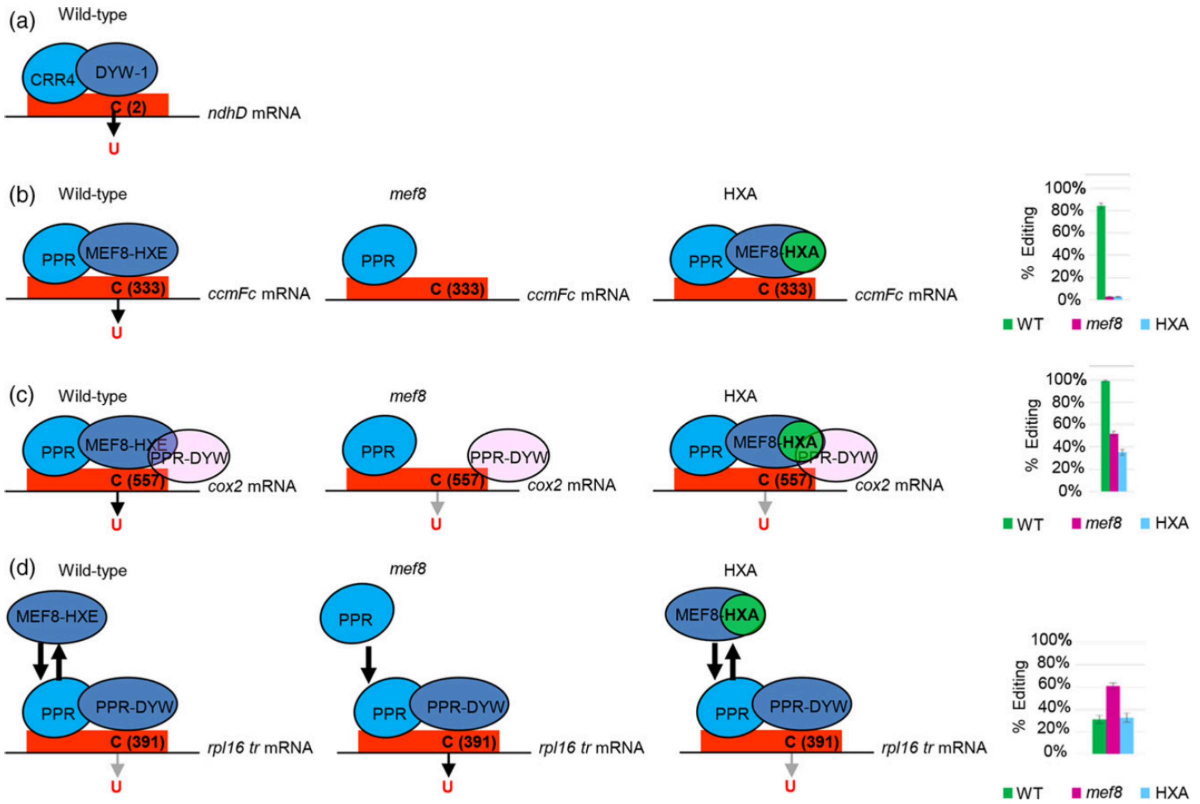


FIGURE 4.6 Models for the different modes of action of MEF8 on editing.

(a) Model for the editing of *ndhD* C2 derived from Boussardon *et al.* (2014). CRR4, a PPR-E protein lacking the DYW domain, is the recognition factor for *ndhD* C2 and binds to the transcript upstream of the C targeted for editing. DYW1 binds to CRR4 and brings the DYW domain allowing the C to be edited to U.

(b, c) Models for the stimulatory effect of MEF8 on editing derived from the DYW1 model. MEF8 brings the DYW domain to editosomes containing recognition factors lacking this domain. MEF8 might bind specifically to the recognition factor in a similar way that DYW1 binds to CRR4. In addition MEF8 might also bind to the RNA target (cf. Figure 5). In (b) the absence of MEF8 in the *mef8* mutant or the absence of the glutamate residue in HXA precludes the editing of *ccmFc* C333. In (c) the absence of MEF8 or the absence of the glutamate residue in HXA is compensated by the redundant function of another PPR-DYW providing the DYW domain in *trans*. A grey arrow represents a reduction of editing extent when only one functional PPR-DYW is present. On the right of each model is a graph representing the editing extent of the wild-type (WT), the *mef8* mutant (*mef8*) and the HXA transgenic plants (HXA).

(d) Model for the inhibitory effect of MEF8 on editing. MEF8 might compete with recognition factors which have a better affinity for the RNA targets. In the absence of MEF8 in the *mef8* mutant, the equilibrium is displaced towards the 'better' recognition factor allowing a more efficient editing to occur. The presence of the glutamate is not required for the competition to happen so that the editing is reduced in the HXA transgenic plant. The colour of the arrow, grey or black, and the graph on the right have the same meaning as in (b) and (c).

sites might not be caused by the substitution of the glutamate, but rather due to a dosage effect. This hypothesis could explain why some sites on *ccmB* and *nad2* transcripts are complemented while others are not. If mutated *MEF8* (HXA) had been expressed at higher levels in the HXA transgenic plants, complementation of sites on the *nad3* transcript might have occurred.

In conclusion, we have shown that a single PPR-DYW protein affects the editing extent of an unexpected number of targets. As a comparison point, among the recognition factors with a high number of targets, we can cite the rice OGR1, another PPR-DYW mitochondrial editing factor, and the *Arabidopsis* SLO2, a PPR-E+ editing factor , both of which affect the editing of seven sites [65,121]. To this date, MEF13, an E-type PPR protein, recognizes the highest number of targets, as this protein is required for RNA editing at eight sites in six different mRNAs in the mitochondria of *Arabidopsis thaliana* [122]. We have also demonstrated that MEF8 could have antagonistic effects on editing extent, and that some of these effects required the glutamate in HXE, while others did not. We propose several different models to explain the diverse and antagonistic roles of MEF8 on mitochondrial editing extent (**Figure 4.6**). The stimulatory effect of MEF8 on editing extent requiring the glutamate residue can be modeled from the report on the CRR4-DYW1 interaction [37] (**Figure 4.6 A**). In the models presented in **Figures 4.6 B** and **4.6 C**, MEF8 brings the DYW domain to Cs targeted for editing recognized by PPR trans factors lacking this domain. This function can be supported by other PPR-DYW proteins explaining the residual extent in the mef8 TDNA insertional mutant for most of its targets (**Figure 4.6 C**). We also offer a model for the inhibitory effect of MEF8 on editing extent, in which this protein competes with other recognition factors better fitted to sustain the editing reaction

(**Figure 4.6 D**). More work is necessary to support these models and to understand the determining factors contributing to the specificity of the recognition of MEF8 for its targets.

Statement of contribution

This chapter is already published. I generated plant materials with MLH. I generated data with SB. I co-wrote the manuscript with SB, MLH, MM, and MH.

Reference*: Diaz, M. F., Bentolila, S., Hayes, M. L., Hanson, M. R. & Mulligan, R. M. A protein with an unusually short PPR domain, MEF8, affects editing at over 60 Arabidopsis mitochondrial C targets of RNA editing. Plant J. 92, 638–649 (2017).*

Chapter 5: Oxidative Stress During RNA Editing Dysfunction: A Model For Lipid-Mediated Retrograde Signaling

Abstract

RNA editing in plants is a post-transcriptional process that converts cytidines to uridines (C-to-U) in transcripts expressed from chloroplast or mitochondria genomes. Pentatricopeptide repeat proteins (PPR) have been identified as critical for RNA editing. In addition, non-PPR genes have been identified to affect editing, several of which have been demonstrated to interact with PPRs. Lastly, there is mounting evidence that PPRs can edit *in trans*, whereby one PPR supplies the DYW deaminase domain for editing, while another PPR provides RNA binding and site specificity. Given the large number of proteins thought to be involved in RNA editing, and growing evidence for a *trans*-editing model, we became interested in understanding how RNA editing is regulated. We investigated the possibility that reactive oxygen species (ROS)-mediated signaling drives an organelle-to-nucleus response to regulate RNA editing. To test this hypothesis, we confirmed that ROS accumulates in plants during RNA editing dysfunction. We observed over 2,000 genes that are differentially expressed in the RNA editing mutant *lpa66* in comparison to wild type. Many of these DEGs are involved in mitigating oxidative stress (ROS network) and retrograde signaling (RSN network). In addition, over 90 PPRs are differentially expressed, which suggest a significant PPR-specific shift in gene expression. We performed lipidomics on PPR mutants *lpa66* and *dot4* as well as wild type plants, and found that in the PPR mutants, lipid unsaturation and oxidized lipid formation were a consistent trend. Among the lipidomics dataset, we observed high levels of Arabidopside E and G production and phytoprostane production, which are potent retrograde signaling molecules. In addition, the observation of Arabidopsides and Phytoprostanes suggests enzyme-mediated and ROS-mediated lipid peroxidation is occurring in the editing mutants, respectively. From this data, we propose a model where RNA editing dysfunction triggers ROS formation, which results in lipid peroxidation and the formation of potent retrograde signaling molecules that trigger the expression of ROS- and RSN-network genes, as well as a significant number of PPR genes.

Introduction

RNA editing in plants is a post-transcriptional process that converts cytidines to uridines (C-to-U) in transcripts expressed from chloroplast or mitochondria genomes [8,36,123]. Over 630 editing sites have been identified in *Arabidopsis* organelles, and C-to-U conversion generally results in non-synonymous substitutions in protein coding sequences [5,124,125]. Editing in plants appears to be a genetic correction mechanism, which reestablishes the evolutionarily conserved amino acid sequence of a polypeptide [6,28]; in contrast to other eukaryotic editing systems in which editing performs a regulatory role [25,28]. The editosome has been shown to be a large complex of 0.8 to 5MDa[126] with a number of proteins including RIP/MORFs[38,39], OZ proteins[43], ORRMs[41,42,127], and P-type PPRs and PLS-type PPRs[34,35], among others[128]. A wealth of genetic, molecular, and biochemical data has identified proteins that appear to participate as generalists [5,34,35,38,40–44,77,127], i.e. an editing factor required for many sites, or specialists [36,2,26], i.e. an editing factor required for a single or few sites. Significant strides have been made in understanding one group of editing factors in particular—the pentatricopeptide repeat protein family.

Pentatricopeptide repeat (PPR) proteins are found in all eukaryotes, but the explosion of PPR in plants is the most striking, with upwards of 500 genes present in *Arabidopsis*. With few exceptions, members of each clade of plant evolution have PPRs and exhibit RNA editing [17,25,26]. The number of PPR genes varies among different taxa, but editing site and PPR numbers show strong correlation, starting with basal angiosperms, and marching on through higher plants, with losses exhibited over time [27].

Pentatricopeptide repeat proteins are predominately single exon nuclear-encoded genes and mainly localize to the chloroplasts and mitochondria. There are two classes of PPRs—the P-type which are primarily involved in RNA stabilization [2] and PLS-type which are involved in RNA editing. PLS-type PPRs are modular in terms of structure. The N-terminus contains a tandem array of repeats called P (pure), L (long), and S (short), which contain varying numbers of amino acids and confer binding specificity to RNA substrates. Each repeat, in association with neighboring repeats, bind to specific nucleotides on RNA in a region upstream to an edited cytidine termed the *cis*-element, which is supported by computational, genetic, molecular, and structural data [11,8,17,12,9,10,13,129]. In addition to conferring binding specificity, the PLS repeat region positions the C-terminus of PPRs to the edited cytidine. The C-terminus is referred to as the DYW-deaminase Domain, which our lab and others have demonstrated this domain confers the capacity to edit RNA *in planta* [22–24]. Editing PPRs can be further divided into E-type, which lack a C-terminal deaminase domain, and degenerate DYW-type, which have a highly reduced PLS repeat domain that often include degenerate PLS repeats. These degenerate repeats are thought to act as *trans*-editing factors to complement editing of other PPRs, and support for this argument has been recently bolstered [34,35,77].

Despite not appearing to have a direct regulatory role in protein expression, several editing PPRs are critical for organelle biogenesis, and null mutant plants exhibit a range of macroscopic phenotypes, from apparently indistinguishable in comparison to wild type, to embryo lethality [14,26,106,130,131]. Our lab and others have posited a possible explanation to this conundrum. In situations where insufficient levels of a PPR are present to edit its target transcript, *trans*-acting PPRs can complement these losses. In cases where a *trans*-editing factors are unavailable, lethality is unavoidable. Recently, a few PPRs have been identified that may occupy this role as general *trans*-acting factors with the ability to catalyze the deamination of cytidine nucleotides[34,35,77], yet this scenario has not been demonstrated directly and still more factors have yet to be characterized[110]. Furthermore, several non-PPR proteins that affect numerous editing sites have been identified, adding to the growing list of *trans*-acting editosomes factors[5,38,39,41–44,127,128,132]. This complexity brings into question how RNA editing is regulated, since maintaining constitutive expression of many *trans*-acting factors would be energetically costly.

Table 5.1 Editing sites located in electron transport genes

TAIR ID	Number of Sites
Chloroplast Photosynthetic Electron Transport Chain	
Photosystem II	3
Photosystem I	0
Cytochrome b6/f complex	1
NADH dehydrogenase-like complex	20
ATP synthase	1
Total	24/37 (65%)
Mitochondria Electron Transport Chain	
Complex I (NADH dehydrogenase)	266
Complex II (Succinate dehydrogenase)	0
Complex III (cytochrome bc1 complex)	65
Complex IV (cytochrome c oxidase)	136
Complex V (atp synthase)	0
Total	467/619 (75%)

A majority of RNA editing events in plant mitochondria and chloroplasts occur in transcripts that encode polypeptides in the electron transport chain (**Table 5.1**) and disruption of electron transport is expected to be a common consequence of RNA editing dysfunction. Pathways that mitigate oxidative stress caused by ETC disruption may overlap with pathways that regulate RNA editing. For example, Photosystem II is a potent producer of singlet oxygen ($^1O_2$) and superoxide anion ($O_2\bullet^{-}$) and hydrogen peroxide (H_2O_2) are mainly produced around photosystem I. In contrast, $O_2\bullet^{-}$ is the main reactive oxygen species (ROS) in mitochondria under normal metabolic conditions, and effectively processed to non-reactive products by organelle ROS network proteins [46,47]. However, when electron transport is disrupted, upstream redox centers may become highly reduced and result in high levels of ROS production. Moderate levels of ROS production can be managed by stress acclimation and signal transduction, but higher levels may significantly overwhelm metabolic scavenging mechanisms, and ROS can be cytotoxic and lead to programmed cell death [48].

Reactive oxygen species have been extensively documented as retrograde signaling molecules in plants outside of RNA editing dysfunction[49–55]—retrograde signals originate in a subcellular compartment outside the nucleus, and drive changes in gene expression in the nucleus. ROS are unlikely candidates for signaling molecules during RNA editing dysfunction because ROS are rapidly detoxified in the chloroplast and mitochondria, and would not be expected to move through the cell even over short distances [48], although it is important to note that ROS molecules can move out of, or between, organelles via aquaporins or stromules [56,57]. Instead, ROS acting on other molecules is a more likely source of retrograde signaling. Since the majority of edited transcripts are destined for membrane bound protein complexes (**Table 5.1**), we hypothesize lipid peroxidation is increased in editing mutants, which would result in production of lipid-derived signaling molecules. Indeed, ROS generation in chloroplast provokes the formation of potent lipid-derived retrograde signaling molecules [58,59]. We expect the identity of these signals depends on what compartment is affected by RNA editing dysfunction, since ROS production can be site-specific [50,52,58,60]. ROS production and upregulation of ROS network genes has been documented in PPR mutants, but this was contextualized as mitigating oxidative stress due to loss of editing or RNA stability [61–66], rather than addressing the possibility that ROS or other retrograde signaling molecules can mitigate RNA editing dysfunction directly. Some evidence suggests that PPRs involved in RNA editing are regulated by ABA.

Several publications have shown that mutations in PPRs affect the abscisic acid (ABA) response. However, these investigations focused on global plant physiological responses and how disruption of PPRs impact abiotic and biotic responses [62–69], and not how ABA influences RNA editing in the cases where editing PPRs were studied [62,65,67,69]. A growing body of research has demonstrated oxylipins and cardiolipins, oxygenated lipids from the chloroplast and mitochondria, respectively, play important roles in retrograde signaling from the organelles and that free-radical catalyzed as well as enzyme-catalyzed lipid oxygenation occurs during abiotic and biotic stress [70,71]. In this study, we analyzed the influence of RNA editing dysfunction on ROS accumulation, transcriptomic changes, and lipidome modulation of the *low psII accumulation 66* (*lpa66*) PPR mutant. *LPA66* is responsible for editing the thylakoid membrane-associated PSII subunit *PsbF* [133] and loss of editing of *psbF* transcript negatively inhibits photosynthetic electron flow [133]. In addition, PSII is a well-established site of ROS production [50,134]. Therefore, we reasoned an early messenger of a retrograde signaling cascade would be an oxylipin, as is the case in several abiotic and biotic stress responses [48,50,52,54,58,70,72]. In this study, we demonstrate that ROS accumulates to higher levels in *lpa66* mutants versus wild type. Commensurate changes in gene expression are observed in the *lpa66* mutant: a suite of ROS and retrograde signaling network responsive genes [46,135] are upregulated; 20% of nucleus-encoded PPRs are upregulated, including 49 genes that are considered *trans*-acting editing factors, and genes for eight non-PPR editing factors. In addition, oxylipins that are known to be produced under oxidative stress, Arabidopsides A and G, accumulate to high levels in the mutant as well as a two putative phytoprostanes. Both the Arabidopsides and the phytoprostanes are lipid-derived signaling molecules, the former of which also serve as precursors to Jasmonic Acid, a well-known hormone and signaling molecule [71,136]. These data suggest a model that oxidative stress during RNA editing dysfunction triggers oxylipin production, which results in the activation of potent retrograde signaling pathway and a concomitant PPRome-wide shift in nuclear expression and oxidative stress response. Lipid-derived signaling molecules may communicate chloroplast-to-nucleus RNA editing dysfunction to recruit needed *trans*-acting editing factors.

Results

RNA Editing Dysfunction Increases ROS and Expression of ROS Responsive Genes

Reactive oxygen species (ROS) act primarily as signaling molecules and, under severe oxidative stress, can cause cell death [46,50].The photosynthesizing chloroplast is a major source for ROS, including singlet oxygen ($^1O_2$), superoxide anion radical ($O_2{\bullet}^{-}$), hydroxyl radical (OH•), and hydrogen peroxide (H_2O_2), produced as a consequence of metabolism or as secondary messengers in response to stress [50,137]. *LPA66* is responsible for editing the *psbF* transcript, which encodes the β-subunit of cytochrome b_{559} in photosystem II, and loss of editing of *psbF* transcript negatively affects PSII function by ~40% as measured by maximum chlorophyll fluorescence (F_v/F_m), resulting in a pale green phenotype[133]. Furthermore, *lpa66* mutant plants exhibit developmental delays, resulting in smaller plants in

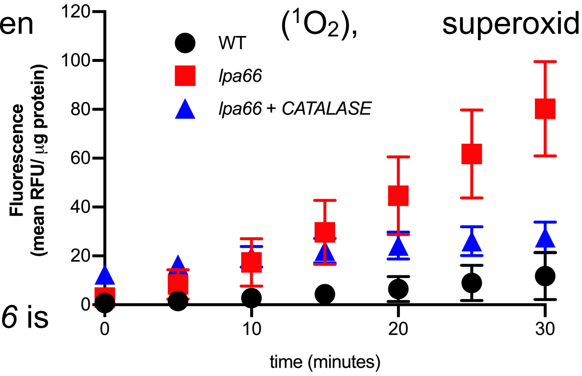


Figure 5.1. H_2O_2 detection by H_2DCFDA. H_2DCFDA substrate was added to whole cell extracts from wild type, *lpa66*, and *lpa66* + *CATALASE* samples, and fluorescence accumulation was detected with a plate reader at 595nm over a 30-minute time course. Data represent biological triplicates and technical duplicates. Error bars represent standard deviation.

comparison to wild type plants, under laboratory conditions. We hypothesize that loss in editing of *psbF* mRNA results in higher production of ROS. A sensitive method for fluorometric detection of ROS is the reaction with dichlorodihydrofluorescein (H_2DCFDA) as a substrate. H_2DCFDA is reactive with ROS [80], as well as other redox active molecules, and is generally used as an indicator of the oxidative environment of cells and tissues[80]. *lpa66* extracts were much more reactive with H_2DCFDA than wild type extracts with an 8x difference after 30 minutes (**Figure 5.1**). Treatment of the *lpa66* samples with catalase resulted in a dramatic reduction in fluorescence, indicating that H_2O_2 was a major component of the ROS detected in these samples (**Figure 5.1**). Since H_2DCFDA is reactive toward a number of non-ROS oxidants including cytochrome *c*, Fe^{2+}, and copper ions, ROS reactivity was also measured *in planta*. While H_2O_2 has a relatively long half-life of approximately 30 ms, other species exhibit much shorter half-lives of ≤ 4 μs [48]. We sought to detect $O_2 \bullet^{-}$, since $O_2 \bullet^{-}$ production occurs at photosystem I [134] and photosystem II [137], in effect enabling us to capture ROS production at the entry and exit points of the photosynthetic electron transport chain. Using Nitroblue tetrazolium dye, which reacts with $O_2 \bullet^{-}$ to produce a blue formazan precipitate, we determined that *lpa66* mutants produced approximately 3x more $O_2 \bullet^{-}$ (**Figure 5.2**). Formazan precipitation was observed in the both wild-type and *lpa66*; however, wild type formazan precipitation was present mostly in younger leaves, whereas formazan in the *lpa66* mutant was present in almost all leaf stages (**Figure 5.2**). When ROS production overwhelms ROS scavenging, nuclear gene expression programs are initiated to mitigate oxidative stress[48]. Therefore, we next sought to determine if ROS network genes were responsive to the accumulation of $O_2 \bullet^{-}$ and H_2O_2 in the *lpa66* mutant.

ROS are considered unavoidable byproducts of aerobic and photosynthetic metabolism, and it is therefore not surprising that plants have evolved to manage these reactive compounds. To determine if ROS detoxifying genes are upregulated in the *lpa66* mutant, we selected a subset of ROS network genes[46] to assay by qPCR. These genes include iron superoxide dismutase 1-3 (*FSD1*-3), copper/zinc superoxide dismutase 1-2 (*CSD1-2*), stromal ascorbate peroxidase (*SAPX*), thylakoid ascorbate peroxidase (TAPX), peroxiredoxin-2E (*PRXIIE*), plastid terminal oxidase (*PTOX*), and ascorbate peroxidase 1 (*APX1*). All of these ROS network genes are chloroplast targeted, with the exception of *APX1* and *CSD1*. APX1 and CSD1 are cytoplasmic proteins and were selected as proxies for ROS production outside the chloroplast, since H_2O_2 can translocate through the chloroplast envelope via aquaporins[56]. *FSD1*, *FSD3*, *CSD1*,

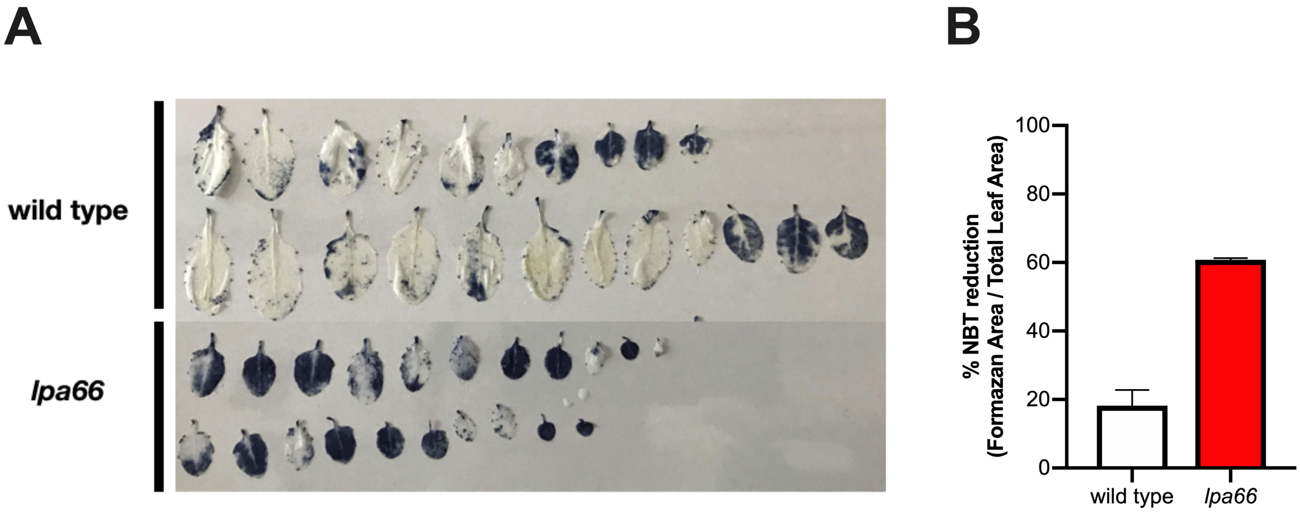


Figure 5.2. Superoxide anion detection by nitroblue tetrazolium dye. Wild type and *lpa66* samples were excised from 5 week old plants. Leaves were submerged and incubated in a buffered NBT/NaN_3 solution. A) Representative image of formazan precipitate in leaf samples. Images were taken with a Canon T3 camera. B) Area density measurements of NBT reduction into formazan. ImageJ v. 1.52h was use for area density analysis.

SAPX and *TAPX* were upregulated and *CSD2* was downregulated in *lpa66* plants (**Figure 5.3 A**). The remaining genes were non-responsive (data not shown). The accumulation of ROS as detected by H_2DCFDA and NBT, taken together with the upregulation of these genes, suggests the *lpa66* mutants are responding to increased oxidative stress with changes in expression of ROS network genes. To address this more comprehensively,

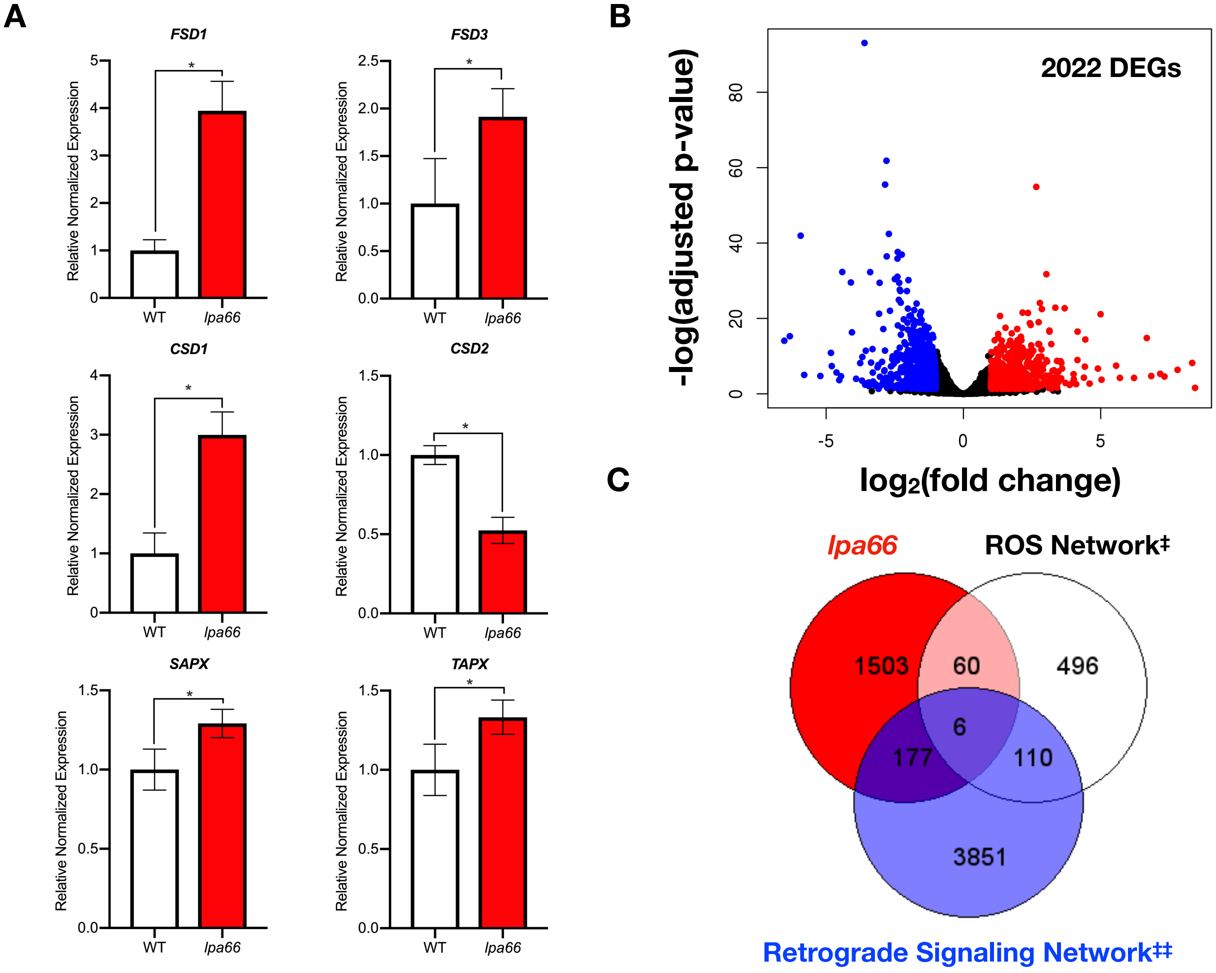


Figure 5.3 Gene expression changes in wild and *lpa66* by qRT-PCR and bulk RNAseq. A) Subset of upregulated ROS network genes from Mittler (2004) that responded to RNA editing dysfunction. B) 2,022 Differentially expressed genes *lpa66*/wild type with |log2(FC)| >1 . Data represents all genes with p-adjusted values of ≤0.05. C) Venn diagram showing overlap of *lpa66* DEGs with p-adjusted values of ≤0.01 , expanded ROS network DEGs (‡ Willem et al, 2016), and Retrograde Signaling Network Genes (‡‡ Gläßer et al, 2014).

we analyzed the transcriptome of *lpa66* mutants in comparison to wild type plants (**Figure 5.3 B**).

Transcriptome Analysis During RNA Editing Dysfunction

To determine how ROS production, and therefore, oxidative stress, impacts gene expression during RNA editing dysfunction, we performed pooled RNA sequencing on *lpa66* and wild type Col-0 plants. Library construction and RNA sequencing was performed by GENEWIZ Inc. (South Plainfield, New Jersey, USA). Using an adjusted p-

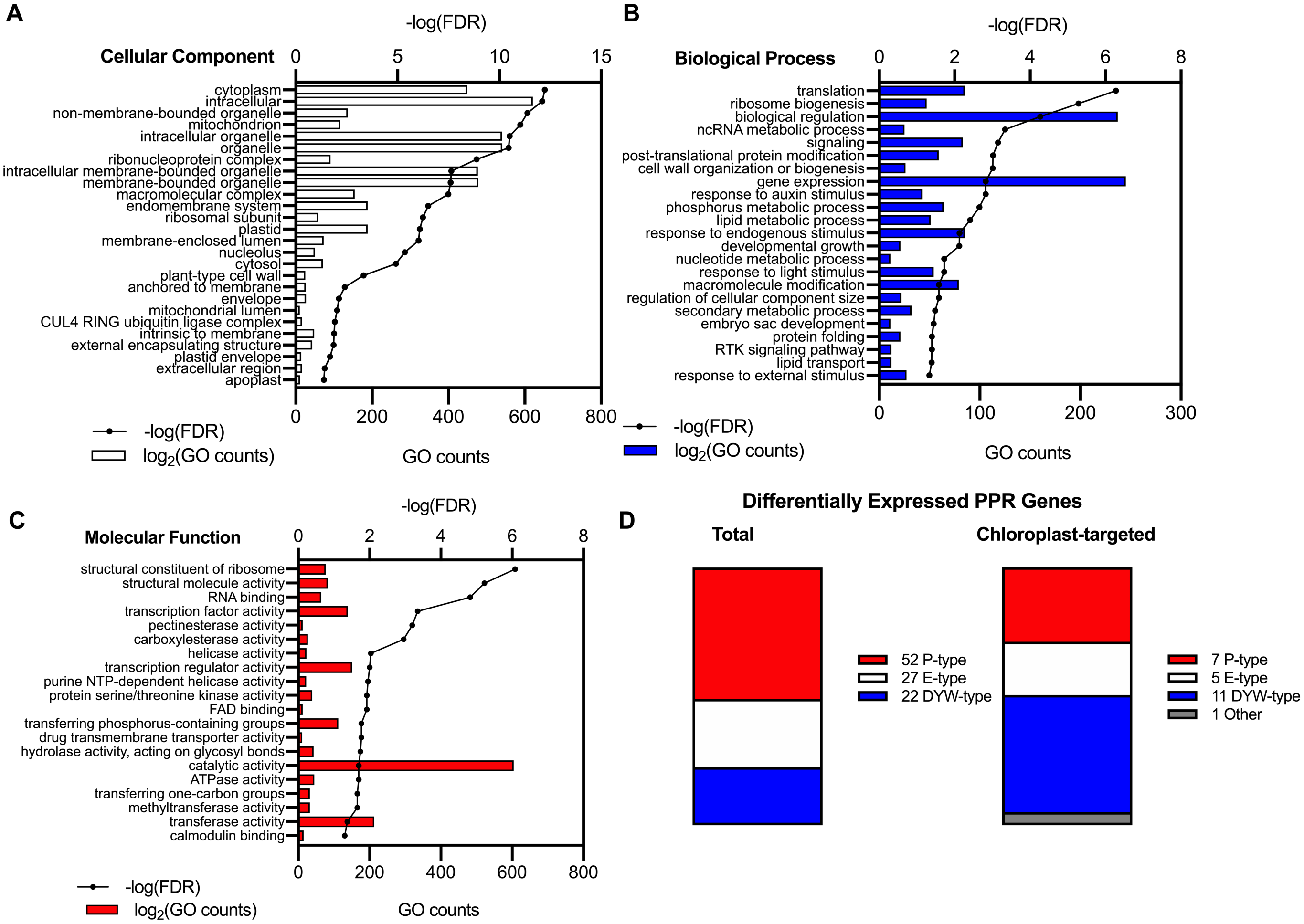


Figure 5.4 Gene ontology analysis of *lpa66* transcriptome and subcellular distribution differentially expressed PPRs. A) GO Cellular Component B) GO Biological Process C) GO Molecular Function. D) Total differentially expressed PPRs and chloroplast-targeted enumerated by class. Gene ontologies were determined by using AgriGO, followed by summarizing with REVIGO.

Table 5.2 RNA editing genes upregulated in this study

TAIR ID	Gene Symbol	PPR Type (Cheng et al., 2016)	log2FC(lpa66/wild type)	SUBA4 targeting or manual curation
Pentatricopeptide Repeat Proteins				
AT4G38010		E2	1.983412022	cytosol
AT1G13630		P	1.097921579	cytosol
AT3G06920		P	1.203854887	cytosol
AT4G26800		P	1.276369678	cytosol
AT5G46100		P	1.499396061	cytosol
AT3G13150		P	1.879850175	cytosol
AT3G11460	MEF10	DYW	1.974793097	mitochondrion
AT1G56690		DYW	1.327226952	mitochondrion
AT1G71420		DYW	1.541734205	**mitochondrion**
AT2G27610		DYW	1.442863101	**mitochondrion**
AT3G12770	MEF22	DYW	1.246497477	mitochondrion
AT3G24000		DYW	1.614115036	mitochondrion
AT4G16835		DYW	1.10818249	mitochondrion
AT4G33990	EMB2758	DYW	1.228932265	mitochondrion
AT4G37170		DYW	1.437581256	mitochondrion
AT5G39680	EMB2744	DYW	1.746399406	mitochondrion
AT5G52850		DYW	1.431131654	mitochondrion
AT1G33350		E+	1.207009956	mitochondrion
AT3G13880	OTP72	E+	1.367999629	mitochondrion
AT4G19191		E+	1.329786854	mitochondrion
AT5G08305		E+	1.782153638	mitochondrion
AT5G27110		E+	1.191730767	mitochondrion
AT1G74400		E+	1.996612	mitochondrion
AT2G39620		E1	2.920985389	mitochondrion
AT1G09190		E2	1.215000785	**mitochondrion**
AT3G49740		E2	1.444865088	mitochondrion
AT1G09220		E2	1.292626746	mitochondrion
AT2G02750		E2	1.346071018	mitochondrion
AT2G03380	PPR596	E2	1.386280295	mitochondrion
AT2G34400		E2	1.3128823	**mitochondrion**
AT4G08210		E2	2.170070102	**mitochondrion**
AT5G37570		E2	1.264478034	mitochondrion
AT5G39350		E2	1.172707423	mitochondrion
AT5G61800		E2	1.577777563	mitochondrion
AT5G66500		E2	1.204924033	mitochondrion
AT1G02370		P	1.333043895	mitochondrion
AT1G16830		P	1.810200637	mitochondrion
AT1G22960		P	1.055583633	mitochondrion
AT1G26500		P	1.326558229	mitochondrion
AT1G61870	PPR336	P	1.142917064	mitochondrion
AT1G71210		P	1.001332431	**mitochondrion**
AT1G77405		P	1.515143257	mitochondrion
AT1G79490	EMB2217	P	1.402756988	mitochondrion
AT1G80150		P	1.667054331	mitochondrion
AT2G01740		P	1.518995665	mitochondrion
AT2G02150	EMB2794	P	1.18075452	mitochondrion
AT3G02650		P	1.149886308	mitochondrion
AT3G07290		P	1.735400121	mitochondrion
AT3G13160	RPPR3B	P	1.0558412	mitochondrion
AT3G14580		P	1.30013127	mitochondrion
AT3G15590		P	1.287139275	mitochondrion
AT3G46870		P	1.004189563	mitochondrion
AT3G48250	BIR6	P	1.8191144	mitochondrion
AT3G60960		P	1.273128263	mitochondrion
AT3G61520		P	1.093444062	mitochondrion
AT4G01990		P	1.218439536	mitochondrion
AT4G04790		P	1.116922689	mitochondrion
AT4G11690	ABO8	P	1.390379097	mitochondrion
AT4G35850		P	1.055117578	mitochondrion
AT4G38150		P	1.523483918	mitochondrion
AT5G08310		P	1.276187383	mitochondrion
AT5G11310	SOAR1	P	1.18580364	mitochondrion
AT1G09680		P	1.088456211	mitochondrion
AT1G13800	FAC19	P	1.43319461	mitochondrion
AT1G62720	NG1	P	1.259141972	mitochondrion
AT2G26790		P	1.346376403	mitochondrion
AT2G40240		P	1.403637175	mitochondrion
AT3G56030		P	1.321269005	mitochondrion
AT3G60980		P	1.02785234	mitochondrion
AT5G16420		P	1.066429247	mitochondrion
AT5G61370		P	1.337394582	mitochondrion
AT1G62350		P	2.127790527	mitochondrion

value cutoff of $\geq$0.05 and a $|\log_2(FC)| \geq 1$, we identified 2,022 significantly differentially expressed genes (DEG) of which 1,960 are predicted protein coding genes (**Figure 5.3 B, Table S-5.1**). We applied a more stringent adjusted p-value of <0.01 *lpa66* DEG dataset, and compared to an updated ROS network gene list [47] and comprehensive retrograde signaling network gene list [135]. Sixty genes are shared between *lpa66* DEGs ROS network DEGs, and 177 are shared between *lpa66* and the retrograde signaling network DEGs (**Figure 5.3 C**). Surprisingly, none of the ROS responsive genes assayed by qPCR were observed in the RNAseq dataset, however lack of concordance is often observed in borderline genes whose fold change does not differ substantially[138].

Table 2 continued. RNA editing genes upregulated in this study.

TAIR ID	Gene Symbol	PPR Type (Cheng et al., 2016)	log2FC(lpa66/wild type)	SUBA4 targeting or manual curation
Pentatricopeptide Repeat Proteins				
AT2G39230	LOJ	P	2.093227097	mitochondrion
AT5G62370		P	2.439056566	mitochondrion
AT3G21470		E2	1.505894085	plasma membrane
AT2G29760	OPT81	DYW	1.437861079	plastid
AT3G49170	EMB2261	DYW	1.119354559	plastid
AT4G18750	DOT4	DYW	1.408416822	plastid
AT2G33760		DYW	2.313692673	plastid
AT1G08070	OTP82	DYW	1.359724411	plastid
AT1G15510	VAC1/atECB2	DYW	2.495941759	plastid
AT3G62890		DYW	1.386401409	plastid
AT4G14820		DYW	1.712505568	plastid
AT4G35130		DYW	1.704469356	plastid
AT5G48910	LPA66	DYW	-1.154004871	plastid
AT5G59200	OTP80	E+	1.579947964	plastid
AT1G43980		E1	1.287638168	plastid
AT4G18840		E2	1.960118246	plastid
AT5G15300		E2	1.420612788	**plastid**
AT2G17670		P	1.824715524	plastid
AT2G37230	RPPR5	P	1.10763339	plastid
AT4G20090	EMB1025	P	1.200469437	plastid
AT5G39980	PDM3/EMB3140	P	1.195199608	plastid
AT5G46580	SOT1	P	1.431183835	plastid
AT1G31840		P	1.904106071	plastid
AT1G08610		P	2.01675304	**plastid**
AT1G31790		PLS	1.750912554	plastid
AT2G37310		E+	1.415138599	**plastid, mitochondrion**
AT3G15930		E+	1.449222548	**plastid, mitochondrion**
AT1G80270	PPR596	P	1.228702531	plastid, mitochondrion
AT2G15690	DYW2	DYW	1.323850084	plastid, mitochondrion
Non-PPR Editing Factors				
AT3G49240	NUWA	N/A	1.78360268	**plastid, mitochondrion**
AT5G61030	ORRM3	N/A	1.788136309	**mitochondria**
AT5G54580	ORRM2	N/A	1.224125988	**mitochondria**
AT4G20020	RIP8/MORF1	N/A	1.371018516	mitochondria
AT3G06790	RIP3/MORF3	N/A	1.312331489	mitochondria
AT1G32580	RIP5/MORF5	N/A	1.079728124	**mitochondria**
AT2G35240	RIP6/MORF6	N/A	1.388496915	mitochondria
AT2G33430	RIP2/MORF2	N/A	1.078368322	**plastid**

For these DEG, there is a significant enrichment in organelle gene ontology (GO) terms with regard to cellular component (**Figure 5.4 A**). Furthermore, several gene expression, signaling, and hormone response GO terms are significantly enriched

(**Figure 5.4 B and 5.4 C, Table S-5.3**). Notably, RNA binding is one one of the most signficantly enriched molecular functions (**Figure 5.4 C**), albeit likely underrepresented given that PPRs account for ~5% of DEG in this dataset (**Table S-5.1**). This underrepresentation is most likely due to misannotated entries of PPRs in public databases as used in AgriGO and REVIGO for this analysis, as previously noted [17]. In total, 51% of differentially expressed PPRs are P-type PPRs (**Table 5.2**), which are demonstrated to be involved in RNA metabolism but not directly in RNA editing [2]. The remaining 49% of PPRs are predicted or known RNA editing factors[17] (**Table 5.2**). PPR distribution and subcellular targeting in this dataset is similar to PPR distribution in the *Arabidopsis* genome [17,139]. In other words, there is no obvious enrichment for P-type or PLS-type PPRs, nor is the overrepresentation for chloroplastic or mitochondrial PPRs, however the proportion of differentially expressed editing type PPRs is greater in the chloroplast (**Figure 5.4 D**). Surprisingly, of the differentially expressed PPRs, all were upregulated in comparison to wild type, with notable exception of *lpa66* since the T-DNA insertion likely leads to destabilization of the transcript (**Table 5.2**). In addition, several non-PPR RNA editing factors were upregulated (**Table 5.2**). This PPRome-wide concomitant shift in expression suggest a possible link between oxidative stress sensing and RNA editing. Changes of peroxisomal genes was observed in our dataset (**Table S-5.1**) and suggest the peroxisome may integrate stress signals during organelle dysfunction[140]. However, proteomics data supports the chloroplast and mitochondria as playing a dominant role in the abiotic stress response—of 279 unique stress-responsive proteins, 73% and 22% were chloroplast and mitochondria localized, whereas 5% were from the peroxisome.

Chloroplast Polar Lipid and Oxylipin Levels are Modulated During RNA Editing Dysfunction

As an initial screen for lipid modification, we analyzed five week old *lpa66* and wild type Col-0 plants for changes in polar lipid composition, using multiple reaction mode mass spectrometry as previously described [141]. The polar lipid panel included phosphatidylglycerols (PG), phosphatidylinositols (PI), phosphatidylserines (PS), phosphatidylethanolamines (PE), phosphatidylcholines (PC), monogalactosyldiacylglycerols (MGDG), digalactosyldiacylglycerols (DGDG), phosphatidic acid (PA), and their lysophospholipid forms. The abundance and distribution of polar lipids in *Arabidopsis* is well documented in the literature, which facilitates the analysis of these species[142] . Several trends emerged from this analysis. The galactosyl

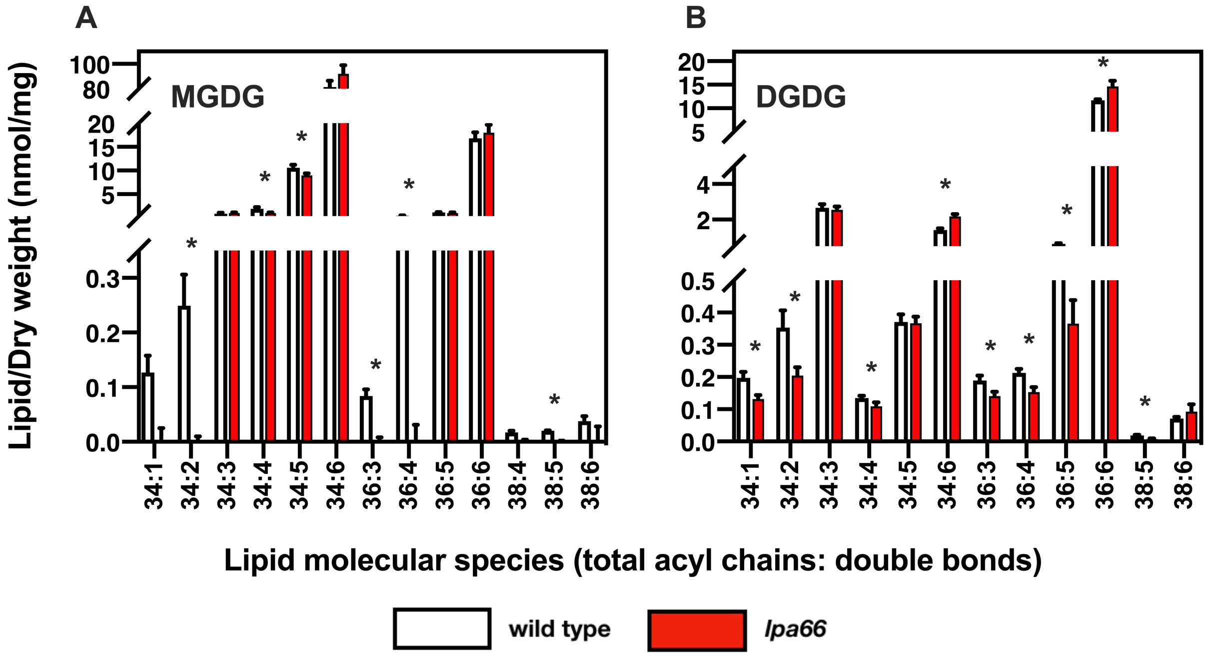


Figure 5.5 Concentration of chloroplast-specific polar lipid species in wild type (white) and *lpa66* (red) mutants. Five-week-old plants of each genotype were harvested for lipid analysis by ESI-MS/MS, which include **A**) monogalactosyldiacylglycerols (MGDG) and **B**) digalactosyldiacylglycerols (MGDG). Data are represented as mean concentration. Error bars represent the standard deviation (n=5). Asterisks represent significant differences in lipid species concentration between wild type and *lpa66* (adjusted p-value <0.01). Numbers to the right of the colon represent double bonds.

lipids, MGDG and DGDG, are the most abundant lipids found in plant cells and are only found in chloroplast membranes. We observed both classes of the chloroplast-specific galactosyl lipids to have several species with changes in saturation (**Figure 5.5**). Changes in fatty acyl chain saturation was seen in the phospholipid pool outside the chloroplast (here referred to as extrachloroplastic) (**Figure 5.6 C-E**) and lipids that are found in both the chloroplast and extrachloroplastic space (**Figure 5.6 A-B**). With the chloroplast-

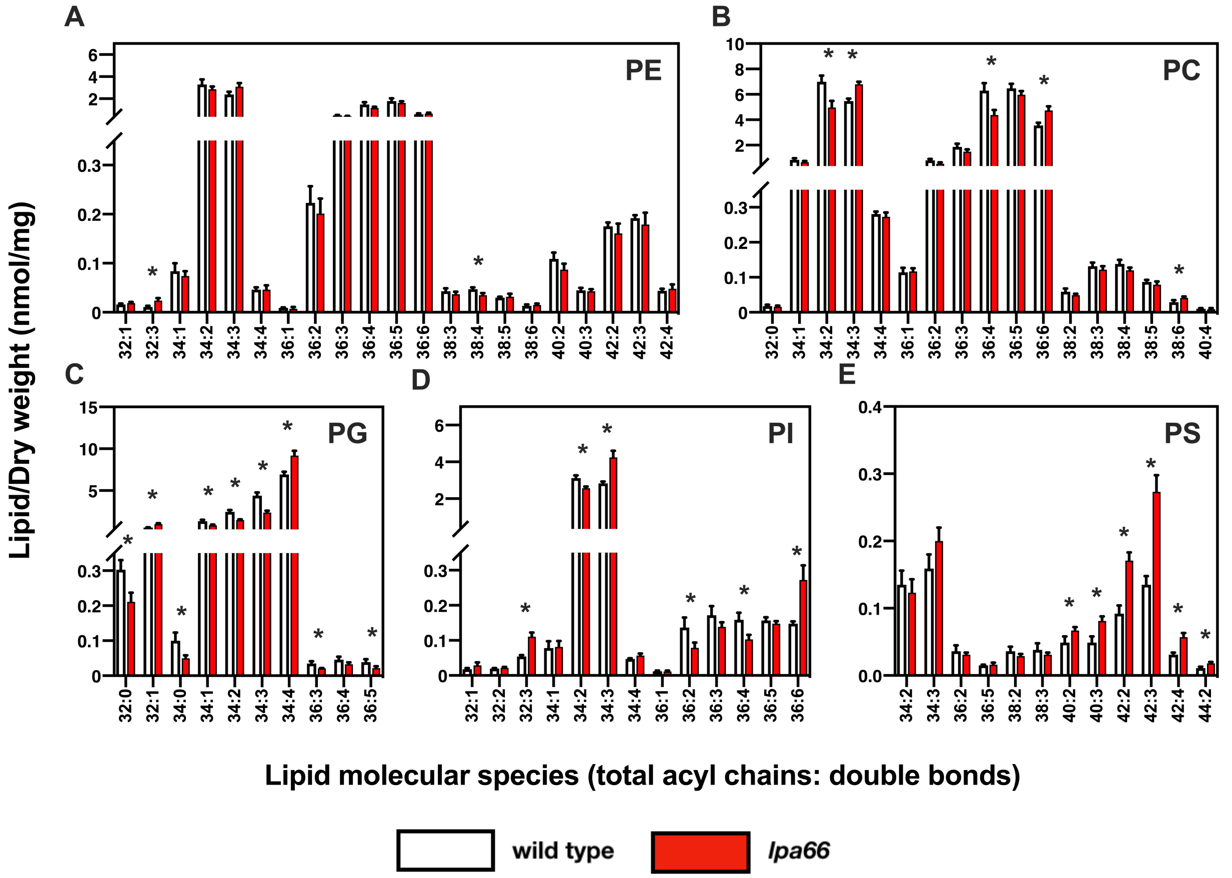


Figure 5.6. Concentration of chloroplast and extrachloroplastic polar lipid species in wild type and *lpa66* mutants. Five-week-old plants of each genotype were harvested for lipid analysis by ESI-MS/MS, which include **A**) phosphatidylethanolamines (PE), **B**) phosphatidylcholines (PC), **C**) phosphatidylglycerols (PG), **D**) phosphatidylinositols (PI), **E**) phosphatidylserines (PS). Data are represented as mean concentration. Error bars represent the standard deviation (n=5). Asterisks represent significant differences in lipid species concentration between wild type and *lpa66* (adjusted p-value <0.01). Numbers to the right of the colon represent double bonds. PE and PC are found in the chloroplast and extrachloroplastic space; PG, PI, and PS are strictly extrachloroplastic.

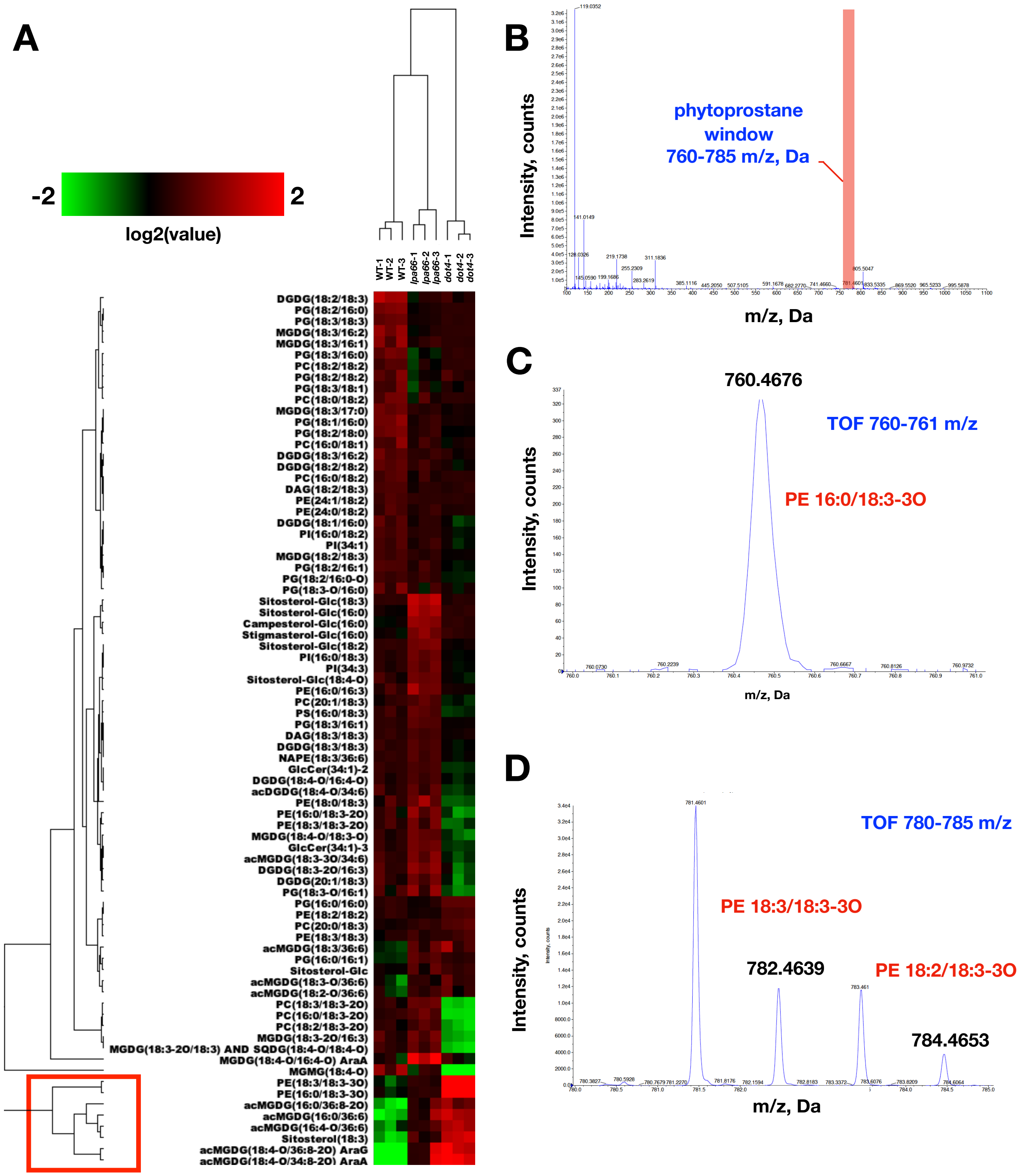


Figure 5.7. Oxylipin analysis and identification of putative lipid-derived RNA editing dysfunction signaling molecules. **A**) Heatmap analysis of 79 oxylipins, significantly modulated in *lpa66* mutant when compared to wild type. Lipid concentrations were $\log_2$ transformed. Rows were centered around the median. A Euclidean distance similarity metric was applied, and columns and rows were clustered by complete linkage using Cluster 3.0. Samples were visualized using TreeView3. **B-D**) Mass spectrometry analysis of putative phytoprostanes.

specific lipids, DGDG and MGDG, there is a general decrease in lipid saturation and a concomitant increase in lipid unsaturation (**Figure 5.5 A and 5.5 B**). This mimics the protective role the chloroplast membranes serves during stress [143]. Overall, there is a trend toward unsaturation, and this trend extends to the extrachloroplastic phospholipid pool including PG, PI, and PS (**Figure 5.6 C-E**), mitochondrial-derived cardiolipins (**Figure S-5.2**) and, to a smaller extent, to lipids that are represented in both the chloroplast and extrachloroplastic space (**5.6 A and 5.6 B**).

These results prompted us to interrogate further the observed lipid changes. Specifically, during RNA editing dysfunction, we suspect the chloroplast may create a strong oxidizing environment that causes the production of oxidized fatty acids (or oxylipins). To test this hypothesis, we determined the concentration of all oxylipins in the cell. In this analysis, we added a second RNA editing mutant to our pipeline to assess whether the molecular phenotype of lipid modulation can extend to other editing mutants.

We selected *defectively organized tributaries 4* (*dot4*) for this analysis for two reasons: 1) *dot4* is also a chloroplast-targeted editing factor, and 2) it exhibits a more dramatic macroscopic phenotype than *lpa66*, which may improve our threshold of detection of oxylipins produced during RNA editing dysfunction. In total, we identified 79 oxylipin species that were significantly modulated between wild-type, *lpa66*, and *dot4* (**Figure 5.7 A**), with a large percentage of MGDG and DGDG containing oxidized acyl modifications (**Figure S-5.1, Table S-5.6)**. Notably, the most abundant oxylipins in both mutants include Arabidopsides A and G, and putative phytoprostanes, PE(18:3/18:3-3O), PE(16:0/18:3-3O), that are both dramatically higher in the *lpa66* and *dot4* mutants than in wild type plants (**Figure 5.6 B**). The identity of the putative phytoprostanes were further interrogated by ESI-TOF-MS without fragmentation (**Figure 5.6 B, 5.6 C, 5.6 D**). The two previously identified putative phytoprostanes, PE(18:3/18:3-3O), PE(16:0/18:3-3O), were confirmed as well as phytoprostane-like oxylipin, PE(18:2/18:3-3O) (**Figure 5.6 D**). Lastly, ESI-TOF-MS with fragmentation was performed on these analytes and they produced the expected lysoPE fatty acid tails as determined by negative scans (data not shown). These results demonstrate that an extraordinary increase in lipid oxidation occurs in these two editing mutants, and is consistent with high levels of ROS (**Figure 5.1** and **Figure 5.2**), and robust ROS network and retrograde signaling network transcriptome responses (**Figure 5.3**, **Table S-5.1**).

Discussion

In the study, we demonstrated that *lpa66* mutants accumulate higher levels of H_2O_2 and superoxide anion in comparison to wild type Col-0 plants, as measured by reactivity with H_2DCFDA and nitroblue tetrazolium dye, respectively. These results demonstrate *lpa66* mutant plants experience a strong oxidative cellular environment and implicate H_2O_2 and superoxide anion as elevated redox active species (**Figure 5.1** and **Figure 5.2**). LPA66 is required for editing *PsbF* transcripts, which encodes an essential component of Photosystem II complexes in oxygenic photosynthetic organisms. *PsbE* and *PsbF* encode the alpha and beta polypeptides of cytochrome B559, which dimerize to form a redox active center that is closely associated with the core. Although cytochrome b_{559} is not directly involved in photosynthetic electron transport, it may be involved in secondary electron transfer reactions that helps to protect PSII from photodamage[144]. *Arabidopsis* plants with a *lpa66* null allele have a strong phenotype, which includes high chlorophyll fluorescence with impaired photochemical reactions associated with Photosystem II[133].

Earlier investigations have reported elevated ROS production in editing mutants[62–69], but these investigations focus mostly on whole plant physiological responses, and not how abscisic acid influences RNA editing in the cases where editing PPRs were studied [62,65,67,69]. In this study, gene expression and transcriptomic responses to editing dysfunction were analyzed by qPCR and RNAseq. A subset of ROS-responsive genes were assayed by qPCR (**Figure 5.3 A**), and a number of genes directly involved in ROS metabolism and oxidative protection were upregulated in *lpa66* mutant plants. In addition, RNAseq analysis of *lpa66* mutants revealed a substantial response of 66 ROS-responsive genes, which represents approximately 10% of all genes part of the ROS-responsive network (**Figure 5.3 B**, **5.3 C**, and **Table S-5.1)**[47]. This result is highly significant because the ROS-responsive gene network was developed by Willems et al. as a large scale meta-analysis of redox perturbations from 79 microarray studies, and represents a reproducible reference set of ROS responsive genes[47]. Thus, elevated ROS detected in mutant plants leads to changes in gene expression that upregulates ROS network genes, and further emphasizes that ROS production is an important process in editing mutants, and results in massive changes in gene expression. Transcriptomic analysis of the *lpa66* mutant and the massive upregulation of PPRs and editing related genes highlights an important link between editing and nuclear gene expression not previously reported.

Thus, there appears to be a signaling pathway that links editing dysfunction to changes in gene expression that include both ROS responsive genes and editing-related genes. While the editing mutant *lpa66* had a robust ROS network response, ROS are highly reactive and short-lived, and make unlikely candidates for signaling molecules[48].

ROS are highly reactive with other molecules such as proteins and lipids, and secondary products derived from cellular components are much more likely signaling molecules. We reasoned that these would primarily be lipid-derived, given that most RNA editing targets are membrane-associated proteins in electron transport, and disruption of a number of these complexes would elevate ROS production (**Table 5.1**). A general trend of lipid unsaturation was detected in the polar lipid pool that includes chloroplast-specific galactosyl lipids and cellular phospholipids (**Figure 5.5**). We also identified 79 modulated oxylipins, which are produced from lipid oxidation reactions (**Figure 5.7 A**). From this dataset, we identified four oxylipins, Arabidopside A and G and two putative phytoprostanes, which are strong candidates for retrograde signaling molecules. Arabidopsides A and G are MGDG derivatives that contain two or three cis-12-oxo-phytodienoic acid (OPDA) moieties. OPDA is produced enzymatically by LOX3, a chloroplast lipid peroxidase, that initiates the Jasmonic Acid (JA) biosynthetic pathway[145]. OPDA has been shown to directly act as a growth regulator, and JA is a potent stress response hormone[146]; thus, Arabidopsides may function as a storage pool to release OPDA for signaling, or as a substrate for JA biosynthesis [147,148].

In addition to the enzymatically produced OPDA containing Arabidopsides, a non-enzymatic route of oxylipin formation is triggered by ROS to produce oxidized lipids including phytoprostanes and hydroxy fatty acids[149–151]. Singlet oxygen production has been shown to be an important source of ROS for phytoprostane production in chloroplasts[59]. Two putative phytoprostanes were highly elevated in the phosphoethanolamine pool in the editing mutants, PE(18:3/18:3-3O), PE(16:0/18:3-3O). Phytoprostanes are structurally similar to OPDA , but include an α,β-unsaturated carbonyl

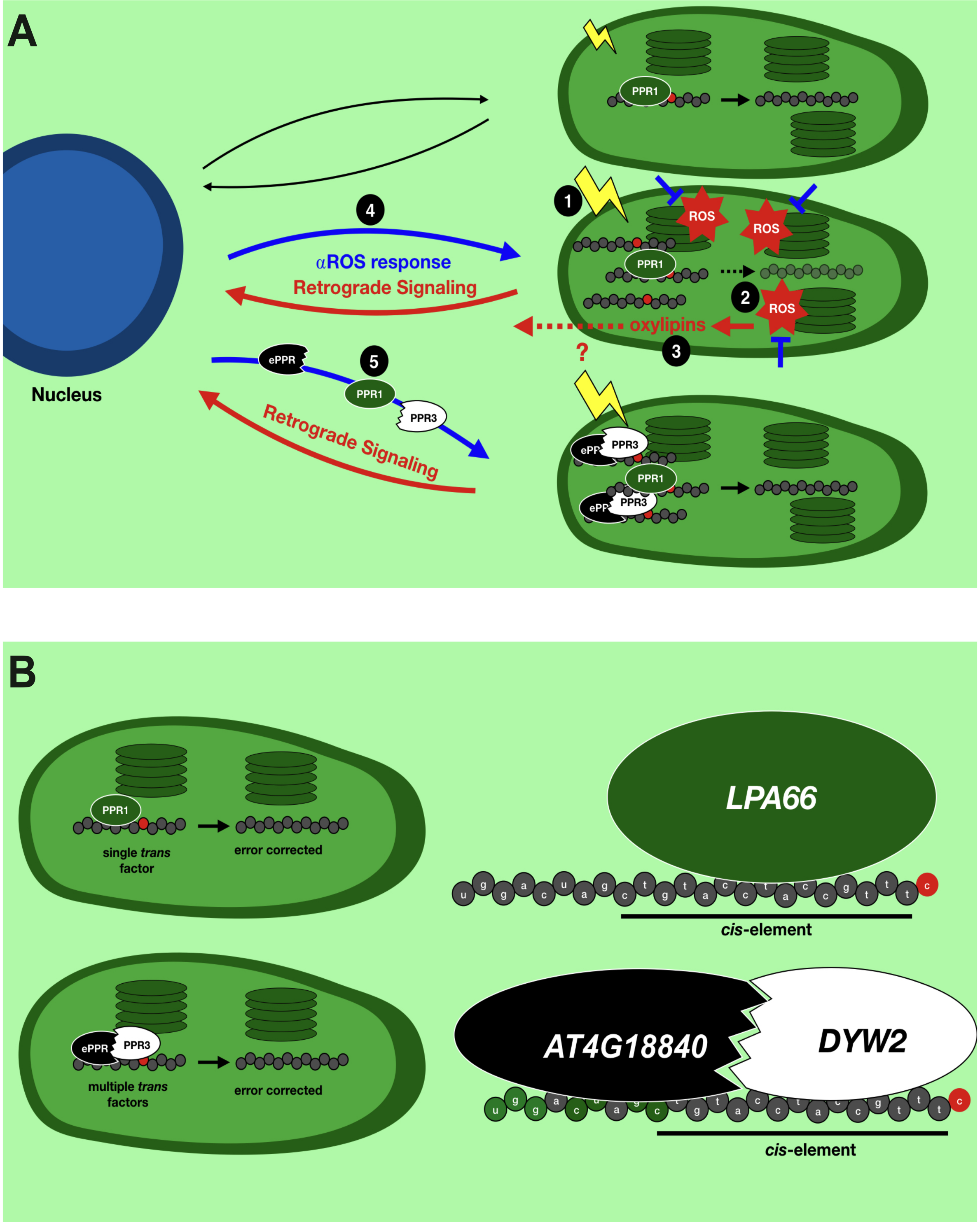


Figure 5.8. A model for *trans*-acting RNA editing interactions and retrograde signaling during RNA editing dysfunction. A) In wild type plants, PPRs are able to edit RNA unabated. (1) When the chloroplast experiences oxidative stress (*lpa66* mutant which is a high-light stress mimic), (2) ROS accumulates, which can (3) generate oxylipins. These oxylipins in turn (4) drive retrograde signaling recruited anti-ROS genes, as well as *trans*-editing factors to support RNA editing. B) Classic model (Top) of RNA editing where a PPR binds to a cis-element ahead of the edited cytidine which is converted to uridine by deamination. (Bottom) The trans-editing model involved an E-type PPR that lacks a catalytic domain and a DYW type PPR that lacks an RNA binding domain. Together these proteins can support at sites new sites, or sites edited by other factors. In this example, AT4G18840 and DYW2 support editing at *psbF*, the target sites for LPA66.

structure that renders them highly reactive electrophilic species (RES). Phytoprostanes induce production of secondary metabolites and activate stress response genes that protect cells from subsequent oxidative stress[152–154]. In addition to the ROS responsive genes, we observed a robust retrograde signaling network response of 183 genes. In future studies, it will be interesting to delineate the relationship between the production of these potent lipid-derived signaling molecules, and the robust retrograde signaling response. It will be important to distinguish whether the Arabidopsides are directly involved in signaling or serve as a source of JA synthesis. Alternatively, signaling may rely on OPDA[146]. It will be interesting to determine the functional consequence of the putative phytoprostanes produced in our dataset. In addition to the biochemical detection of ROS production (**Figure 5.1** and **5.2**) and the transcriptome changes (**Figure 5.3**), production of putative phytoprostanes is a direct confirmation of lipid reactivity with ROS in the chloroplast, since phytoprostanes are produced by a non-enzymatic, free radical-catalyzed pathway[155], unlike Arabidopsides. Furthermore, it will be important to analyze several editing mutants from *Arabidopsis* as well as editing mutants in other land plants to see if this relationship is evolutionary conserved. Since Arabidopsides are only found in *Arabidopsis*, it will be important to determine the concentration of free OPDA and phytoprostanes. An Arabidopside-independent response is conceivable since OPDA can serve as a signaling molecule and enzymes involved in the synthesis of JA from OPDA are found from algae up through higher land plants[155,156].

Potential signaling pathways are shown in **Figure 5.8**. In **Figure 5.8 A**, the top chloroplast depicts RNA editing under non-stressed circumstances. The chloroplast experiences intermediate levels of stress and does not require a robust ROS response and editing is managed by the extant editing factors. During increased stress (**Figure 5.8 A**, **middle chloroplast**), chloroplast function is disrupted, including RNA editing, and requires retrograde signaling to the nucleus to mitigate oxidative stress and recover homeostasis in RNA editing. In this model, oxylipins serve as the primary retrograde signaling factor, although other retrograde signaling factors may be involved. Under these circumstances, the nuclear expression of *trans*-acting editing factors are important as they are capable of supporting editing at many editing sites. In addition to site specific editing factors, e.g. PPPR1/LPA66 (**Figure 5.8 A**, **5.8 B**), ePPR and PPR3 are expressed which together can complement the function of PPR1 (**Figure 5.8 A**, **bottom chloroplast**). In this model, ePPR is an e-type PPR that lacks a functional deaminase domain (**Figure 1.1 A**), where PPR3 is a PPR with a reduced RNA binding domain (**Figure 1.1 A**). Perhaps one or both pathways are involved in the RNA editing dysfunction response. Both ODPA and phytoprostanes can be synthesized to purity[155,157], which should be tested alongside JA, which is commercially available, to test if PPRome responses can be modulated, since editsome formation appears to be dynamic[34,35]. In addition, the consequence of polar lipid acylation (**Figure S-5.1**) should be investigated further as head group acylation may serve as a storage for signaling precursors, subsequently released by phospholipase family enzymes[158].

Researchers recently identified that disruption of *DYW2*, a DYW-type PPR with a degenerate RNA binding domain, affects editing at numerous E+ editing sites [34]. This was an intriguing observation, since E+ PPRs lack the ability to edit their target sites because they do not possess a DYW domain. Instead, it was hypothesized at the time, that a deaminase domain would need to be recruited in *trans*, to support editing and it appears DYW2 fits this role. These researchers demonstrated that DYW2, in complex with the E-type PPR, CLB19, and an accessory protein, NUWA, interact with one another to form a complex. This prompted us to search for possible *trans* editing factors in our dataset. We identified 49 editing type PPRs in our dataset, of which 17 are targeted to the chloroplast. From this subset, 6 PLS type PPRs lacking a DYW domain were identified. According to the updated PPR Code[129], AT4G18840 could identify a region upstream of the *psbF* cis-element—the editing target of LPA66. Interestingly, DYW2 was also upregulated in our dataset, suggesting the possibility that AT4G18840 and DYW2 can support editing of *psbF* in the absence of LPA66 (**Figure 5.8 B**). However, we were unable to detect editing of *psbF* in our samples and have not tested this interaction directly. It is possible that there is a spatiotemporal window which we are unaware of, and it would be prudent in future studies to comprehensively assay editing activity in mutants where *trans*-editing is thought to occur, especially since differential editing has been observed, at least in a tissue-specific manner [159]. Overall, we propose a model where, in cases of RNA editing dysfunction, ROS accumulation drives oxylipin production, triggering a potent retrograde signaling response that help ameliorate oxidative stress, but also drives PPRome response to support RNA editing in *trans* (**Figure 5.8 A and 5.8 B**). These results open a new avenue of research for the plant RNA editing field.

Statement of contribution

This chapter is in preparation for publication. I generated all the plant materials for this study. I generated the data for this study. I wrote the chapter with Dr. Michael Mulligan.

Chapter 6: Concluding Remarks and Future Directions

Concluding Remarks

RNA editing was discovered in plants in 1989, with the simple observation that mitochondrial messenger RNA sequences did not match the genomic sequence[6]. Instead, cytidines were converted to uridines in the mature transcript. This had important implications, as the nucleotide polymorphism led to a non-synonymous substitution, which corrected the polypeptide sequence so that it maintained protein sequence conservation among plants. For this reason, and because of the absence of a compelling example to the contrary, RNA editing in plants appears to be a genetic correction mechanism. It is possible that RNA editing has a regulatory role in protein diversity as seen in other RNA editing systems [115], since both edited and unedited translation products have been reported in plants [119,120]. However, unedited translational products have not been reported to accumulate in mature complexes [1] and have no established role and function, a regulatory role for RNA editing remains a formal possibility.

Nonetheless, substantial progress has been made in understanding RNA editing in plants since the 1980s. Researchers identified many instances of RNA editing in the mitochondria, culminating in the discovery of over 400 unique editing sites [124]. RNA editing as a biochemical phenomenon of the mitochondria was later extended to chloroplasts [160]. By the 2000s, researchers began searching for trans factors involved in the editing reaction. In 2005, the first RNA editing trans factor was identified [82]. Chlororespiratory reduction 4 (CRR4) was a protein that contained numerous pentatricopeptide repeat domains. The structure and function details were unclear at that time, but its domains shared architecture with nearly 500 other genes in Arabidopsis of the plant combinatorial and modular protein family, which would later be reclassified as the pentatricopeptide repeat protein (PPR) family 14. The PPR family has tremendous diversity in domain architecture (Figure 1.1), which initially made it difficult to understand how these genes were involved in editing. Approximately 60% (283 genes) of the PPRs were P-type and expected to be involved in RNA stabilization, while the remaining 40% (213 genes) were PLS-type and involved in RNA editing 17. For the remainder of the 2000s and into the early 2010s, researchers had identified numerous PPRs involved in RNA editing with varying domain architecture 2,36, which began to refine our understanding of the role of PPRs in the editing reaction. It turned out that approximately 40% (91 genes) of all editing type PPRs have motifs in the C-terminal domain that have key features in common with other cytidine deaminases [20,87]—a highly conserved HXE motif bearing a catalytic glutamate residue, and a CXXC motif which is critical for divalent cation binding (X is any amino acid)[20,88]. These motifs are part of the active site of cytidine deaminases, which together participate in a proton shuttling mechanism that results in cytidine-to-uridine conversion[88].

I first set out to determine if the highly conserved regions of PPRs are critical for editing. Our experimental system consisted of transfer-DNA (T-DNA) insertional mutant Arabidopsis plants generated by the Salk Institute [161]. We bred these plants to homozygosity, to generate a null homozygous mutant. Using a null mutant of a given PPR, we studied the function of the mutant gene by overexpressing the wild type or modified gene in the null plant with a Cauliflower Mosaic Virus 35S (CaMV 35S) promoter-driven transgene system. With this system, we expressed wild type and variants of the wild type gene to determine domain function. In Chapter 3 we investigated the function

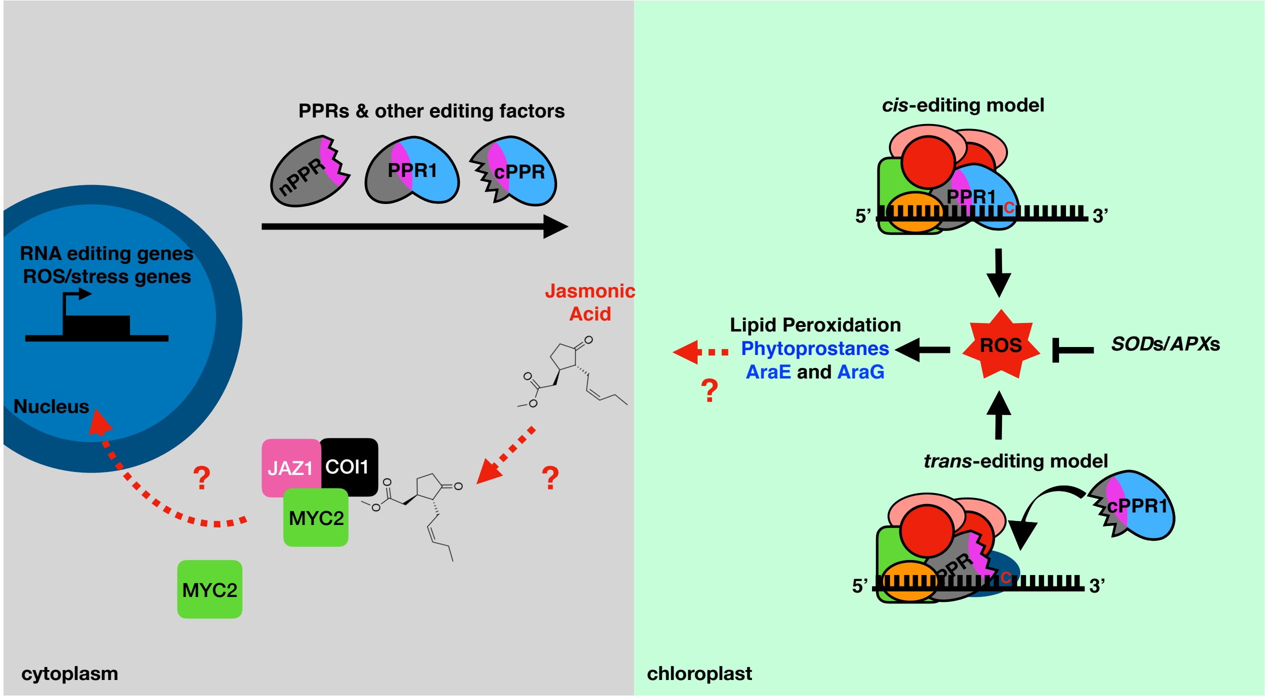


Figure 6.1 Model for RNA Editing Reaction and Regulation Via Organelle Derived Retrograde Signals. (**Right to Left**) RNA editing requires several *trans*-acting proteins. These include PPO1 (pink), NUWA (navy blue), trans-editing model only), and RIPs (red) are non-RNA binding proteins. Both NUWA and PPOI form interactions with RIP family proteins. RIP can form homodimers. PPRs (gray/pink/light blue), ORRMs (green) and OZs (orange) are RNA binding proteins. OZs and ORRMs interact with each other and with RNA. PPRs interact with RNA as well as non-RNA binding proteins NUWA and RIPs. In addition, PPRs and OZs can form homodimers. Two models for the RNA editing reaction are supported by the work in **Chapter 3** and **Chapter 4**. The *cis*-editing model uses a PPR with an intact RNA binding domain and DYW deaminase domain in one protein. In the trans-editing model, an E/E+ type PPR without a deaminase domain (nPPR, n means N-terminus) interacts with a DYW-type PPR with a reduced DYW deaminase domain to edit together (cPPR, c means C-terminus, e.g *MEF8*). In each model, several non-PPR proteins are thought to function as a scaffold this model is supported by genetic, molecular and biochemical data. In **Chapter 5**, we demonstrated that during RNA editing dysfunction, reactive oxygen species accumulate. Over 1,500 genes are differentially expressed in an editing mutant when compared to wild type plants using a stringent adjusted p-value of <0.001. Hundreds of these genes have been identified as genes involved in retrograde signaling and mitigating oxidative stress. In addition, 91 PPR genes are upregulated in the editing mutant, about 50% (49) which are considered editing type PPRs, of which 30 genes are thought to participate in *trans*-editing reactions. In Figure **5.8 B**, we propose a pair of genes as being able to compensate for losses in the *lpa66* mutant background under the *trans*-editing model, based off bioinformatics prediction of RNA binding and upregulation of a *DYW2*, a PPR with similar characteristics to *MEF8* (**Chapter 4**). Lastly, in Chapter 5 we identified 79 oxylipins which are modulated in PPR mutant backgrounds (i.e. *dot4* and *lpa66*). These include Arabidopsides (AraE and AraG) as well as phytoprostanes, produced by enzyme-dependent and enzyme-independent (i.e. ROS) mechanisms, respectively. These lipid derived molecules are retrograde signaling molecules in their own right, but also serve as precursors for jasmonic acid, a potent retrograde signaling molecule. It is well known that Jasmonic acid interacts with COI1 in the cytoplasm, and releases a MYC2 transcription factor from JAZ1 repression. MYC2 translocates to the nucleus to alter gene expression in response to several stress responses. We hypothesize a similar mechanism may underpin organelle-to-nuclear (retrograde) signaling during RNA editing dysfunction. In response, the cell increases expression of trans-acting PPRs to support RNA editing.

of chloroplast PPRs, while in Chapter 4 we focused on a mitochondrial PPR. In Chapter 3, we generated C-terminal truncations that helped us confirm that the DYW domain is critical for RNA editing, in most cases. We followed up this observation in Chapter 3 and Chapter 4 by investigating the role of the highly conserved glutamate residue of the HXE motif and found that without it, plants could not participate in C-to-U conversion. In Chapter 3 we also found that in addition to the N-terminal RNA binding domain and the C-terminal DYW domain of PPRs, a highly conserved region which we referred to as the PG box, is critical for editing in all our tested cases. We propose that this domain is critical for trans factor protein-protein interactions (Figure 1.4, and summarized in Figure 6.1), although we were not able to test this hypothesis directly. However, this observation helped refine our experimental design for Chapter 4.

I focused my investigation for Chapter 4 on a PPR with a markedly different domain architecture when compared to other PPRs—it had an unusually short N-terminal RNA binding domain. At the time, it was clear that the RNA binding domain of PPRs was critical for positioning the PPR in close proximity to the edited cytidine in the mature transcript [2,162]. We therefore hypothesized that our unusual PPR, Mitochondrial Editing Factor 8 (MEF8), would have profound effects on editing in the mitochondria since it had reduced RNA binding capacity and might therefore edit many sites (Figure 6.1, cPPR). Of the hundreds of editing sites found in the mitochondria, over 10% (60 cytidines) were affected by loss-of-function MEF8 mutants, representing an unprecedented number of editing defects for a PPR. Simultaneously, two other labs discovered editing defects of many sites by DYW2 34,35, which shares a reduced N-terminal RNA binding domain with MEF8. In addition, a growing list of non-PPR RNA editing factors were being discovered at a rapid pace that also had effects on many sites 7 (Figure 1.5 and summarized in Figure 6.1). My colleagues and I posited that the non-PPR factors being discovered in combination with the panoply of PPR variants come together to form high-molecular editing complexes, with PPRs at the core of the complex and the other proteins serving as a scaffold [7,126] (Figure 1.5 and summarized in Figure 6.1) Borne out of these hypotheses, I became interested in understanding how such an enigmatic process would be regulated.

RNA editing in plants is restricted to the chloroplast and mitochondria. It is therefore not surprising that a majority of the transcripts affected by RNA editing occur in genes associated with the electron transport chain (ETC) of each organelle 5 (Table 5.1). I suspected that during RNA editing dysfunction, reactive oxygen species (ROS) would be produced, as a consequence of unedited transcript accumulation and non-synonymous amino acid substitutions present in the translational products. Several scenarios are possible: either the unedited translation product accumulates in mature complexes, the mutant translation product is recognized and degraded by organelle machinery, or failure to assemble unedited translation products could cause depletion of core complexes. Previous reports suggest that unedited translation products accumulate [119,120], but they have not been found in mature complexes [163], therefore suggesting that ETC would be negatively impacted by the absence of an entire protein and lead to ROS accumulation. I speculated that the cell co-opts the intimate association between ETC flow and ROS accumulation to regulate RNA editing reactions. For example, several organelle lipid-derived signaling molecules are produced during oxidative stress by enzyme-dependent and ROS-dependent mechanisms. I hypothesized that similar molecules may be produced during RNA editing dysfunction. Indeed, I found ROS accumulation occurs during RNA editing dysfunction, as well as the accumulation of several lipid-derived signaling molecules (Chapter 5). In addition, we observed large numbers of differentially expressed genes, many of which are involved in mitigating oxidative stress, as well as a large number of RNA editing factors. I suspect the cell may use these and other retrograde signaling molecules to communicate RNA editing dysfunction to the nucleus as a way to recruit additional editing factors and ultimately prevent incorrect messages from being produced. This work was the focus of Chapter 5 and, while it is mostly descriptive, it lays the foundation for investigating nuclear regulation of organelle function as it pertains to RNA editing (Figure 6.1).

Future Directions: Characterization of the DYW Deaminase Domain, Regulation of RNA Editing, and cis/trans-Network Interactions

The work I present in Chapter 3 and Chapter 4 provide strong support for the DYW deaminase domain of PPRs being responsible for C-to-U catalysis. Our lab and others have published these observations with similar results, suggesting the highly conserved features of the DYW deaminase domain are indeed critical for editing [22–24,77]. However, some researchers remain skeptical, since a large number of proteins are involved and the requirement for the DYW deaminase has not been demonstrated with an in vitro biochemical reaction [89]. This criticism is not lost on us, and several attempts have been made by our lab and others to create an in vitro editing system, although to no avail. Researchers have performed in vitro editing in undefined systems of mitochondria or chloroplast extracts using synthetic RNA substrates [101,164,165]. Not only is editing dependent on the addition of cofactors [76,101,164], but it appears it may involve several trans-acting factors whose stoichiometries remain unknown [7,128] and it is possible additional factors have yet to be discovered. This would explain why attempts to recreate the plant editing reaction in vitro have failed—there are too many factors in unknown quantities.

Attempts to define complex members have been indirect using genetic strategies as we and others have done in Chapter 3 and Chapter 4, or qualitative using bait-based mass spectrometry techniques [126]. Still, other methods are available to delineate protein stoichiometries to better inform these in vitro reactions in the future. These include cryogenic electron microscopy (cryo-EM), cross-linking mass spectrometry (CX-MS)[166,167] and MS of intact multiprotein complexes (native MS)[168] . These strategies in combination were successful in elucidating the composition of the 2.5 MDa 26S proteasome [169], which is similar in size to the expected range of RNA editing complexes (~0.8-5Mda). It addition, the 26S proteasome is heterogeneous in its structural composition, which includes up to 25 different subunits in its regulatory particle[169], suggesting the composition of multitudinous PPR editing complexes can be resolved by the same strategy. These biochemical techniques in parallel with two-hybrid studies, pull downs, comparative modeling, and bioinformatics were critical for determining the structure of the 26S proteasome. Researchers in our community could benefit from using the same pipeline simultaneously and collaboratively, instead of in isolation as has been done up to this point [11–13,35,38,39,41–43,43,44,126,127,170–172,172,173]. Lastly, using a tagging strategy may help identify stable and transient interaction partners. One promising strategy is the biotin ligase ID (BioID) technique developed in mammalian cells [174,175]. Briefly, chimeras of PPR-BioID can be developed and expressed as transient or stable products, in a constitutive or inducible manner. With this technique, a PPR targeted to the mitochondria or chloroplast, and in the presence of native biotin, will biotinylate proteins in close proximity, which can be subsequently resolved using streptavidin-tagged beads, 2D gel electrophoresis, and mass spectrometry. This strategy has the advantage of not employing the specialized proteomic techniques mentioned previously, that may only be available at certain institutions.

In Chapter 3, we also determined that a highly conserved region between the N-terminal RNA binding domain and C-terminal DYW domain was critical for editing. We referred to this region as the PG box21,23. We speculated this region is critical for RNA editing, since C-terminal truncations of the DYW domain do not always result in loss of editing (Figure 3.2 C). By removing the PG box, we eliminated editing in each of our test cases (Figure 3.2). The importance of the PG box in protein-protein interactions was later substantiated by other researchers who were interested in studying the role of the E/E+ domain (Figure 1.1)—the PG-box is a small region of the somewhat conserved larger E/E+ domain. It was discovered the E/E+ domain is critical for PPR-RIP/MORF interactions [171]. Still, whether PPRs interact with RNA as monomers or multimers needs to be clarified. Recently, crystal structures of PPRs have revealed they may interact as homodimers 12,13, whereas the solution state structure and designer-PPR structures are monomeric [114,170]. Either way, it appears RIP/MORF interactions with E/E+ domains of PPRs are critical for multimer formation as well as enhancing RNA binding [173]. It will be important to identify critical residues in the E/E+ that confer protein-protein interactions, which will allow us to detangle the complex interaction network that lies ahead. Our lab and others have narrowed down the region to focus on with the PG box 23,24. Now, it is just a matter of performing scanning alanine mutagenesis on the highly conserved residues to nail down the most critical amino acids that support trans interactions.

In Chapter 4, we discovered that MEF8 affects editing at many sites. Since MEF8 has a reduced RNA binding domain, we speculated that it must interact with other PPRs, most likely of the E/E+ type, which lack a deaminase. Support for this hypothesis was published simultaneously with our discovery in which a PPR with a reduced RNA binding domain was involved in editing many sites and interacting with E/E+ type PPR 34,35. These observations provide support for the trans editing model; however, it will be important to identify interaction partners for MEF8. This will be challenging, since E/E+ type PPRs have not been identified for the sites that MEF8 affects. Researchers will need to continue characterizing mitochondrial and chloroplast PPRs to uncover the complex network of RNA editing factors.

The accepted dogma in the plant RNA editing is that it functions as a genetic correction mechanism. It is still possible, however, that it acts as a regulatory mechanism, since partially edited sites have been observed in the mitochondria. In addition, we saw evidence of increased editing in the absence of MEF8 at several sites, suggesting some compensatory regulation (Figure 4.4). Also, as previously mentioned, unedited translation products have been observed in ribosomal fractions[119,120]. To address the possibility that RNA editing is regulatory, researchers will have to analyze proteomes of the chloroplast and mitochondria, and selectively enrich fractions that are abundant unedited translation products. Fortunately, it is possible to raise antibodies that can distinguish between edited and unedited translation products [119,120]. By combining previously discussed CX-MS with antibody-based enrichment[176], one could selectively enrich an unedited translation product and determine if it accumulates in mature complexes. This strategy would help resolve the speculation into a possible regulatory role for RNA editing in plants.

In Chapter 5, we demonstrated that lpa66 mutants accumulate higher levels of H2O2 and superoxide anion in comparison to wild type Col-0 plants, as measured by reactivity with H2DCFDA and nitroblue tetrazolium dye, respectively. ROS accumulation has been reported in other PPR studies [62–69], yet these investigations mostly focus on whole plant physiological responses, and not how ABA influences RNA editing in the cases where editing PPRs were studied [62,65,67,69]. In this study, we assayed a subset of ROS-responsive genes [46], and demonstrate that they were upregulated in comparison to wild type. In addition, we employed RNAseq to provide a transcriptome snapshot of RNA editing dysfunction, which revealed a substantial ROS response of 66 ROS network genes as described by Willems et al, 2016 (Figure 5.3 C). It is possible that some previously identified ROS-responsive genes were missed in our comparison. However, using Willems et al.[47] dataset as a reference for comparison was a prudent approach, considering they systematically culled data from 79 redox homeostasis perturbation microarray studies and identified a reproducible core set of ROS responsive genes to use as a reference.

Despite having a robust ROS network response, we did not suspect that ROS signaling was the primary or only mechanism for retrograde control of RNA editing dysfunction, primarily due to the transient nature of ROS[48]. Instead, we suspected ROS reacts with other molecules, such as proteins and lipids, which subsequently drives the retrograde signaling response. We reasoned that these would primarily be lipid-derived, given that most RNA editing targets are membrane-associated proteins in electron transport, and disruption of a number of these complexes would exacerbate ROS production (Table 5.1). We found that unsaturation was a general trend inside and outside of the chloroplast (Figure 5.5). We also identified 79 significantly modulated oxylipins (Figure 5.7 A). From this dataset, we identified Arabidopside A and G, as well as two putative phytoprostanes, all which are signaling molecules, and the former which contain OPDA moieties, that can serve as precursors for the potent stress response hormone, jasmonic acid (JA) [146]. In addition to the ROS responsive genes we observed, there was also a robust retrograde signaling network response of 183 genes. In future studies, it will be important to delineate the relationship between the production of these potent lipid-derived signaling molecules and the robust retrograde signaling response. It will also be important to determine if the Arabidopside-OPDA sink we observed is consequential for JA signaling, or a JA-independent OPDA driven signaling response [146]. Lastly, it will be interesting to determine the functional consequence of the putative phytoprostanes produced in our dataset. Production of putative phytoprostanes confirms that there is ROS production in the chloroplast, since phytoprostanes are produced by a non-enzymatic, free radical-catalyzed pathway[155], unlike Arabidopsides. Furthermore, it will be important to analyze several mutants from *Arabidopsis* as well as editing mutants in other land plants to see if this relationship is evolutionary conserved. Since Arabidopsides are only found in *Arabidopsis*, it will be interesting to see if free OPDA and/or phytoprostanes levels are high in editing mutants since it is known that OPDA can serve as a signaling molecule, and enzymes involved in the synthesis of jasmonic acid from OPDA are found from algae up through higher land plants[155,156]. Perhaps one or both pathways are involved in the RNA editing dysfunction response. Both ODPA and phytoprostanes can be synthesized to purity[155,157], which should be tested alongside JA, which is commercially available, to test if PPRome responses can be modulated, since editsome formation has been now been confirmed and appears to be dynamic[34,35]. In addition, the consequence of polar lipid acylation (Figure S-5.1) should be further investigated, as head group acylation may serve as a storage for signaling precursors, subsequently released by phospholipase family enzymes[158].

Researchers recently identified that disruption of DYW2, a DYW-type PPR with a degenerate RNA binding domain, affects editing at numerous E/E+ editing sites [34]. This was an intriguing observation, since E+ PPRs lack the ability to edit their target sites since they do not possess a DYW domain. Instead, it was hypothesized at the time that a deaminase domain would need to be recruited *in trans* to support editing, and it appears DYW2 fits this role. These researchers demonstrated that DYW2, in complex with the E-type PPR, CLB19, and an accessory protein, NUWA, interact with one another to form a complex. This prompted us to search for possible *trans* editing factors in our dataset. We identified 49 editing type PPRs in our dataset, of which 17 are targeted to the chloroplast. From this subset, 6 PLS type PPRs lacking a DYW domain were identified. According to the updated PPR Code[129], AT4G18840 could identify a region upstream of the *psbF* cis-element—the editing target of LPA66. Interestingly, DYW2 was also upregulated in our dataset, suggesting the possibility that AT4G18840 and DYW2 can support editing of *psbF*, in the absence of LPA66 (**Figure 5.8 B**). However, we were unable to detect editing of *psbF* in our samples and have not tested this interaction directly. It is possible that there is a spatiotemporal window which we are unaware of, and it would be prudent in future studies to comprehensively assay editing activity in mutants where *trans* editing is thought to occur, especially since differential editing has been observed, at least in a tissue-specific manner [159]. Overall, we propose a model where in cases of RNA editing dysfunction, ROS accumulation drives oxylipin production, triggering a potent retrograde signaling that help ameliorate oxidative stress, but also drives PPRome response to support RNA editing in *trans* (**Figure 5.8 A, 5.8 B**, and summarized in **Figure 6.1**)

.

References

1. Wijk, K. J. van & Baginsky, S. Plastid Proteomics in Higher Plants: Current State and Future Goals. *Plant Physiol.* **155**, 1578–1588 (2011).
2. Barkan, A. & Small, I. Pentatricopeptide Repeat Proteins in Plants. *Annu. Rev. Plant Biol.* **65**, 415–442 (2014).
3. Chateigner-Boutin, A.-L. & Small, I. A rapid high-throughput method for the detection and quantification of RNA editing based on high-resolution melting of amplicons. *Nucleic Acids Res.* **35**, e114–e114 (2007).
4. Bentolila, S., Elliott, L. E. & Hanson, M. R. Genetic Architecture of Mitochondrial Editing in Arabidopsis thaliana. *Genetics* **178**, 1693–1708 (2008).
5. Bentolila, S., Oh, J., Hanson, M. R. & Bukowski, R. Comprehensive High-Resolution Analysis of the Role of an Arabidopsis Gene Family in RNA Editing. *PLoS Genet.* **9**, e1003584 (2013).
6. Gualberto, J. M., Lamattina, L., Bonnard, G., Weil, J. H. & Grienenberger, J. M. RNA editing in wheat mitochondria results in the conservation of protein sequences. *Nature* **341**, 660–662 (1989).
7. Sun, T., Bentolila, S. & Hanson, M. R. The Unexpected Diversity of Plant Organelle RNA Editosomes. *Trends Plant Sci.* **21**, 962–973 (2016).
8. Barkan, A. *et al.* A Combinatorial Amino Acid Code for RNA Recognition by Pentatricopeptide Repeat Proteins. *PLoS Genet.* **8**, e1002910 (2012).
9. Takenaka, M., Zehrmann, A., Brennicke, A. & Graichen, K. Improved Computational Target Site Prediction for Pentatricopeptide Repeat RNA Editing Factors. *PLoS ONE* **8**, e65343 (2013).

10. Yagi, Y., Hayashi, S., Kobayashi, K., Hirayama, T. & Nakamura, T. Elucidation of the RNA Recognition Code for Pentatricopeptide Repeat Proteins Involved in Organelle RNA Editing in Plants. *PLoS ONE* **8**, e57286 (2013).
11. Ban, T. *et al.* Structure of a PLS-class Pentatricopeptide Repeat Protein Provides Insights into Mechanism of RNA Recognition. *J. Biol. Chem.* **288**, 31540–31548 (2013).
12. Ke, J. *et al.* Structural basis for RNA recognition by a dimeric PPR-protein complex. *Nat. Struct. Mol. Biol.* **20**, 1377–1382 (2013).
13. Yin, P. *et al.* Structural basis for the modular recognition of single-stranded RNA by PPR proteins. *Nature* **504**, 168–171 (2013).
14. Lurin, C. Genome-Wide Analysis of Arabidopsis Pentatricopeptide Repeat Proteins Reveals Their Essential Role in Organelle Biogenesis. *PLANT CELL ONLINE* **16**, 2089–2103 (2004).
15. Kindgren, P., Yap, A., Bond, C. S. & Small, I. Predictable Alteration of Sequence Recognition by RNA Editing Factors from Arabidopsis. *Plant Cell Online* **27**, 403–416 (2015).
16. Okuda, K. *et al.* Quantitative analysis of motifs contributing to the interaction between PLS-subfamily members and their target RNA sequences in plastid RNA editing. *Plant J.* **80**, 870–882 (2014).
17. Cheng, S. *et al.* Redefining the structural motifs that determine RNA binding and RNA editing by pentatricopeptide repeat proteins in land plants. *Plant J.* **85**, 532–547 (2016).

18. Chateigner-Boutin, A.-L. *et al.* The E domains of pentatricopeptide repeat proteins from different organelles are not functionally equivalent for RNA editing. *Plant J.* **74**, 935–945 (2013).

19. Ramos-Vega, M. *et al.* Functional analysis of the *Arabidopsis thaliana CHLOROPLAST BIOGENESIS 19* pentatricopeptide repeat editing protein. *New Phytol.* **208**, 430–441 (2015).

20. Iyer, L. M., Zhang, D., Rogozin, I. B. & Aravind, L. Evolution of the deaminase fold and multiple origins of eukaryotic editing and mutagenic nucleic acid deaminases from bacterial toxin systems. *Nucleic Acids Res.* **39**, 9473–9497 (2011).

21. Hayes, M. L., Giang, K., Berhane, B. & Mulligan, R. M. Identification of Two Pentatricopeptide Repeat Genes Required for RNA Editing and Zinc Binding by C-terminal Cytidine Deaminase-like Domains. *J. Biol. Chem.* **288**, 36519–36529 (2013).

22. Boussardon, C. *et al.* The cytidine deaminase signature HxE(x) $_n$ CxxC of DYW1 binds zinc and is necessary for RNA editing of *ndhD-1*. *New Phytol.* **203**, 1090–1095 (2014).

23. Hayes, M. L., Dang, K. N., Diaz, M. F. & Mulligan, R. M. A Conserved Glutamate Residue in the C-terminal Deaminase Domain of Pentatricopeptide Repeat Proteins Is Required for RNA Editing Activity. *J. Biol. Chem.* **290**, 10136–10142 (2015).

24. Wagoner, J. A., Sun, T., Lin, L. & Hanson, M. R. Cytidine Deaminase Motifs within the DYW Domain of Two Pentatricopeptide Repeat-containing Proteins Are

Required for Site-specific Chloroplast RNA Editing. *J. Biol. Chem.* **290**, 2957–2968 (2015).

25. Knoop, V. When you can't trust the DNA: RNA editing changes transcript sequences. *Cell. Mol. Life Sci.* **68**, 567–586 (2011).
26. Schmitz-Linneweber, C. & Small, I. Pentatricopeptide repeat proteins: a socket set for organelle gene expression. *Trends Plant Sci.* **13**, 663–670 (2008).
27. Fujii, S. & Small, I. The evolution of RNA editing and pentatricopeptide repeat genes. *New Phytol.* **191**, 37–47 (2011).
28. Gray, M. W. Evolutionary Origin of RNA Editing. *Biochemistry* **51**, 5235–5242 (2012).
29. Stoltzfus, A. On the Possibility of Constructive Neutral Evolution. *J. Mol. Evol.* **49**, 169–181 (1999).
30. O'Toole, N. *et al.* On the Expansion of the Pentatricopeptide Repeat Gene Family in Plants. *Mol. Biol. Evol.* **25**, 1120–1128 (2008).
31. Sakurai, A. *et al.* On biased distribution of introns in various eukaryotes. *Gene* **300**, 89–95 (2002).
32. Okuda, K. *et al.* Pentatricopeptide Repeat Proteins with the DYW Motif Have Distinct Molecular Functions in RNA Editing and RNA Cleavage in Arabidopsis Chloroplasts. *PLANT CELL ONLINE* **21**, 146–156 (2009).
33. Okuda, K. *et al.* The pentatricopeptide repeat protein OTP82 is required for RNA editing of plastid ndhB and ndhG transcripts. *Plant J.* **61**, 339–349 (2010).

34. Guillaumot, D. *et al.* Two interacting PPR proteins are major Arabidopsis editing factors in plastid and mitochondria. *Proc. Natl. Acad. Sci. U. S. A.* **114**, 8877–8882 (2017).

35. Andrés-Colás, N. *et al.* Multiple PPR protein interactions are involved in the RNA editing system in *Arabidopsis* mitochondria and plastids. *Proc. Natl. Acad. Sci.* **114**, 8883–8888 (2017).

36. Hammani, K. & Giegé, P. RNA metabolism in plant mitochondria. *Trends Plant Sci.* **19**, 380–389 (2014).

37. Boussardon, C. *et al.* Two Interacting Proteins Are Necessary for the Editing of the NdhD-1 Site in Arabidopsis Plastids. *Plant Cell* **24**, 3684–3694 (2012).

38. Bentolila, S. *et al.* RIP1, a member of an Arabidopsis protein family, interacts with the protein RARE1 and broadly affects RNA editing. *Proc. Natl. Acad. Sci.* **109**, E1453–E1461 (2012).

39. Takenaka, M. *et al.* Multiple organellar RNA editing factor (MORF) family proteins are required for RNA editing in mitochondria and plastids of plants. *Proc. Natl. Acad. Sci.* **109**, 5104–5109 (2012).

40. Sun, T. *et al.* An RNA recognition motif-containing protein is required for plastid RNA editing in Arabidopsis and maize. *Proc. Natl. Acad. Sci.* **110**, E1169–E1178 (2013).

41. Shi, X., Bentolila, S. & Hanson, M. R. Organelle RNA recognition motif-containing (ORRM) proteins are plastid and mitochondrial editing factors in Arabidopsis. *Plant Signal. Behav.* **11**, e1167299 (2016).

42. Shi, X., Castandet, B., Germain, A., Hanson, M. R. & Bentolila, S. ORRM5, an RNA recognition motif-containing protein, has a unique effect on mitochondrial RNA editing. *J. Exp. Bot.* **68**, 2833–2847 (2017).
43. Sun, T. *et al.* A Zinc Finger Motif-Containing Protein Is Essential for Chloroplast RNA Editing. *PLOS Genet.* **11**, e1005028 (2015).
44. Zhang, F. *et al.* Tetrapyrrole biosynthetic enzyme protoporphyrinogen IX oxidase 1 is required for plastid RNA editing. *Proc. Natl. Acad. Sci.* **111**, 2023–2028 (2014).
45. von Heijne, G. Why mitochondria need a genome. *FEBS Lett.* **198**, 1–4 (1986).
46. Mittler, R., Vanderauwera, S., Gollery, M. & Van Breusegem, F. Reactive oxygen gene network of plants. *Trends Plant Sci.* **9**, 490–498 (2004).
47. Willems, P. *et al.* The ROS Wheel: Refining ROS Transcriptional Footprints1[OPEN]. *Plant Physiol.* **171**, 1720–1733 (2016).
48. Mittler, R. ROS Are Good. *Trends Plant Sci.* **22**, 11–19 (2017).
49. Choi, W.-G. *et al.* Orchestrating rapid long-distance signaling in plants with Ca $^{2+}$, ROS and electrical signals. *Plant J.* **90**, 698–707 (2017).
50. Choudhury, F. K., Rivero, R. M., Blumwald, E. & Mittler, R. Reactive oxygen species, abiotic stress and stress combination. *Plant J.* **90**, 856–867 (2017).
51. Kleine, T. & Leister, D. Retrograde signaling: Organelles go networking. *Biochim. Biophys. Acta BBA - Bioenerg.* **1857**, 1313–1325 (2016).
52. Mittler, R. *et al.* ROS signaling: the new wave? *Trends Plant Sci.* **16**, 300–309 (2011).
53. Mullineaux, P. M. ROS in Retrograde Signalling from the Chloroplast to the Nucleus. in *Reactive Oxygen Species in Plant Signaling* (eds. Rio, L. A. & Puppo,

A.) 221–240 (Springer Berlin Heidelberg, 2009). doi:10.1007/978-3-642-00390-5_14

54. Raja, V., Majeed, U., Kang, H., Andrabi, K. I. & John, R. Abiotic stress: Interplay between ROS, hormones and MAPKs. *Environ. Exp. Bot.* **137**, 142–157 (2017).
55. Woodson, J. D. & Chory, J. Organelle Signaling: How Stressed Chloroplasts Communicate with the Nucleus. *Curr. Biol.* **22**, R690–R692 (2012).
56. Borisova, M. M. *et al.* Photosynthetic electron flow to oxygen and diffusion of hydrogen peroxide through the chloroplast envelope via aquaporins. *Biochim. Biophys. Acta BBA - Bioenerg.* **1817**, 1314–1321 (2012).
57. Kohler, R. H. & Hanson, M. R. Plastid tubules of higher plants are tissue-specific and developmentally regulated. *Curr. Opin. Plant Biol.* **3**, 174 (2000).
58. Farmer, E. E. & Mueller, M. J. ROS-Mediated Lipid Peroxidation and RES-Activated Signaling. *Annu. Rev. Plant Biol.* **64**, 429–450 (2013).
59. Triantaphylides, C. *et al.* Singlet Oxygen Is the Major Reactive Oxygen Species Involved in Photooxidative Damage to Plants. *PLANT Physiol.* **148**, 960–968 (2008).
60. Apel, K. & Hirt, H. Reactive Oxygen Species: Metabolism, Oxidative Stress, and Signal Transduction. *Annu. Rev. Plant Biol.* **55**, 373–399 (2004).
61. Hammani, K. *et al.* An *Arabidopsis* Dual-Localized Pentatricopeptide Repeat Protein Interacts with Nuclear Proteins Involved in Gene Expression Regulation. *Plant Cell* **23**, 730–740 (2011).

62. Laluk, K., AbuQamar, S. & Mengiste, T. The Arabidopsis Mitochondria-Localized Pentatricopeptide Repeat Protein PGN Functions in Defense against Necrotrophic Fungi and Abiotic Stress Tolerance. *PLANT Physiol.* **156**, 2053–2068 (2011).

63. Liu, Y. *et al.* ABA overly-sensitive 5 (ABO5), encoding a pentatricopeptide repeat protein required for cis-splicing of mitochondrial nad2 intron 3, is involved in the abscisic acid response in Arabidopsis: ABA and PPR protein. *Plant J.* **63**, 749–765 (2010).

64. Tan, J. *et al.* A Novel Chloroplast-Localized Pentatricopeptide Repeat Protein Involved in Splicing Affects Chloroplast Development and Abiotic Stress Response in Rice. *Mol. Plant* **7**, 1329–1349 (2014).

65. Zhu, Q. *et al.* SLO2, a mitochondrial pentatricopeptide repeat protein affecting several RNA editing sites, is required for energy metabolism. *Plant J.* **71**, 836–849 (2012).

66. Zsigmond, L. *et al.* Arabidopsis PPR40 Connects Abiotic Stress Responses to Mitochondrial Electron Transport. *PLANT Physiol.* **146**, 1721–1737 (2008).

67. Liu, J.-M. *et al.* The E-Subgroup Pentatricopeptide Repeat Protein Family in Arabidopsis thaliana and Confirmation of the Responsiveness PPR96 to Abiotic Stresses. *Front. Plant Sci.* **7**, (2016).

68. Murayama, M. *et al.* Isolation of Arabidopsis ahg11, a weak ABA hypersensitive mutant defective in nad4 RNA editing. *J. Exp. Bot.* **63**, 5301–5310 (2012).

69. Yuan, H. & Liu, D. Functional disruption of the pentatricopeptide protein SLG1 affects mitochondrial RNA editing, plant development, and responses to abiotic stresses in Arabidopsis. *Plant J.* **70**, 432–444 (2012).

70. Blée, E. Phytooxylipins and plant defense reactions. *Prog. Lipid Res.* **37**, 33–72 (1998).

71. Wasternack, C. & Feussner, I. The Oxylipin Pathways: Biochemistry and Function. *Annu. Rev. Plant Biol.* **69**, 363–386 (2018).

72. Vu, H. S. *et al.* Modifications of membrane lipids in response to wounding of *Arabidopsis thaliana* leaves. *Plant Signal. Behav.* **10**, e1056422 (2015).

73. Okuda, K., Nakamura, T., Sugita, M., Shimizu, T. & Shikanai, T. A Pentatricopeptide Repeat Protein Is a Site Recognition Factor in Chloroplast RNA Editing. *J. Biol. Chem.* **281**, 37661–37667 (2006).

74. Tzfira, T. & Citovsky, V. Agrobacterium-mediated genetic transformation of plants: biology and biotechnology. *Curr. Opin. Biotechnol.* **17**, 147–154 (2006).

75. Clough, S. J. & Bent, A. F. Floral dip: a simplified method forAgrobacterium-mediated transformation ofArabidopsis thaliana: Floral dip transformation of Arabidopsis. *Plant J.* **16**, 735–743 (1998).

76. Hayes, M. & Hanson, M. *Assay of Editing of Exogenous RNAs in Chloroplast Extracts of Arabidopsis, Maize, Pea, and Tobacco*. **424**, (2007).

77. Diaz, M. F., Bentolila, S., Hayes, M. L., Hanson, M. R. & Mulligan, R. M. A protein with an unusually short PPR domain, MEF8, affects editing at over 60 Arabidopsis mitochondrial C targets of RNA editing. *Plant J.* **92**, 638–649 (2017).

78. Schneider, C. A., Rasband, W. S. & Eliceiri, K. W. NIH Image to ImageJ: 25 years of image analysis. *Nat. Methods* **9**, 671 (2012).

79. Joo, J. H., Wang, S., Chen, J. G., Jones, A. M. & Fedoroff, N. V. Different Signaling and Cell Death Roles of Heterotrimeric G Protein α and β Subunits in the Arabidopsis Oxidative Stress Response to Ozone. *Plant Cell* **17**, 957–970 (2005).
80. Mattila, H., Khorobrykh, S., Havurinne, V. & Tyystjärvi, E. Reactive oxygen species: Reactions and detection from photosynthetic tissues. *J. Photochem. Photobiol. B* **152**, 176–214 (2015).
81. Covello, P. S. & Gray, M. W. RNA editing in plant mitochondria. *Nature* **341**, 662 (1989).
82. Kotera, E., Tasaka, M. & Shikanai, T. A pentatricopeptide repeat protein is essential for RNA editing in chloroplasts. *Nature* **433**, 326–330 (2005).
83. Rudinger, M., Fritz-Laylin, L., Polsakiewicz, M. & Knoop, V. Plant-type mitochondrial RNA editing in the protist Naegleria gruberi. *RNA* **17**, 2058–2062 (2011).
84. Uchida, M., Ohtani, S., Ichinose, M., Sugita, C. & Sugita, M. The PPR-DYW proteins are required for RNA editing of *rps14* , *cox1* and *nad5* transcripts in *Physcomitrella patens* mitochondria. *FEBS Lett.* **585**, 2367–2371 (2011).
85. Andrés, C., Lurin, C. & Small, I. D. The multifarious roles of PPR proteins in plant mitochondrial gene expression. *Physiol. Plant.* **129**, 14–22 (2007).
86. Finn, R. D. *et al.* Pfam: the protein families database. *Nucleic Acids Res.* **42**, D222–D230 (2014).
87. Salone, V. *et al.* A hypothesis on the identification of the editing enzyme in plant organelles. *FEBS Lett.* **581**, 4132–4138 (2007).

88. Betts, L., Xiang, S., Short, S. A., Wolfenden, R. & Carter, C. W. Cytidine Deaminase. The 2·3 Å Crystal Structure of an Enzyme: Transition-state Analog Complex. *J. Mol. Biol.* **235**, 635–656 (1994).

89. Teng, B., Burant, C. & Davidson, N. Molecular cloning of an apolipoprotein B messenger RNA editing protein. *Science* **260**, 1816–1819 (1993).

90. Xie, K. *et al.* The structure of a yeast RNA-editing deaminase provides insight into the fold and function of activation-induced deaminase and APOBEC-1. *Proc. Natl. Acad. Sci.* **101**, 8114–8119 (2004).

91. Spears, J. L. *et al.* A Single Zinc Ion Is Sufficient for an Active *Trypanosoma brucei* tRNA Editing Deaminase. *J. Biol. Chem.* **286**, 20366–20374 (2011).

92. Goodman, R. A., Macbeth, M. R. & Beal, P. A. ADAR Proteins: Structure and Catalytic Mechanism. *Curr. Top. Microbiol. Immunol.* **353**, 1–33 (2012).

93. Bransteitter, R., Prochnow, C. & Chen, X. S. The current structural and functional understanding of APOBEC deaminases. *Cell. Mol. Life Sci.* **66**, 3137–3147 (2009).

94. Okuda, K., Myouga, F., Motohashi, R., Shinozaki, K. & Shikanai, T. Conserved domain structure of pentatricopeptide repeat proteins involved in chloroplast RNA editing. *Proc. Natl. Acad. Sci.* **104**, 8178–8183 (2007).

95. Verbitskiy, D., Zehrmann, A., Brennicke, A. & Takenaka, M. A truncated MEF11 protein shows site-specific effects on mitochondrial RNA editing. *Plant Signal. Behav.* **5**, 558–560 (2010).

96. Hammani, K. *et al.* A Study of New Arabidopsis Chloroplast RNA Editing Mutants Reveals General Features of Editing Factors and Their Target Sites. *Plant Cell* **21**, 3686–3699 (2009).

97. Yagi, Y. *et al.* Pentatricopeptide repeat proteins involved in plant organellar RNA editing. *RNA Biol.* **10**, 1419–1425 (2013).

98. Carlow, D. C., Short, S. A. & Wolfenden, R. Complementary Truncations of a Hydrogen Bond to Ribose Involved in Transition-State Stabilization by Cytidine Deaminase†. *Biochemistry* **37**, 1199–1203 (1998).

99. Rajasekhar, V. K. & Mulligan, R. M. RNA Editing in Plant Mitochondria: a-Phosphate Is Retained during C-to-U Conversion in mRNAs. *Plant Cell* **5**, 1843 (1993).

100. Yu, W. & Schuster, W. Evidence for a Site-specific Cytidine Deamination Reaction Involved in C to U RNA Editing of Plant Mitochondria. *J. Biol. Chem.* **270**, 18227–18233 (1995).

101. Hirose, T. & Sugiura, M. Involvement of a site-specific trans-acting factor and a common RNA-binding protein in the editing of chloroplast mRNAs: development of a chloroplast in vitro RNA editing system. *EMBO J.* **20**, 1144–1152 (2001).

102. Nakajima, Y. & Mulligan, R. M. Nucleotide specificity of the RNA editing reaction in pea chloroplasts. *J. Plant Physiol.* **162**, 1347–1354 (2005).

103. Hegeman, C. E., Hayes, M. L. & Hanson, M. R. Substrate and cofactor requirements for RNA editing of chloroplast transcripts in Arabidopsis in vitro. *Plant J.* **42**, 124–132 (2005).

104. Zehrmann, A., Verbitskiy, D., Härtel, B., Brennicke, A. & Takenaka, M. PPR proteins network as site-specific RNA editing factors in plant organelles. *RNA Biol.* **8**, 67–70 (2011).

105. Tseng, C.-C. *et al.* Editing of accD and ndhF chloroplast transcripts is partially affected in the Arabidopsis vanilla cream1 mutant. *Plant Mol. Biol.* **73**, 309–323 (2010).

106. Chateigner-Boutin, A.-L. *et al.* CLB19, a pentatricopeptide repeat protein required for editing of rpoA and clpP chloroplast transcripts. *Plant J. Cell Mol. Biol.* **56**, 590–602 (2008).

107. Hayes, M. L., Giang, K. & Mulligan, R. Molecular evolution of pentatricopeptide repeat genes reveals truncation in species lacking an editing target and structural domains under distinct selective pressures. *BMC Evol. Biol.* **12**, 66 (2012).

108. Verbitskiy, D., Merwe, J. A. van der, Zehrmann, A., Härtel, B. & Takenaka, M. The E-Class PPR Protein MEF3 of Arabidopsis thaliana Can Also Function in Mitochondrial RNA Editing With an Additional DYW Domain. *Plant Cell Physiol.* **53**, 358–367 (2012).

109. Takenaka, M., Zehrmann, A., Verbitskiy, D., Härtel, B. & Brennicke, A. RNA Editing in Plants and Its Evolution. *Annu. Rev. Genet.* **47**, 335–352 (2013).

110. Verbitskiy, D., Zehrmann, A., Härtel, B., Brennicke, A. & Takenaka, M. Two Related RNA-editing Proteins Target the Same Sites in Mitochondria of *Arabidopsis thaliana*. *J. Biol. Chem.* **287**, 38064–38072 (2012).

111. Emanuelsson, O., Nielsen, H., Brunak, S. & von Heijne, G. Predicting Subcellular Localization of Proteins Based on their N-terminal Amino Acid Sequence. *J. Mol. Biol.* **300**, 1005–1016 (2000).

112. Small, I., Peeters, N., Legeai, F. & Lurin, C. Predotar: A tool for rapidly screening proteomes forN-terminal targeting sequences. *PROTEOMICS* **4**, 1581–1590 (2004).

113. Lu, B. & Hanson, M. R. A single nuclear gene specifies the abundance and extent of RNA editing of a plant mitochondrial transcript. *Nucleic Acids Res.* **20**, 5699–5703 (1992).

114. Shen, C. *et al.* Structural basis for specific single-stranded RNA recognition by designer pentatricopeptide repeat proteins. *Nat. Commun.* **7**, 11285 (2016).

115. Chen, S. *et al.* Apolipoprotein B-48 is the product of a messenger RNA with an organ-specific in-frame stop codon. *Science* **238**, 363–366 (1987).

116. Lomeli, H. *et al.* Control of kinetic properties of AMPA receptor channels by nuclear RNA editing. *Science* **266**, 1709–1713 (1994).

117. Schuster, W., Wissinger, B., Unseld, M. & Brennicke, A. Transcripts of the NADH-dehydrogenase subunit 3 gene are differentially edited in Oenothera mitochondria. *EMBO J.* **9**, 263–269 (1990).

118. Yang, A. J. & Mulligan, R. M. RNA editing intermediates of cox2 transcripts in maize mitochondria. *Mol. Cell. Biol.* **11**, 4278–4281 (1991).

119. Lu, B., Wilson, R. K., Phreaner, C. G., Mulligan, R. M. & Hanson, M. R. Protein polymorphism generated by differential RNA editing of a plant mitochondrial rps12 gene. *Mol. Cell. Biol.* **16**, 1543–1549 (1996).

120. Phreaner, C. G., Williams, M. & Mulligan, R. M. Incomplete Editing of rps12 Transcripts Results in teh synthesis of polymorphic polypeptides in plant mitochondria. *Plant Cell* **8**, 107–117 (1996).

121. Kim, S.-R. *et al.* Rice OGR1 encodes a pentatricopeptide repeat–DYW protein and is essential for RNA editing in mitochondria. *Plant J.* **59**, 738–749 (2009).

122. Glass, F., Härtel, B., Zehrmann, A., Verbitskiy, D. & Takenaka, M. MEF13 Requires MORF3 and MORF8 for RNA Editing at Eight Targets in Mitochondrial mRNAs in Arabidopsis thaliana. *Mol. Plant* **8**, 1466–1477 (2015).

123. Stern, D. B., Goldschmidt-Clermont, M. & Hanson, M. R. Chloroplast RNA Metabolism. *Annu. Rev. Plant Biol.* **61**, 125–155 (2010).

124. Giege, P. & Brennicke, A. RNA editing in Arabidopsis mitochondria effects 441 C to U changes in ORFs. *Proc. Natl. Acad. Sci.* **96**, 15324–15329 (1999).

125. Ruwe, H., Castandet, B., Schmitz-Linneweber, C. & Stern, D. B. Arabidopsis chloroplast quantitative editotype. *FEBS Lett.* **587**, 1429–1433 (2013).

126. Olinares, P. D. B., Ponnala, L. & van Wijk, K. J. Megadalton Complexes in the Chloroplast Stroma of Arabidopsis thaliana Characterized by Size Exclusion Chromatography, Mass Spectrometry, and Hierarchical Clustering*□S. *Mol. Cell. Proteomics* **9**, 22 (2010).

127. Shi, X., Germain, A., Hanson, M. R. & Bentolila, S. RNA Recognition Motif-Containing Protein ORRM4 Broadly Affects Mitochondrial RNA Editing and Impacts Plant Development and Flowering. *Plant Physiol.* **170**, 294–309 (2016).

128. Takenaka, M., Jörg, A., Burger, M. & Haag, S. Requirement of Various Protein Combinations for Each C-to-U RNA Editosome in Plant Organelles. in *RNA Metabolism in Mitochondria* (eds. Cruz-Reyes, J. & Gray, M. W.) **34**, 223–249 (Springer International Publishing, 2018).

129. Yan, J. *et al.* Delineation of pentatricopeptide repeat codes for target RNA prediction. (2019). doi:10.1093/nar/gkz075

130. Cushing, D. A., Forsthoefel, N. R., Gestaut, D. R. & Vernon, D. M. Arabidopsis emb175 and other ppr knockout mutants reveal essential roles for pentatricopeptide repeat (PPR) proteins in plant embryogenesis. *Planta* **221**, 424–436 (2005).

131. Sun, Y. K., Gutmann, B., Yap, A., Kindgren, P. & Small, I. Editing of Chloroplast rps14 by PPR Editing Factor EMB2261 Is Essential for Arabidopsis Development. *Front. Plant Sci.* **9**, (2018).

132. Bobik, K. *et al.* The chloroplast RNA helicase ISE2 is required for multiple chloroplast RNA processing steps in *Arabidopsis thaliana*. *Plant J.* **91**, 114–131 (2017).

133. Cai, W. *et al.* LPA66 Is Required for Editing psbF Chloroplast Transcripts in Arabidopsis. *PLANT Physiol.* **150**, 1260–1271 (2009).

134. Zulfugarov, I. S. *et al.* Production of superoxide from Photosystem II in a rice (Oryza sativaL.) mutant lacking PsbS. *BMC Plant Biol.* **14**, (2014).

135. Gläßer, C. *et al.* Meta-Analysis of Retrograde Signaling in Arabidopsis thaliana Reveals a Core Module of Genes Embedded in Complex Cellular Signaling Networks. *Mol. Plant* **7**, 1167–1190 (2014).

136. Galano, J.-M. *et al.* Isoprostanes, neuroprostanes and phytoprostanes: An overview of 25 years of research in chemistry and biology. *Prog. Lipid Res.* **68**, 83–108 (2017).

137. Dietz, K.-J., Turkan, I. & Krieger-Liszkay, A. Redox- and Reactive Oxygen Species-Dependent Signaling into and out of the Photosynthesizing Chloroplast. *Plant Physiol.* **171**, 1541–1550 (2016).

138. Everaert, C. *et al.* Benchmarking of RNA-sequencing analysis workflows using whole-transcriptome RT-qPCR expression data. *Sci. Rep.* **7**, (2017).

139. Hooper, C. M., Castleden, I. R., Tanz, S. K., Aryamanesh, N. & Millar, A. H. SUBA4: the interactive data analysis centre for Arabidopsis subcellular protein locations. *Nucleic Acids Res.* **45**, D1064–D1074 (2017).

140. Taylor, N. L., Tan, Y.-F., Jacoby, R. P. & Millar, A. H. Abiotic environmental stress induced changes in the Arabidopsis thaliana chloroplast, mitochondria and peroxisome proteomes. *J. Proteomics* **72**, 367–378 (2009).

141. Li, M., Welti, R. & Wang, X. Quantitative Profiling of Arabidopsis Polar Glycerolipids in Response to Phosphorus Starvation. Roles of Phospholipases D 1 and D 2 in Phosphatidylcholine Hydrolysis and Digalactosyldiacylglycerol Accumulation in Phosphorus-Starved Plants. *PLANT Physiol.* **142**, 750–761 (2006).

142. Li-Beisson, Y. *et al.* Acyl-Lipid Metabolism. *Arab. Book* **2013**, (2013).

143. Schmid-Siegert, E., Stepushenko, O., Glauser, G. & Farmer, E. E. Membranes as Structural Antioxidants: RECYCLING OF MALONDIALDEHYDE TO ITS SOURCE IN OXIDATION-SENSITIVE CHLOROPLAST FATTY ACIDS. *J. Biol. Chem.* **291**, 13005–13013 (2016).

144. Chu, H.-A. & Chiu, Y.-F. The Roles of Cytochrome b559 in Assembly and Photoprotection of Photosystem II Revealed by Site-Directed Mutagenesis Studies. *Front. Plant Sci.* **6**, (2016).

145. Dave, A. & Graham, I. A. Oxylipin Signaling: A Distinct Role for the Jasmonic Acid Precursor cis-(+)-12-Oxo-Phytodienoic Acid (cis-OPDA). *Front. Plant Sci.* **3**, (2012).
146. Heitz, T. *et al.* The Rise and Fall of Jasmonate Biological Activities. in *Lipids in Plant and Algae Development* (eds. Nakamura, Y. & Li-Beisson, Y.) **86**, 405–426 (Springer International Publishing, 2016).
147. Kourtchenko, O. *et al.* Oxo-Phytodienoic Acid-Containing Galactolipids in Arabidopsis: Jasmonate Signaling Dependence. *PLANT Physiol.* **145**, 1658–1669 (2007).
148. Ibrahim, A. *et al.* The Alphabet of Galactolipids in Arabidopsis thaliana. *Front. Plant Sci.* **2**, (2011).
149. Imbusch, R. & Mueller, M. J. Analysis of Oxidative Stress and Wound-Inducible Dinor Isoprostanes F $_1$ (Phytoprostanes F $_1$) in Plants. *Plant Physiol.* **124**, 1293–1304 (2000).
150. Mosblech, A., Feussner, I. & Heilmann, I. Oxylipins: Structurally diverse metabolites from fatty acid oxidation. *Plant Physiol. Biochem.* **47**, 511–517 (2009).
151. Mueller, S. *et al.* General Detoxification and Stress Responses Are Mediated by Oxidized Lipids through TGA Transcription Factors in Arabidopsis. *PLANT CELL ONLINE* **20**, 768–785 (2008).
152. Thoma, I. *et al.* Cyclopentenone isoprostanes induced by reactive oxygen species trigger defense gene activation and phytoalexin accumulation in plants. *Plant J.* **34**, 363–375 (2003).
153. Loeffler, C. B1-Phytoprostanes Trigger Plant Defense and Detoxification Responses. *PLANT Physiol.* **137**, 328–340 (2005).

154. Mueller, S. *et al.* General Detoxification and Stress Responses Are Mediated by Oxidized Lipids through TGA Transcription Factors in Arabidopsis. *PLANT CELL ONLINE* **20**, 768–785 (2008).
155. Maynard, D., Gröger, H., Dierks, T. & Dietz, K.-J. The function of the oxylipin 12-oxophytodienoic acid in cell signaling, stress acclimation, and development. *J. Exp. Bot.* (2018). doi:10.1093/jxb/ery316
156. Li, W. *et al.* Phylogenetic analysis, structural evolution and functional divergence of the 12-oxo-phytodienoate acid reductase gene family in plants. *BMC Evol. Biol.* **9**, 90 (2009).
157. Fangour, S. E., Guy, A., Vidal, J.-P., Rossi, J.-C. & Durand, T. A Flexible Synthesis of the Phytoprostanes B1 Type I and II. *J. Org. Chem.* **70**, 9 (2005).
158. Nilsson, A. K. *et al.* Acylated monogalactosyl diacylglycerol: prevalence in the plant kingdom and identification of an enzyme catalyzing galactolipid head group acylation in *Arabidopsis thaliana*. *Plant J.* **84**, 1152–1166 (2015).
159. Tseng, C.-C., Lee, C.-J., Chung, Y.-T., Sung, T.-Y. & Hsieh, M.-H. Differential regulation of Arabidopsis plastid gene expression and RNA editing in non-photosynthetic tissues. *Plant Mol. Biol.* **82**, 375–392 (2013).
160. Bock, R. Extraplastidic site-specific factors mediate RNA editing in chloroplasts. *EMBO J.* **16**, 3282–3288 (1997).
161. Krysan, P. J., Young, J. C. & Sussman, M. R. T-DNA as an Insertional Mutagen in Arabidopsis. *Plant Cell* **11**, 2283–2290 (1999).

162. Merwe, J. A. van der, Takenaka, M., Neuwirt, J., Verbitskiy, D. & Brennicke, A. RNA editing sites in plant mitochondria can share cis-elements. *FEBS Lett.* **580**, 268–272 (2006).

163. Sun, Q. *et al.* PPDB, the Plant Proteomics Database at Cornell. *Nucleic Acids Res.* **37**, D969–D974 (2009).

164. Hegeman, C. E., Hayes, M. L. & Hanson, M. R. Substrate and cofactor requirements for RNA editing of chloroplast transcripts in Arabidopsis in vitro: Substrate and cofactor requirements for RNA editing in Arabidopsis. *Plant J.* **42**, 124–132 (2005).

165. Neuwirt, J. An in vitro RNA editing system from cauliflower mitochondria: Editing site recognition parameters can vary in different plant species. *RNA* **11**, 1563–1570 (2005).

166. Rappsilber, J., Siniossoglou, S., Hurt, E. C. & Mann, M. A Generic Strategy To Analyze the Spatial Organization of Multi-Protein Complexes by Cross-Linking and Mass Spectrometry. *Anal. Chem.* **72**, 267–275 (2000).

167. Young, M. M. *et al.* High throughput protein fold identification by using experimental constraints derived from intramolecular cross-links and mass spectrometry. *Proc. Natl. Acad. Sci.* **97**, 5802–5806 (2000).

168. Stengel, F., Aebersold, R. & Robinson, C. V. Joining Forces: Integrating Proteomics and Cross-linking with the Mass Spectrometry of Intact Complexes. *Mol. Cell. Proteomics* **11**, R111.014027 (2012).

169. Lasker, K. *et al.* Molecular architecture of the 26S proteasome holocomplex determined by an integrative approach. *Proc. Natl. Acad. Sci.* **109**, 1380–1387 (2012).

170. Gully, B. S. *et al.* The solution structure of the pentatricopeptide repeat protein PPR10 upon binding atpH RNA. *Nucleic Acids Res.* **43**, 1918–1926 (2015).

171. Bayer-Császár, E. *et al.* The conserved domain in MORF proteins has distinct affinities to the PPR and E elements in PPR RNA editing factors. *Biochim. Biophys. Acta BBA - Gene Regul. Mech.* **1860**, 813–828 (2017).

172. Zehrmann, A. *et al.* Selective homo- and heteromer interactions between the multiple organellar RNA editing factor (MORF) proteins in Arabidopsis thaliana. *J. Biol. Chem.* jbc.M114.602086 (2015). doi:10.1074/jbc.M114.602086

173. Yan, J. *et al.* MORF9 increases the RNA-binding activity of PLS-type pentatricopeptide repeat protein in plastid RNA editing. *Nat. Plants* **3**, 17037 (2017).

174. Roux, K. J., Kim, D. I., Raida, M. & Burke, B. A promiscuous biotin ligase fusion protein identifies proximal and interacting proteins in mammalian cells. *J. Cell Biol.* **196**, 801–810 (2012).

175. Kim, D. I. *et al.* An improved smaller biotin ligase for BioID proximity labeling. *Mol. Biol. Cell* **27**, 1188–1196 (2016).

176. Whiteaker, J. R. *et al.* Antibody-based enrichment of peptides on magnetic beads for mass spectrometry-based quantification of serum biomarkers. *Anal. Biochem.* **362**, 44–54 (2007).

Appendix

Supplemental Figures and Tables

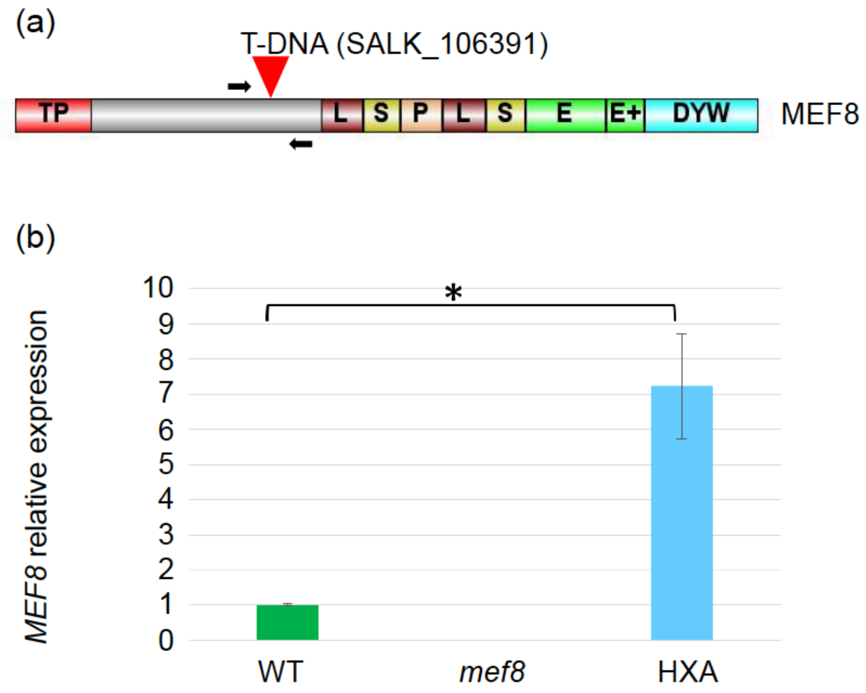


Figure S-4.1. *MEF8* Expression in the material used in this study. (a) Schematic representation of MEF8 with its different domains: the predicted mitochondrial transit peptide (TP), the different types of repeats, L, S, and P, the C terminus domains, E, E+, and DYW. The location of the T-DNA insertion is indicated by a triangle and the primers used for the qRT-PCR are represented by arrows encompassing the T-DNA insertion. (b) *MEF8* expression measured by qRT-PCR**.** Two biological samples were measured per genotype, and three technical replicates were assayed per biological sample. Values represent mean ± SD.

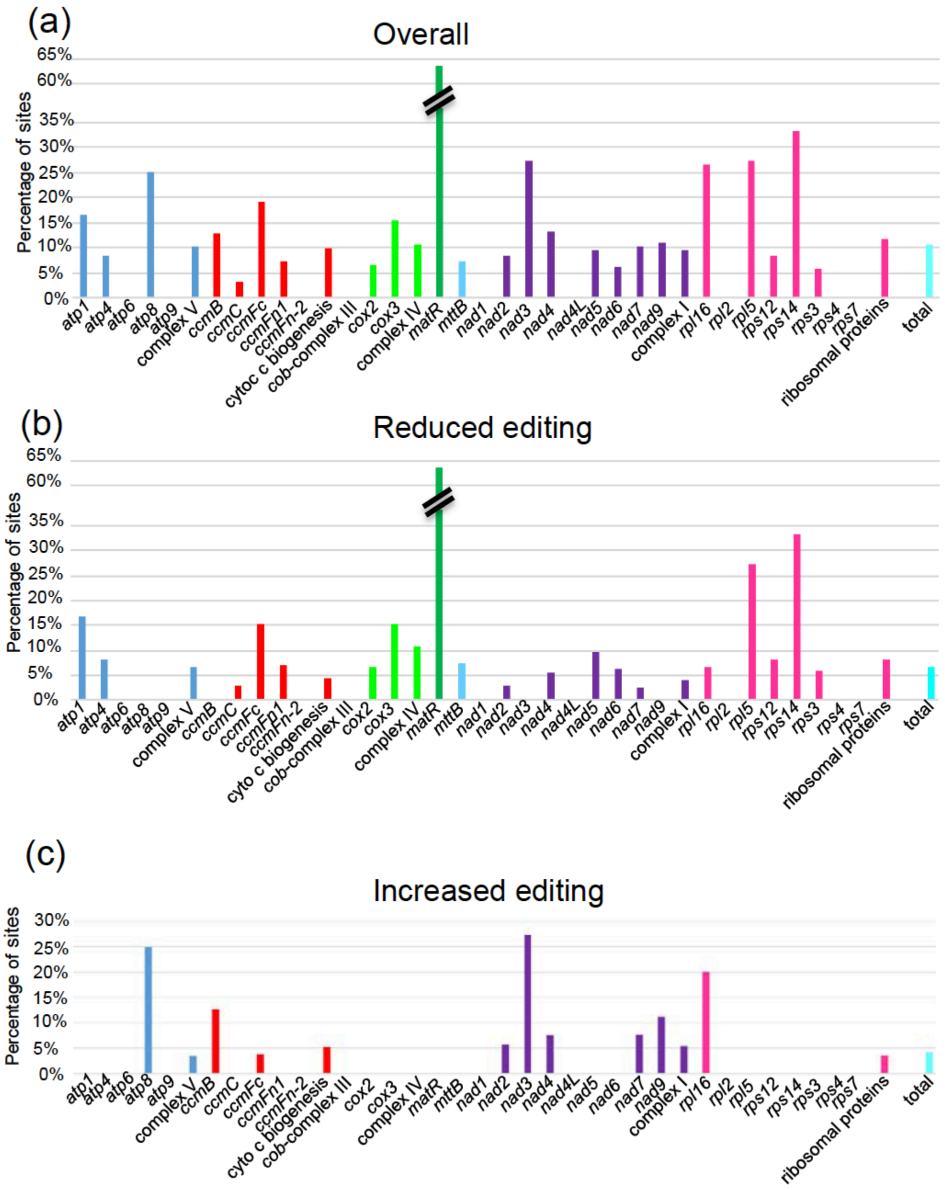


Figure S-4.2. Percentage of affected edited sites/transcript in the *mef8* T-DNA insertional mutant. (a) Percentage of sites affected by *MEF8* mutation on each transcript. Each bar represents a transcript color-coded according to the complex to which it belongs. (b) Percentage of sites experiencing reduced editing extents by *MEF8* mutation on each transcript. (c) Percentage of sites showing increased editing efficiency on each transcript as a result of *mef8* mutations. The percentage is also given for the complex to which the transcripts belong, complex V, cytochrome C biogenesis, complex IV, complex I, and ribosomal proteins.

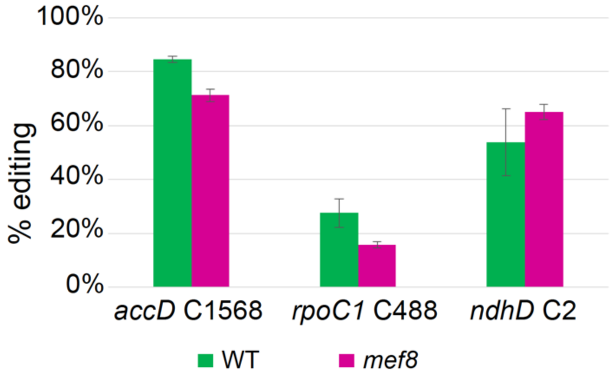


Figure S-4.3. *MEF8* mutation changes the editing extent of three plastid sites. The editing extent of *accD*C1568 and *rpoC1*C488 is significantly reduced in the *mef8* mutant, while the editing extent of *ndhD*C2 is significantly increased. Values represent mean ± SD.

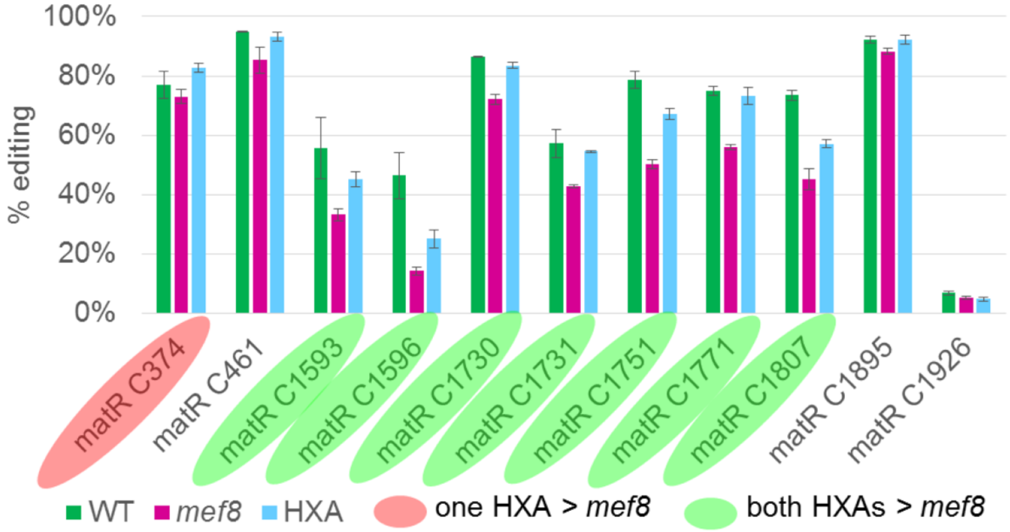


Figure S-4.4. A mutated MEF8 (HXA) is able to partially complement all the defective editing sites on the *matR* transcript. Editing extents of the sites found on the *matR* transcript are given for the wild-type (WT), the *mef8* mutant, and the HXA transgenic plants. HXA plants were obtained by transforming the *mef8* mutant with a mutated version of MEF8 in which the putatively catalytic glutamate of the HXE motif is replaced by HXA. Values represent mean ± SD.

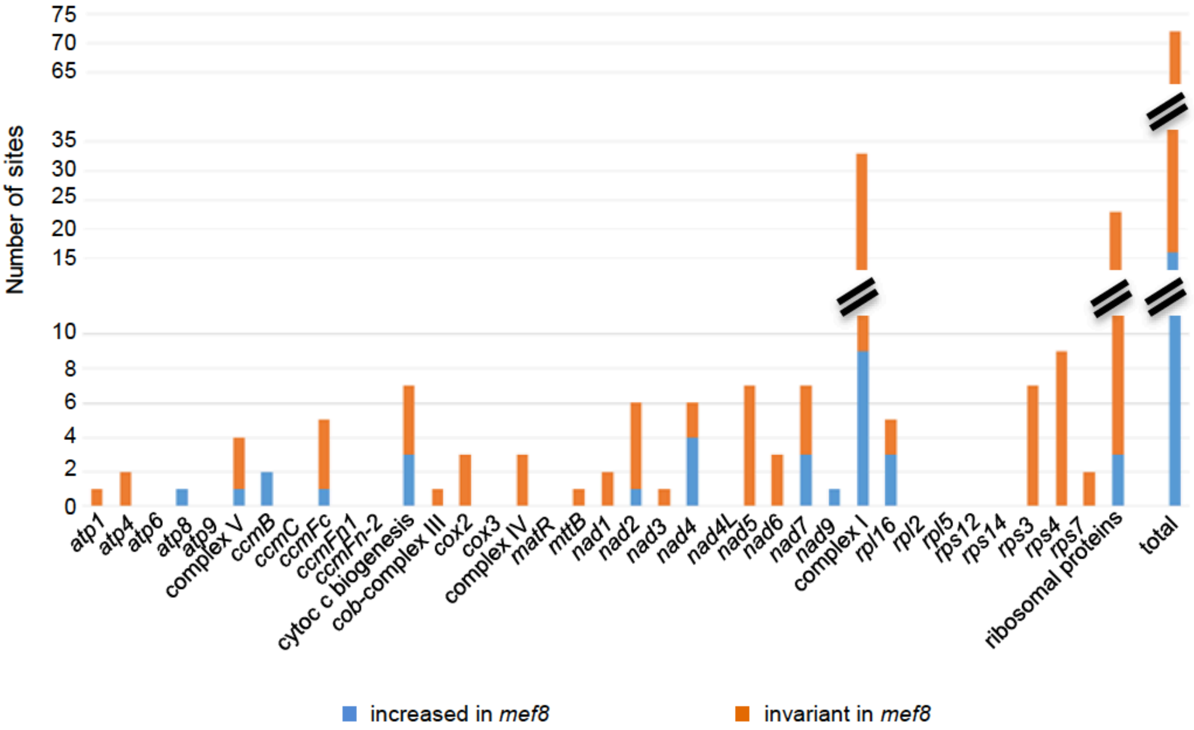


Figure S-4.5. Number of edited sites/transcript that show a decrease of editing extent in at least one of the HXA transgenic plants. Overexpressing a mutated *MEF8* (HXA) results in the occurrence of sites whose editing extent is significantly decreased compared to the *mef8* mutant. For each transcript the number of these sites is split between the sites that were showing a significant increase of editing extent in the *mef8* mutant vs. wild-type (blue) and the sites that did not show a significant difference of editing extent between the *mef8* mutant and the wild-type, invariant (orange). The number is also given for the complex to which the transcripts belong, complex V, cytochrome C biogenesis, complex IV, complex I, and ribosomal proteins.

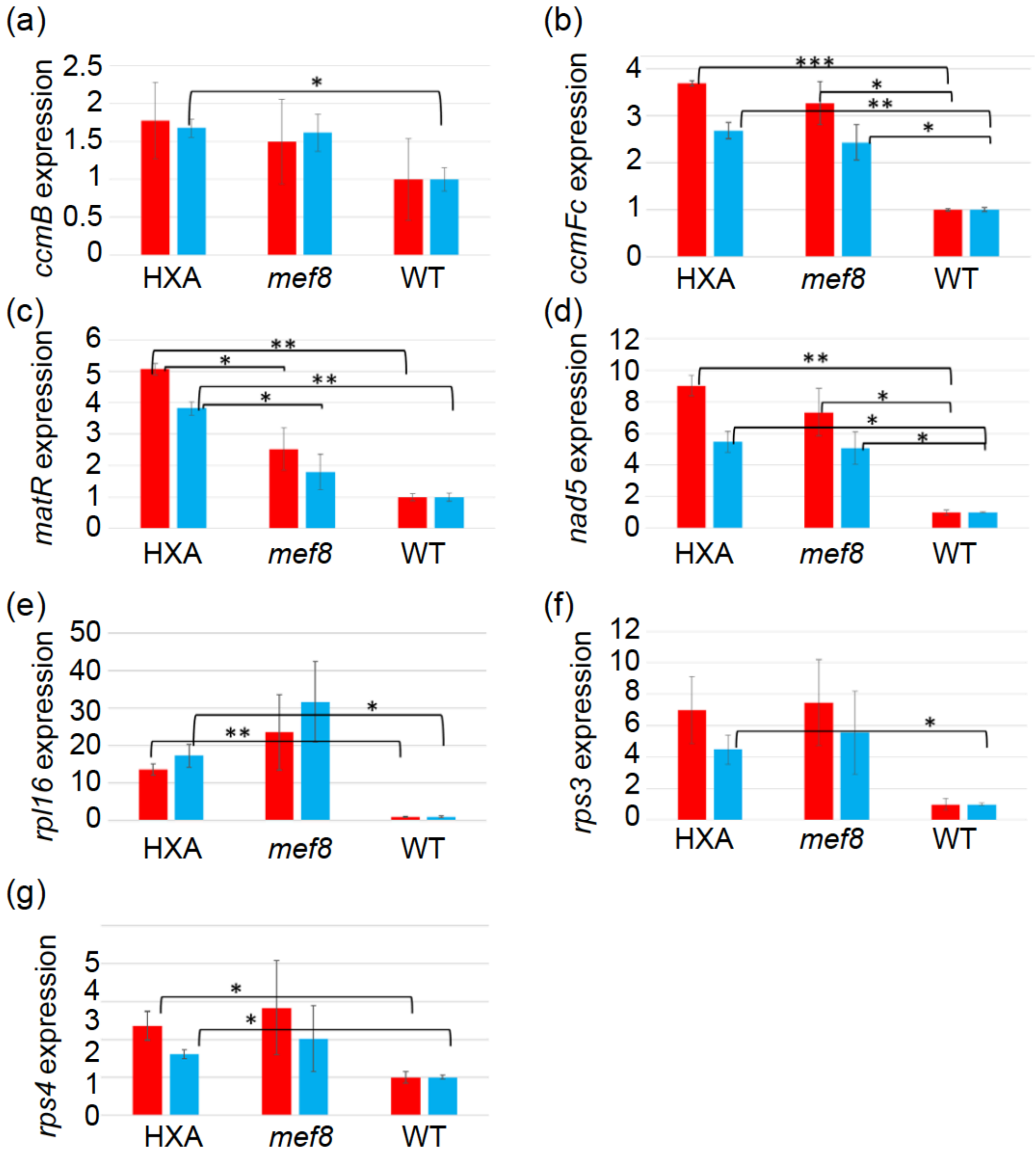


Figure S-4.6. Mitochondrial gene expression measurement shows a general increase of steady state level of transcripts in both the *mef8* mutant and the transgenic plant (HXA) relative to the wild-type (WT). (a–g). Each mitochondrial gene expression was measured by qRT-PCR assay using two different primer pairs represented in red and blue. Two biological samples were measured per genotype, and three technical replicates were assayed per biological sample. Values represent mean ± SD.

Table S-4.1 Number of reads at each editing site (gene-position for each library (genotype). X_n_C: number of unedited reads, X_n_T: number of edited reads, X_n_Tfr (editing extent): X_n_T/ (X_n_C+ X_n_T). The values of the reads for WT (wild-type), *mef8*, and HXA are obtained by pooling the values of each replicate.

#Gene	position ATG	WT_1_C	WT_1_T	WT_1_Tfr	WT_2_C	WT_2_T	WT_2_Tfr	WT_C	WT_T	WT-Tfr	*mef8*_1_C	*mef8*_1_T	*mef8*_1_Tfr	*mef8*_2_C	*mef8*_2_T	*mef8*_2_Tfr	*mef8*_C	*mef8*_T	*mef8*_T fr	HXA_1_C	HXA_1_T	HXA_1_Tfr	HXA_2_C	HXA_2_T	HXA_2_Tfr	HXA_C	HXA_T	HXA_Tfr
accD	794	34	3563	0.99	38	1673	0.98	72	5236	0.99	47	1976	0.98	100	7760	0.99	147	9736	0.99	107	5587	0.98	90	5242	0.98	197	10829	0.98
accD	1568	900	5164	0.85	542	2727	0.83	1442	7891	0.85	968	2108	0.69	3538	8997	0.72	4506	11105	0.71	2619	6869	0.72	2466	5564	0.69	5085	12433	0.71
atpF	92	55	6525	0.99	54	3230	0.98	109	9755	0.99	131	4601	0.97	267	9585	0.97	398	14186	0.97	333	10196	0.97	241	6541	0.96	574	16737	0.97
clp	559	254	5891	0.96	24	2877	0.99	278	8768	0.97	154	2300	0.94	169	7255	0.98	323	9555	0.97	197	3559	0.95	295	5248	0.95	492	8807	0.95
matK	640	217	2879	0.93	28	740	0.96	245	3619	0.94	155	1142	0.88	459	4560	0.91	614	5702	0.90	659	4530	0.87	411	3443	0.89	1070	7973	0.88
ndhB	149	19	1935	0.99	1	345	1.00	20	2280	0.99	5	904	0.99	34	3202	0.99	39	4106	0.99	27	3675	0.99	20	3724	0.99	47	7399	0.99
ndhB	467	103	4841	0.98	15	1872	0.99	118	6713	0.98	23	2243	0.99	117	7186	0.98	140	9429	0.99	181	8169	0.98	132	8766	0.99	313	16935	0.98
ndhB	586	39	4479	0.99	3	1421	1.00	42	5900	0.99	21	2101	0.99	71	7077	0.99	92	9178	0.99	84	7786	0.99	86	8464	0.99	170	16250	0.99
ndhB	708	4258	229	0.05	1316	158	0.11	5574	387	0.06	2011	228	0.10	5870	1115	0.16	7881	1343	0.15	7228	470	0.06	7896	599	0.07	15124	1069	0.07
ndhB	726	4354	182	0.04	1368	156	0.10	5722	338	0.06	1977	301	0.13	5677	1378	0.20	7654	1679	0.18	7355	379	0.05	7941	533	0.06	15296	912	0.06
ndhB	746	43	4434	0.99	9	1546	0.99	52	5980	0.99	18	2209	0.99	85	6973	0.99	103	9182	0.99	79	7598	0.99	74	8327	0.99	153	15925	0.99
ndhB	830	28	4609	0.99	5	1752	1.00	33	6361	0.99	18	2186	0.99	113	7035	0.98	131	9221	0.99	103	7807	0.99	93	8499	0.99	196	16306	0.99
ndhB	836	216	4380	0.95	24	1716	0.99	240	6096	0.96	33	2151	0.98	315	6774	0.96	348	8925	0.96	172	7674	0.98	174	8358	0.98	346	16032	0.98
ndhB	872	100	4485	0.98	10	1670	0.99	110	6155	0.98	45	2186	0.98	194	6974	0.97	239	9160	0.97	203	7778	0.97	225	8492	0.97	428	16270	0.97
ndhB	1255	9	4706	1.00	10	1386	0.99	19	6092	1.00	7	2147	1.00	28	7228	1.00	35	9375	1.00	35	7297	1.00	36	8471	1.00	71	15768	1.00
ndhB	1481	91	8194	0.99	20	3587	0.99	111	11781	0.99	60	3668	0.98	235	11357	0.98	295	15025	0.98	185	12946	0.99	156	13926	0.99	341	26872	0.99
ndhD	2	1759	2382	0.58	691	460	0.40	2450	2842	0.54	586	1255	0.68	2402	4287	0.64	2988	5542	0.65	2510	3951	0.61	2798	4466	0.61	5308	8417	0.61
ndhD	383	45	4846	0.99	9	1542	0.99	54	6388	0.99	21	2152	0.99	74	7573	0.99	95	9725	0.99	115	7871	0.99	97	8700	0.99	212	16571	0.99
ndhD	674	156	4885	0.97	44	1581	0.97	200	6466	0.97	173	2183	0.93	591	7133	0.92	764	9316	0.92	406	7767	0.95	478	8983	0.95	884	16750	0.95
ndhD	878	389	4036	0.91	140	1336	0.91	529	5372	0.91	232	1879	0.89	818	6080	0.88	1050	7959	0.88	667	6676	0.91	742	7900	0.91	1409	14576	0.91
ndhD	887	301	4202	0.93	130	1383	0.91	431	5585	0.93	276	1884	0.87	974	6068	0.86	1250	7952	0.86	589	6989	0.92	755	8011	0.91	1344	15000	0.92
ndhF	290	4	2227	1.00	3	934	1.00	7	3161	1.00	6	1267	1.00	28	4425	0.99	34	5692	0.99	24	4090	0.99	13	3162	1.00	37	7252	0.99
ndhG	50	652	3457	0.84	322	2296	0.88	974	5753	0.86	527	2194	0.81	1228	5062	0.80	1755	7256	0.81	1151	5722	0.83	753	4927	0.87	1904	10649	0.85
petL	5	6	101	0.94	1	11	0.92	7	112	0.94	4	87	0.96	41	335	0.89	45	422	0.90	40	578	0.94	16	254	0.94	56	832	0.94
psbE	214	42	17603	1.00	5	3017	1.00	47	20620	1.00	31	7967	1.00	143	25093	0.99	174	33060	0.99	46	10205	1.00	49	14809	1.00	95	25014	1.00
psbF	77	5	643	0.99	0	203	1.00	5	846	0.99	7	332	0.98	42	810	0.95	49	1142	0.96	37	1120	0.97	15	638	0.98	52	1758	0.97
psbZ	50	123	3563	0.97	5	195	0.98	128	3758	0.97	188	2427	0.93	699	9010	0.93	887	11437	0.93	440	7234	0.94	370	6182	0.94	810	13416	0.94
rpl23	89	504	7044	0.93	101	2725	0.96	605	9769	0.94	499	3705	0.88	1341	12589	0.90	1840	16294	0.90	1621	8298	0.84	1342	9997	0.88	2963	18295	0.86
rpoA	200	146	2886	0.95	13	516	0.98	159	3402	0.96	235	826	0.78	899	7664	0.90	1134	8490	0.88	602	2635	0.81	975	4325	0.82	1577	6960	0.82
rpoB	338	104	2354	0.96	27	827	0.97	131	3181	0.96	124	1176	0.90	231	3418	0.94	355	4594	0.93	281	2861	0.91	276	3183	0.92	557	6044	0.92
rpoB	551	101	2087	0.95	17	876	0.98	118	2963	0.96	90	1168	0.93	168	3358	0.95	258	4526	0.95	165	2687	0.94	223	3191	0.93	388	5878	0.94
rpoBF	2432	72	1763	0.96	10	223	0.96	82	1986	0.96	51	795	0.94	147	2625	0.95	198	3420	0.95	116	1182	0.91	156	1793	0.92	272	2975	0.92
rpoC1	488	5516	2426	0.31	4090	1214	0.23	9606	3640	0.27	3267	665	0.17	11074	2000	0.15	14341	2665	0.16	10306	3185	0.24	7098	1662	0.19	17404	4847	0.22
rps12- intron		542	129	0.19	49	24	0.33	591	153	0.21	292	84	0.22	907	313	0.26	1199	397	0.25	705	234	0.25	509	188	0.27	1214	422	0.26
rps14	80	185	8523	0.98	52	2492	0.98	237	11015	0.98	470	7367	0.94	1273	15717	0.93	1743	23084	0.93	426	12712	0.97	301	9224	0.97	727	21936	0.97
rps14	149	22	344	0.94	2	52	0.96	24	396	0.94	41	276	0.87	110	822	0.88	151	1098	0.88	133	653	0.83	80	394	0.83	213	1047	0.83
atp1	1110	3227	716	0.18	930	261	0.22	4157	977	0.19	1989	115	0.05	6147	644	0.09	8136	759	0.09	4688	335	0.07	3921	289	0.07	8609	624	0.07
atp1	1178	42	4305	0.99	13	1267	0.99	55	5572	0.99	13	2384	0.99	57	7634	0.99	70	10018	0.99	33	5349	0.99	23	4668	1.00	56	10017	0.99
atp1	1292	17	4315	1.00	6	929	0.99	23	5244	1.00	12	2350	0.99	29	8113	1.00	41	10463	1.00	32	5045	0.99	23	4908	1.00	55	9953	0.99
atp1	1415	31	1888	0.98	4	187	0.98	35	2075	0.98	8	1124	0.99	61	4391	0.99	69	5515	0.99	29	2954	0.99	36	2183	0.98	65	5137	0.99
atp1	1425	1335	233	0.15	107	20	0.16	1442	253	0.15	661	280	0.30	2558	1180	0.32	3219	1460	0.31	2133	415	0.16	1492	322	0.18	3625	737	0.17
atp1	1484	147	8447	0.98	44	1669	0.97	191	10116	0.98	37	4636	0.99	141	15035	0.99	178	19671	0.99	107	10532	0.99	94	8801	0.99	201	19333	0.99
atp4	55	7311	108	0.01	3082	63	0.02	10393	171	0.02	2903	102	0.03	7958	189	0.02	10861	291	0.03	7124	99	0.01	5864	71	0.01	12988	170	0.01
atp4	89	92	7730	0.99	57	3132	0.98	149	10862	0.99	27	3130	0.99	74	8696	0.99	101	11826	0.99	97	7579	0.99	67	6259	0.99	164	13838	0.99
atp4	138	79	1501	0.95	11	221	0.95	90	1722	0.95	53	606	0.92	175	2139	0.92	228	2745	0.92	126	1596	0.93	126	1294	0.91	252	2890	0.92
atp4	144	1616	188	0.10	253	32	0.11	1869	220	0.11	718	28	0.04	2415	146	0.06	3133	174	0.05	1786	52	0.03	1552	43	0.03	3338	95	0.03
atp4	215	25	3033	0.99	6	753	0.99	31	3786	0.99	10	1215	0.99	27	3623	0.99	37	4838	0.99	29	2530	0.99	27	2513	0.99	56	5043	0.99
atp4	248	31	2985	0.99	12	843	0.99	43	3828	0.99	15	1197	0.99	40	3559	0.99	55	4756	0.99	31	2515	0.99	30	2569	0.99	61	5084	0.99
atp4	250	468	2530	0.84	74	779	0.91	542	3309	0.86	102	1096	0.91	270	3317	0.92	372	4413	0.92	392	2131	0.84	363	2247	0.86	755	4378	0.85
atp4	251	25	2985	0.99	10	840	0.99	35	3825	0.99	9	1195	0.99	20	3581	0.99	29	4776	0.99	18	2508	0.99	20	2598	0.99	38	5106	0.99
atp4	382	1993	1422	0.42	459	487	0.51	2452	1909	0.44	1379	45	0.03	4428	161	0.04	5807	206	0.03	2965	40	0.01	2814	44	0.02	5779	84	0.01
atp4	395	31	2873	0.99	3	777	1.00	34	3650	0.99	11	1229	0.99	32	3978	0.99	43	5207	0.99	29	2656	0.99	34	2431	0.99	63	5087	0.99

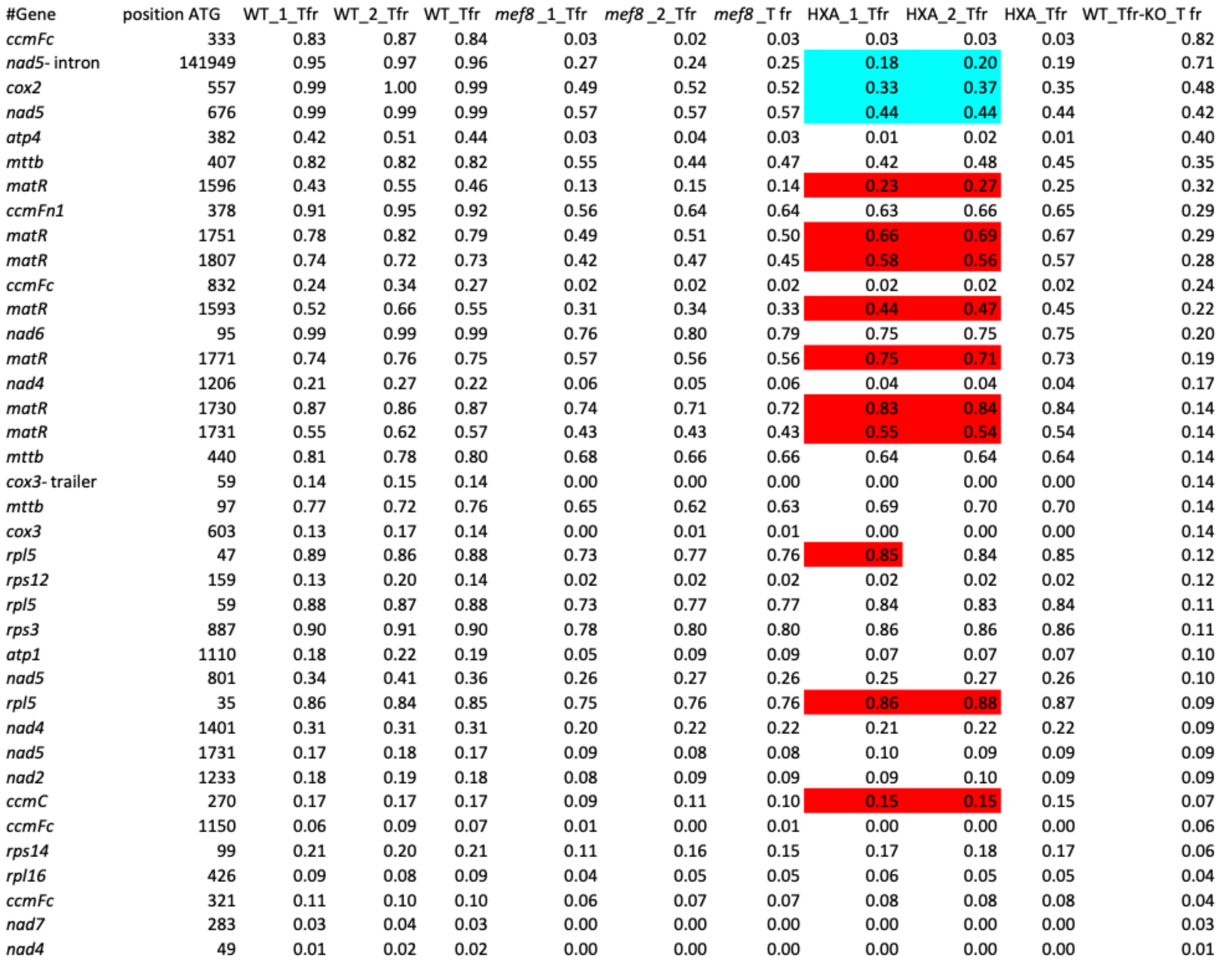
Table S-4.1 Continued

atp4	416	56	2302	0.98	10	566	0.98	66	2868	0.98	21	967	0.98	43	3298	0.99	64	4265	0.99	43	2245	0.98	32	1960	0.98	75	4205	0.98
atp4	525	7311	1200	0.14	2704	627	0.19	10015	1827	0.15	2677	607	0.18	7418	1511	0.17	10095	2118	0.17	6656	965	0.13	5742	856	0.13	12398	1821	0.13
atp6	71	5584	105	0.02	3085	87	0.03	8669	192	0.02	1893	44	0.02	6786	120	0.02	8679	164	0.02	5664	68	0.01	5744	82	0.01	11408	150	0.01
atp6	475	41	3465	0.99	14	1403	0.99	55	4868	0.99	63	1329	0.95	156	4084	0.96	219	5413	0.96	86	3604	0.98	99	3631	0.97	185	7235	0.98
atp8	78	14160	230	0.02	4389	92	0.02	18549	322	0.02	4637	111	0.02	15253	431	0.03	19890	542	0.03	14333	284	0.02	10746	207	0.02	25079	491	0.02
atp8	303	3055	180	0.06	290	13	0.04	3345	193	0.05	1329	24	0.02	5092	115	0.02	6421	139	0.02	3606	113	0.03	2952	75	0.02	6558	188	0.03
atp8	389	14447	490	0.03	3762	267	0.07	18209	757	0.04	4335	810	0.16	14216	2515	0.15	18551	3325	0.15	14039	1242	0.08	10083	1210	0.11	24122	2452	0.09
atp8	408	14361	339	0.02	3862	156	0.04	18223	495	0.03	4909	118	0.02	15728	571	0.04	20637	689	0.03	14512	360	0.02	10804	261	0.02	25316	621	0.02
atp9	53	43	7028	0.99	2	897	1.00	45	7925	0.99	27	4543	0.99	74	18378	1.00	101	22921	1.00	95	18222	0.99	71	13039	0.99	166	31261	0.99
atp9	83	59	7087	0.99	5	907	0.99	64	7994	0.99	42	4582	0.99	109	18636	0.99	151	23218	0.99	140	18501	0.99	104	13206	0.99	244	31707	0.99
atp9	117	201	30	0.13	25	4	0.14	226	34	0.13	126	23	0.15	676	121	0.15	802	144	0.15	777	147	0.16	456	57	0.11	1233	204	0.14
atp9	167	90	6288	0.99	23	2027	0.99	113	8315	0.99	35	4258	0.99	144	17435	0.99	179	21693	0.99	152	17957	0.99	93	12391	0.99	245	30348	0.99
atp9	224	48	6182	0.99	4	2031	1.00	52	8213	0.99	36	4172	0.99	161	16962	0.99	197	21134	0.99	133	17465	0.99	97	12051	0.99	230	29516	0.99
ccmB	16	556	4299	0.89	137	1392	0.91	693	5691	0.89	132	1745	0.93	529	6018	0.92	661	7763	0.92	430	4743	0.92	345	4563	0.93	775	9306	0.92
ccmB	28	380	4539	0.92	81	1456	0.95	461	5995	0.93	72	1836	0.96	386	6314	0.94	458	8150	0.95	249	5038	0.95	234	4781	0.95	483	9819	0.95
ccmB	44	4953	100	0.02	1523	36	0.02	6476	136	0.02	1884	84	0.04	6688	250	0.04	8572	334	0.04	5293	231	0.04	4939	264	0.05	10232	495	0.05
ccmB	45	4993	71	0.01	1530	29	0.02	6523	100	0.02	1948	23	0.01	6842	106	0.02	8790	129	0.01	5446	91	0.02	5129	85	0.02	10575	176	0.02
ccmB	48	5051	33	0.01	1544	17	0.01	6595	50	0.01	1937	40	0.02	6824	149	0.02	8761	189	0.02	5478	87	0.02	5129	104	0.02	10607	191	0.02
ccmB	71	27	353	0.93	4	55	0.93	31	408	0.93	11	167	0.94	51	682	0.93	62	849	0.93	36	620	0.95	34	474	0.93	70	1094	0.94
ccmB	75	353	38	0.10	52	9	0.15	405	47	0.10	150	29	0.16	587	163	0.22	737	192	0.21	615	52	0.08	472	53	0.10	1087	105	0.09
ccmB	80	120	290	0.71	18	45	0.71	138	335	0.71	45	140	0.76	184	585	0.76	229	725	0.76	117	567	0.83	78	468	0.86	195	1035	0.84
ccmB	128	139	666	0.83	22	113	0.84	161	779	0.83	48	244	0.84	169	957	0.85	217	1201	0.85	109	860	0.89	106	788	0.88	215	1648	0.88
ccmB	137	115	827	0.88	12	144	0.92	127	971	0.88	27	314	0.92	111	1108	0.91	138	1422	0.91	92	922	0.91	75	915	0.92	167	1837	0.92
ccmB	138	894	52	0.05	149	13	0.08	1043	65	0.06	286	57	0.17	1040	206	0.17	1326	263	0.17	926	94	0.09	916	99	0.10	1842	193	0.09
ccmB	148	137	1014	0.88	15	184	0.92	152	1198	0.89	41	364	0.90	184	1318	0.88	225	1682	0.88	123	1041	0.89	125	1092	0.90	248	2133	0.90
ccmB	149	137	1034	0.88	18	183	0.91	155	1217	0.89	37	376	0.91	145	1382	0.91	182	1758	0.91	122	1055	0.90	106	1131	0.91	228	2186	0.91
ccmB	154	157	1106	0.88	15	204	0.93	172	1310	0.88	31	414	0.93	141	1532	0.92	172	1946	0.92	114	1150	0.91	105	1247	0.92	219	2397	0.92
ccmB	159	180	1163	0.87	19	223	0.92	199	1386	0.87	47	433	0.90	171	1603	0.90	218	2036	0.90	143	1202	0.89	141	1315	0.90	284	2517	0.90
ccmB	160	174	1183	0.87	20	223	0.92	194	1406	0.88	47	437	0.90	183	1612	0.90	230	2049	0.90	145	1217	0.89	130	1356	0.91	275	2573	0.90
ccmB	164	271	1145	0.81	37	232	0.86	308	1377	0.82	64	452	0.88	230	1656	0.88	294	2108	0.88	200	1222	0.86	197	1373	0.87	397	2595	0.87
ccmB	172	143	1409	0.91	21	310	0.94	164	1719	0.91	38	541	0.93	173	1901	0.92	211	2442	0.92	122	1422	0.92	123	1595	0.93	245	3017	0.92
ccmB	179	215	1480	0.87	39	329	0.89	254	1809	0.88	52	576	0.92	204	2039	0.91	256	2615	0.91	143	1541	0.92	137	1722	0.93	280	3263	0.92
ccmB	181	137	1588	0.92	21	360	0.94	158	1948	0.92	40	607	0.94	164	2143	0.93	204	2750	0.93	118	1611	0.93	102	1800	0.95	220	3411	0.94
ccmB	193	650	1478	0.69	164	326	0.67	814	1804	0.69	282	533	0.65	745	2129	0.74	1027	2662	0.72	719	1414	0.66	739	1604	0.68	1458	3018	0.67
ccmB	194	659	1503	0.70	163	338	0.67	822	1841	0.69	248	585	0.70	676	2240	0.77	924	2825	0.75	613	1575	0.72	615	1771	0.74	1228	3346	0.73
ccmB	196	2155	73	0.03	485	27	0.05	2640	100	0.04	812	49	0.06	2843	165	0.05	3655	214	0.06	2185	59	0.03	2374	86	0.03	4559	145	0.03
ccmB	271	3387	105	0.03	1041	48	0.04	4428	153	0.03	1295	34	0.03	4702	141	0.03	5997	175	0.03	3489	35	0.01	3821	58	0.01	7310	93	0.01
ccmB	286	396	3054	0.89	95	985	0.91	491	4039	0.89	73	1255	0.95	333	4432	0.93	406	5687	0.93	207	3285	0.94	167	3651	0.96	374	6936	0.95
ccmB	304	526	2676	0.84	150	893	0.86	676	3569	0.84	70	1137	0.94	344	3999	0.92	414	5136	0.93	233	2973	0.93	214	3312	0.94	447	6285	0.93
ccmB	324	2862	151	0.05	920	56	0.06	3782	207	0.05	1084	83	0.07	3750	364	0.09	4834	447	0.08	2779	284	0.09	3032	339	0.10	5811	623	0.10
ccmB	338	501	2370	0.83	152	721	0.83	653	3091	0.83	74	1029	0.93	321	3589	0.92	395	4618	0.92	242	2684	0.92	212	2989	0.93	454	5673	0.93
ccmB	367	763	1528	0.67	177	458	0.72	940	1986	0.68	143	747	0.84	410	2623	0.86	553	3370	0.86	406	1867	0.82	369	2128	0.85	775	3995	0.84
ccmB	379	803	1344	0.63	178	390	0.69	981	1734	0.64	137	686	0.83	406	2406	0.86	543	3092	0.85	420	1693	0.80	340	1985	0.85	760	3678	0.83
ccmB	380	429	1694	0.80	126	442	0.78	555	2136	0.79	70	753	0.91	283	2520	0.90	353	3273	0.90	230	1882	0.89	191	2134	0.92	421	4016	0.91
ccmB	406	1407	414	0.23	268	130	0.33	1675	544	0.25	350	344	0.50	1331	1159	0.47	1681	1503	0.47	1218	672	0.36	1165	877	0.43	2383	1549	0.39
ccmB	424	209	1299	0.86	45	248	0.85	254	1547	0.86	96	480	0.83	375	1741	0.82	471	2221	0.83	356	1248	0.78	286	1394	0.83	642	2642	0.80
ccmB	428	118	1317	0.92	22	247	0.92	140	1564	0.92	30	532	0.95	142	1891	0.93	172	2423	0.93	100	1441	0.94	83	1508	0.95	183	2949	0.94
ccmB	441	1202	65	0.05	203	20	0.09	1405	85	0.06	484	29	0.06	1729	86	0.05	2213	115	0.05	1323	70	0.05	1348	82	0.06	2671	152	0.05
ccmB	467	126	766	0.86	17	107	0.86	143	873	0.86	29	343	0.92	157	1245	0.89	186	1588	0.90	116	974	0.89	73	979	0.93	189	1953	0.91
ccmB	475	81	655	0.89	15	79	0.84	96	734	0.88	22	289	0.93	126	1059	0.89	148	1348	0.90	76	848	0.92	58	829	0.93	134	1677	0.93
ccmB	476	76	644	0.89	13	78	0.86	89	722	0.89	22	287	0.93	123	1052	0.90	145	1339	0.90	75	839	0.92	57	820	0.94	132	1659	0.93
ccmB	485	57	550	0.91	11	59	0.84	68	609	0.90	26	236	0.90	110	912	0.89	136	1148	0.89	66	735	0.92	49	709	0.94	115	1444	0.93
ccmB	512	42	387	0.90	4	57	0.93	46	444	0.91	9	177	0.95	62	629	0.91	71	806	0.92	47	519	0.92	37	473	0.93	84	992	0.92
ccmB	514	20	417	0.95	2	69	0.97	22	486	0.96	9	186	0.95	39	658	0.94	48	844	0.95	31	540	0.95	20	488	0.96	51	1028	0.95
ccmB	551	274	3775	0.93	73	1468	0.95	347	5243	0.94	67	1617	0.96	284	5166	0.95	351	6783	0.95	217	4488	0.95	213	4403	0.95	430	8891	0.95
ccmB	554	258	3784	0.94	73	1467	0.95	331	5251	0.94	93	1589	0.94	273	5175	0.95	366	6764	0.95	227	4477	0.95	213	4398	0.95	440	8875	0.95
ccmB	566	350	3685	0.91	102	1436	0.93	452	5121	0.92	87	1590	0.95	304	5121	0.94	391	6711	0.94	239	4444	0.95	233	4364	0.95	472	8808	0.95
ccmB	569	374	3658	0.91	96	1442	0.94	470	5100	0.92	92	1584	0.95	296	5124	0.95	388	6708	0.95	242	4439	0.95	250	4346	0.95	492	8785	0.95

Table S-4.1 Continued

ccmB	576	2787	1243	0.31	903	634	0.41	3690	1877	0.34	582	1093	0.65	1765	3654	0.67	2347	4747	0.67	2716	1958	0.42	2413	2185	0.48	5129	4143	0.45
ccmB	596	639	3353	0.84	252	1277	0.84	891	4630	0.84	238	1423	0.86	607	4743	0.89	845	6166	0.88	432	4160	0.91	443	4083	0.90	875	8243	0.90
ccmC	103	209	4951	0.96	142	2567	0.95	351	7518	0.96	109	3837	0.97	218	8491	0.97	327	12328	0.97	249	9422	0.97	188	6638	0.97	437	16060	0.97
ccmC	133	105	5242	0.98	50	2705	0.98	155	7947	0.98	57	4087	0.99	97	9081	0.99	154	13168	0.99	150	10121	0.99	121	7059	0.98	271	17180	0.98
ccmC	176	842	14	0.02	274	8	0.03	1116	22	0.02	779	24	0.03	1814	60	0.03	2593	84	0.03	2225	58	0.03	1292	49	0.04	3517	107	0.03
ccmC	179	27	880	0.97	9	290	0.97	36	1170	0.97	14	826	0.98	25	1959	0.99	39	2785	0.99	48	2318	0.98	15	1391	0.99	63	3709	0.98
ccmC	184	123	889	0.88	77	273	0.78	200	1162	0.85	220	719	0.77	422	1762	0.81	642	2481	0.79	319	2254	0.88	186	1379	0.88	505	3633	0.88
ccmC	252	1452	733	0.34	635	239	0.27	2087	972	0.32	1297	524	0.29	3093	1036	0.25	4390	1560	0.26	2593	1672	0.39	1773	1290	0.42	4366	2962	0.40
ccmC	270	1994	409	0.17	775	156	0.17	2769	565	0.17	1793	175	0.09	3892	472	0.11	5685	647	0.10	3784	667	0.15	2798	491	0.15	6582	1158	0.15
ccmC	331	87	2650	0.97	59	1391	0.96	146	4041	0.97	86	2086	0.96	140	4517	0.97	226	6603	0.97	115	4897	0.98	97	3554	0.97	212	8451	0.98
ccmC	381	1856	436	0.19	1212	264	0.18	3068	700	0.19	1490	355	0.19	3262	648	0.17	4752	1003	0.17	3608	820	0.19	2486	697	0.22	6094	1517	0.20
ccmC	395	72	1962	0.96	41	1260	0.97	113	3222	0.97	27	1558	0.98	57	3381	0.98	84	4939	0.98	101	3831	0.97	56	2742	0.98	157	6573	0.98
ccmC	400	247	1753	0.88	200	1057	0.84	447	2810	0.86	232	1318	0.85	494	2875	0.85	726	4193	0.85	469	3425	0.88	320	2419	0.88	789	5844	0.88
ccmC	421	257	1626	0.86	269	818	0.75	526	2444	0.82	255	1161	0.82	476	2668	0.85	731	3829	0.84	371	3240	0.90	387	2256	0.85	758	5496	0.88
ccmC	436	87	1699	0.95	51	914	0.95	138	2613	0.95	38	1261	0.97	87	2878	0.97	125	4139	0.97	112	3242	0.97	67	2386	0.97	179	5628	0.97
ccmC	446	102	1449	0.93	44	732	0.94	146	2181	0.94	36	1082	0.97	79	2485	0.97	115	3567	0.97	93	2816	0.97	63	2077	0.97	156	4893	0.97
ccmC	458	193	1252	0.87	149	540	0.78	342	1792	0.84	116	902	0.89	274	2075	0.88	390	2977	0.88	231	2468	0.91	187	1789	0.91	418	4257	0.91
ccmC	463	207	1207	0.85	114	562	0.83	321	1769	0.85	84	902	0.91	165	2141	0.93	249	3043	0.92	225	2401	0.91	141	1766	0.93	366	4167	0.92
ccmC	467	256	1162	0.82	143	528	0.79	399	1690	0.81	142	842	0.86	318	2008	0.86	460	2850	0.86	340	2292	0.87	233	1652	0.88	573	3944	0.87
ccmC	473	167	1287	0.89	72	608	0.89	239	1895	0.89	46	975	0.95	108	2307	0.96	154	3282	0.96	160	2559	0.94	91	1831	0.95	251	4390	0.95
ccmC	497	197	1304	0.87	132	553	0.81	329	1857	0.85	254	840	0.77	447	2110	0.83	701	2950	0.81	506	2396	0.83	391	1657	0.81	897	4053	0.82

Table S-4.2. Editing extent of the mitochondrial sites exhibiting a significant decrease of editing extent in the *mef8* mutant.



#Gene	position ATG	WT_1_Tfr	WT_2_Tfr	WT_Tfr	*mef8* _1_Tfr	*mef8* _2_Tfr	*mef8* _T fr	HXA_1_Tfr	HXA_2_Tfr	HXA_Tfr	WT_Tfr-KO_T fr
ccmFc	333	0.83	0.87	0.84	0.03	0.02	0.03	0.03	0.03	0.03	0.82
nad5- intron	141949	0.95	0.97	0.96	0.27	0.24	0.25	0.18	0.20	0.19	0.71
cox2	557	0.99	1.00	0.99	0.49	0.52	0.52	0.33	0.37	0.35	0.48
nad5	676	0.99	0.99	0.99	0.57	0.57	0.57	0.44	0.44	0.44	0.42
atp4	382	0.42	0.51	0.44	0.03	0.04	0.03	0.01	0.02	0.01	0.40
mttb	407	0.82	0.82	0.82	0.55	0.44	0.47	0.42	0.48	0.45	0.35
matR	1596	0.43	0.55	0.46	0.13	0.15	0.14	0.23	0.27	0.25	0.32
ccmFn1	378	0.91	0.95	0.92	0.56	0.64	0.64	0.63	0.66	0.65	0.29
matR	1751	0.78	0.82	0.79	0.49	0.51	0.50	0.66	0.69	0.67	0.29
matR	1807	0.74	0.72	0.73	0.42	0.47	0.45	0.58	0.56	0.57	0.28
ccmFc	832	0.24	0.34	0.27	0.02	0.02	0.02	0.02	0.02	0.02	0.24
matR	1593	0.52	0.66	0.55	0.31	0.34	0.33	0.44	0.47	0.45	0.22
nad6	95	0.99	0.99	0.99	0.76	0.80	0.79	0.75	0.75	0.75	0.20
matR	1771	0.74	0.76	0.75	0.57	0.56	0.56	0.75	0.71	0.73	0.19
nad4	1206	0.21	0.27	0.22	0.06	0.05	0.06	0.04	0.04	0.04	0.17
matR	1730	0.87	0.86	0.87	0.74	0.71	0.72	0.83	0.84	0.84	0.14
matR	1731	0.55	0.62	0.57	0.43	0.43	0.43	0.55	0.54	0.54	0.14
mttb	440	0.81	0.78	0.80	0.68	0.66	0.66	0.64	0.64	0.64	0.14
cox3- trailer	59	0.14	0.15	0.14	0.00	0.00	0.00	0.00	0.00	0.00	0.14
mttb	97	0.77	0.72	0.76	0.65	0.62	0.63	0.69	0.70	0.70	0.14
cox3	603	0.13	0.17	0.14	0.00	0.01	0.01	0.00	0.00	0.00	0.14
rpl5	47	0.89	0.86	0.88	0.73	0.77	0.76	0.85	0.84	0.85	0.12
rps12	159	0.13	0.20	0.14	0.02	0.02	0.02	0.02	0.02	0.02	0.12
rpl5	59	0.88	0.87	0.88	0.73	0.77	0.77	0.84	0.83	0.84	0.11
rps3	887	0.90	0.91	0.90	0.78	0.80	0.80	0.86	0.86	0.86	0.11
atp1	1110	0.18	0.22	0.19	0.05	0.09	0.09	0.07	0.07	0.07	0.10
nad5	801	0.34	0.41	0.36	0.26	0.27	0.26	0.25	0.27	0.26	0.10
rpl5	35	0.86	0.84	0.85	0.75	0.76	0.76	0.86	0.88	0.87	0.09
nad4	1401	0.31	0.31	0.31	0.20	0.22	0.22	0.21	0.22	0.22	0.09
nad5	1731	0.17	0.18	0.17	0.09	0.08	0.08	0.10	0.09	0.09	0.09
nad2	1233	0.18	0.19	0.18	0.08	0.09	0.09	0.09	0.10	0.09	0.09
ccmC	270	0.17	0.17	0.17	0.09	0.11	0.10	0.15	0.15	0.15	0.07
ccmFc	1150	0.06	0.09	0.07	0.01	0.00	0.01	0.00	0.00	0.00	0.06
rps14	99	0.21	0.20	0.21	0.11	0.16	0.15	0.17	0.18	0.17	0.06
rpl16	426	0.09	0.08	0.09	0.04	0.05	0.05	0.06	0.05	0.05	0.04
ccmFc	321	0.11	0.10	0.10	0.06	0.07	0.07	0.08	0.08	0.08	0.04
nad7	283	0.03	0.04	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.03
nad4	49	0.01	0.02	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.01

X_n_Tfr (editing extent), WT: wild-type, *mef8* : *mef8* mutant, HXA: transgenic *mef8* transformed with a mutated MEF8 where E in HXE has been substituted by A. _1 and _2 refer to the two biological replicates assayed by genotype. The sites are presented by decreasing value of the difference in editing extent between the wild-type and the *mef8* mutant (WT_Tfr-KO_T fr). The blue (red) background for each HXA replicate represents an editing extent value which is significantly lower (higher) than both *mef8* mutants.

Table S-4.3. Editing extent of the mitochondrial sites exhibiting a significant increase of editing extent in the *mef8* mutant.

#Gene	position ATG	WT_1_Tfr	WT_2_Tfr	WT-Tfr	mef8_1_Tfr	mef8_2_Tfr	*mef8* _T fr	HXA_1_Tfr	HXA_2_Tfr	HXA_Tfr	WT_Tfr-*mef8* _T fr
ccmB	576	0.31	0.41	0.34	0.65	0.67	0.67	0.42	0.48	0.45	-0.33
rpl16- trailer	391	0.29	0.34	0.31	0.58	0.62	0.61	0.36	0.30	0.33	-0.30
nad7	1137	0.61	0.70	0.64	0.88	0.88	0.88	0.78	0.81	0.80	-0.24
ccmB	406	0.23	0.33	0.25	0.50	0.47	0.47	0.36	0.43	0.39	-0.23
ccmB	379	0.63	0.69	0.64	0.83	0.86	0.85	0.80	0.85	0.83	-0.21
ccmB	367	0.67	0.72	0.68	0.84	0.86	0.86	0.82	0.85	0.84	-0.18
ccmFc	1280	0.59	0.54	0.58	0.66	0.76	0.73	0.67	0.59	0.64	-0.16
nad7	910	0.07	0.08	0.07	0.19	0.23	0.22	0.13	0.12	0.12	-0.15
nad3	149	0.74	0.79	0.75	0.89	0.90	0.89	0.85	0.85	0.85	-0.14
nad3	211	0.78	0.78	0.78	0.90	0.90	0.90	0.88	0.88	0.88	-0.12
nad3	212	0.78	0.80	0.79	0.90	0.90	0.90	0.89	0.88	0.89	-0.11
nad7- intron2	134282	0.06	0.11	0.07	0.17	0.19	0.19	0.04	0.04	0.04	-0.11
atp8	389	0.03	0.07	0.04	0.16	0.15	0.15	0.08	0.11	0.09	-0.11
ccmB	380	0.80	0.78	0.79	0.91	0.90	0.90	0.89	0.92	0.91	-0.11
nad2	28	0.65	0.64	0.65	0.77	0.73	0.74	0.81	0.83	0.82	-0.10
ccmB	338	0.83	0.83	0.83	0.93	0.92	0.92	0.92	0.93	0.93	-0.10
rpl16- trailer	72	0.05	0.08	0.06	0.13	0.15	0.15	0.06	0.06	0.06	-0.09
rpl16- trailer	105	0.07	0.12	0.09	0.18	0.17	0.17	0.07	0.08	0.08	-0.08
nad4	303	0.02	0.03	0.03	0.09	0.10	0.10	0.04	0.04	0.04	-0.08
nad4	385	0.04	0.06	0.05	0.12	0.12	0.12	0.07	0.07	0.07	-0.07
nad9	517	0.03	0.05	0.04	0.11	0.10	0.10	0.03	0.04	0.03	-0.06
nad4	753	0.03	0.04	0.03	0.10	0.08	0.09	0.04	0.04	0.04	-0.05
nad2	285	0.05	0.06	0.05	0.09	0.10	0.10	0.06	0.06	0.06	-0.05
nad4	279	0.02	0.02	0.02	0.05	0.05	0.05	0.02	0.02	0.02	-0.04

X_n_Tfr (editing extent), WT: wild-type, *mef8* : *mef8* mutant, HXA: transgenic *mef8* transformed with a mutated MEF8 where E in HXE has been substituted by A. _1 and _2 refer to the two biological replicates assayed by genotype. The sites are presented by increasing value of the difference in editing extent between the wild-type and the *mef8* mutant (WT_Tfr-KO_T fr). The blue background for each HXA replicate represents an editing extent value which is significantly lower than both *mef8* mutants.

Table S-4.4 Editing extent of the mitochondrial sites exhibiting a significant decrease of editing extent in at least one of the HXA transgenic plant.

#Gene	position ATG	WT_1_Tfr	WT_2_Tfr	WT-Tfr	*mef8* _1_Tfr	*mef8* _2_Tfr	*mef8* _T fr	HXA_1_Tfr	HXA_2_Tfr	HXA_Tfr
atp1	1425	0.15	0.16	0.15	0.30	0.32	0.31	0.16	0.18	0.17
atp4	55	0.01	0.02	0.02	0.03	0.02	0.03	0.01	0.01	0.01
atp4	525	0.14	0.19	0.15	0.18	0.17	0.17	0.13	0.13	0.13
atp8	389	0.03	0.07	0.04	0.16	0.15	0.15	0.08	0.11	0.09
ccmB	406	0.23	0.33	0.25	0.50	0.47	0.47	0.36	0.43	0.39
ccmB	576	0.31	0.41	0.34	0.65	0.67	0.67	0.42	0.48	0.45
ccmFc	231	0.09	0.12	0.09	0.10	0.11	0.11	0.07	0.06	0.06
ccmFc	315	0.05	0.06	0.05	0.05	0.05	0.05	0.03	0.03	0.03
ccmFc	378	0.22	0.24	0.23	0.24	0.20	0.21	0.15	0.15	0.15
ccmFc	1215	0.52	0.67	0.55	0.76	0.81	0.80	0.63	0.57	0.61
ccmFc	1280	0.59	0.54	0.58	0.66	0.76	0.73	0.67	0.59	0.64
cob	610	0.10	0.09	0.10	0.17	0.19	0.19	0.09	0.12	0.11
cox2	25	0.64	0.77	0.69	0.74	0.78	0.77	0.68	0.68	0.68
cox2	138	0.79	0.88	0.81	0.90	0.90	0.90	0.82	0.84	0.83
cox2	557	0.99	1.00	0.99	0.49	0.52	0.52	0.33	0.37	0.35
mttb	552	0.22	0.27	0.23	0.39	0.35	0.36	0.29	0.31	0.30
nad1	40	0.27	0.31	0.28	0.30	0.30	0.30	0.22	0.23	0.22
nad1	49	0.11	0.15	0.12	0.12	0.16	0.15	0.08	0.08	0.08
nad2	19	0.14	0.16	0.15	0.20	0.18	0.18	0.13	0.16	0.14
nad2	285	0.05	0.06	0.05	0.09	0.10	0.10	0.06	0.06	0.06
nad2	558	0.38	0.51	0.41	0.53	0.53	0.53	0.42	0.47	0.44
nad2	642	0.18	0.27	0.20	0.26	0.29	0.28	0.18	0.19	0.19
nad2	888	0.05	0.05	0.05	0.07	0.08	0.08	0.04	0.06	0.05
nad2	1107	0.02	0.04	0.03	0.05	0.05	0.05	0.03	0.03	0.03
nad3	254	0.85	0.90	0.86	0.84	0.85	0.85	0.79	0.76	0.78
nad4	261	0.06	0.09	0.07	0.08	0.12	0.11	0.05	0.05	0.05
nad4	279	0.02	0.02	0.02	0.05	0.05	0.05	0.02	0.02	0.02
nad4	303	0.02	0.03	0.03	0.09	0.10	0.10	0.04	0.04	0.04
nad4	385	0.04	0.06	0.05	0.12	0.12	0.12	0.07	0.07	0.07
nad4	753	0.03	0.04	0.03	0.10	0.08	0.09	0.04	0.04	0.04
nad4	1131	0.18	0.24	0.20	0.25	0.34	0.31	0.14	0.13	0.13
nad5	676	0.99	0.99	0.99	0.57	0.57	0.57	0.44	0.44	0.44
nad5	1287	0.04	0.05	0.04	0.07	0.09	0.08	0.04	0.05	0.04
nad5	1318	0.09	0.11	0.10	0.19	0.17	0.18	0.15	0.13	0.14
nad5	1929	0.16	0.21	0.17	0.13	0.13	0.13	0.11	0.10	0.10
nad5	1933	0.04	0.05	0.04	0.07	0.07	0.07	0.03	0.03	0.03
nad5- intron	141949	0.95	0.97	0.96	0.27	0.24	0.25	0.18	0.20	0.19
nad5- intron	141966	0.37	0.62	0.46	0.38	0.47	0.45	0.27	0.33	0.30
nad6	90	0.07	0.11	0.08	0.08	0.09	0.08	0.04	0.04	0.04
nad6	362	0.02	0.04	0.02	0.05	0.06	0.06	0.02	0.02	0.02
nad6 -leader	-1	0.25	0.37	0.28	0.30	0.29	0.29	0.21	0.20	0.20
nad7- leader	-39	0.48	0.50	0.49	0.61	0.54	0.55	0.47	0.45	0.46
nad7	789	0.19	0.24	0.21	0.32	0.33	0.33	0.23	0.30	0.27
nad7	795	0.82	0.80	0.81	0.87	0.88	0.88	0.77	0.81	0.79
nad7	910	0.07	0.08	0.07	0.19	0.23	0.22	0.13	0.12	0.12
nad7	1083	0.02	0.04	0.03	0.04	0.04	0.04	0.02	0.02	0.02
nad7	1137	0.61	0.70	0.64	0.88	0.88	0.88	0.78	0.81	0.80
nad7- 2intron	134282	0.06	0.11	0.07	0.17	0.19	0.19	0.04	0.04	0.04
nad9	517	0.03	0.05	0.04	0.11	0.10	0.10	0.03	0.04	0.03
rpl16	43	0.08	0.12	0.09	0.09	0.12	0.12	0.07	0.09	0.08
rpl16- trailer	72	0.05	0.08	0.06	0.13	0.15	0.15	0.06	0.06	0.06
rpl16- trailer	105	0.07	0.12	0.09	0.18	0.17	0.17	0.07	0.08	0.08
rpl16- trailer	327	0.69	0.77	0.73	0.86	0.82	0.83	0.68	0.68	0.68
rpl16- trailer	391	0.29	0.34	0.31	0.58	0.62	0.61	0.36	0.30	0.33
rps3	126	0.04	0.13	0.06	0.10	0.13	0.12	0.04	0.04	0.04
rps3	210	0.07	0.14	0.09	0.09	0.09	0.09	0.07	0.05	0.06
rps3	270	0.04	0.10	0.06	0.08	0.13	0.12	0.03	0.03	0.03
rps3	515	0.04	0.06	0.05	0.09	0.10	0.10	0.03	0.04	0.04
rps3	603	0.80	0.88	0.83	0.85	0.90	0.89	0.73	0.73	0.73
rps3	1260	0.09	0.13	0.10	0.13	0.17	0.16	0.08	0.07	0.07
rps3	1344	0.59	0.71	0.62	0.53	0.72	0.68	0.37	0.36	0.37
rps4	77	0.81	0.73	0.79	0.84	0.89	0.88	0.79	0.76	0.78
rps4	235	0.85	0.81	0.84	0.84	0.91	0.90	0.81	0.74	0.78

Table S-4.5 Editing extent of the mitochondrial sites exhibiting a significant increase of editing extent in at least one of the HXA transgenic plant

#Gene	position ATG	WT_1_Tfr	WT_2_Tfr	WT-Tfr	*mef8* _1_Tfr	*mef8* _2_Tfr	*mef8* _T fr	HXA_1_Tfr	HXA_2_Tfr	HXA_Tfr
ccmC	252	0.34	0.27	0.32	0.29	0.25	0.26	0.39	0.42	0.40
ccmC	270	0.17	0.17	0.17	0.09	0.11	0.10	0.15	0.15	0.15
ccmC	673	0.84	0.71	0.78	0.69	0.76	0.74	0.86	0.84	0.85
matR	374	0.75	0.82	0.77	0.71	0.74	0.73	0.82	0.84	0.83
matR	1593	0.52	0.66	0.55	0.31	0.34	0.33	0.44	0.47	0.45
matR	1596	0.43	0.55	0.46	0.13	0.15	0.14	0.23	0.27	0.25
matR	1730	0.87	0.86	0.87	0.74	0.71	0.72	0.83	0.84	0.84
matR	1731	0.55	0.62	0.57	0.43	0.43	0.43	0.55	0.54	0.54
matR	1751	0.78	0.82	0.79	0.49	0.51	0.50	0.66	0.69	0.67
matR	1771	0.74	0.76	0.75	0.57	0.56	0.56	0.75	0.71	0.73
matR	1807	0.74	0.72	0.73	0.42	0.47	0.45	0.58	0.56	0.57
orf114	309	0.51	0.37	0.48	0.60	0.60	0.60	0.79	0.79	0.79
rpl2	212	0.67	0.70	0.67	0.63	0.66	0.65	0.73	0.70	0.72
rpl5	35	0.86	0.84	0.85	0.75	0.76	0.76	0.86	0.88	0.87
rpl5	47	0.89	0.86	0.88	0.73	0.77	0.76	0.85	0.84	0.85
rpl5	64	0.66	0.67	0.66	0.65	0.64	0.64	0.69	0.73	0.71

X_n_Tfr (editing extent), WT: wild-type, *mef8* : *mef8* mutant, HXA: transgenic *mef8* transformed with a mutated MEF8 where E in HXE has been substituted by A. _1 and _2 refer to the two biological replicates assayed by genotype. The sites are presented by alphabetical order. The red background for each *mef8* mutant replicate represents an editing extent value which is significantly lower than both wild-type replicates. The red background for each HXA replicate represents an editing extent value which is higher than both *mef8* mutants.

Table S-4.6. List of primers used in this study.

Primer Name	Description	Primer Sequence
MEF8_FWD1	forward primer to introduce mutation alanine substitution into HXE motif and generate reverse megaprimer	TGGTCATAGCGCGAGAATAGCT
MEF8_FWD2	forward primer for cloning MEF8 variants into pCHF1 plant expression vector; BglII restriction site	TGCTAGATCTATGTATACGAAGTTATCATTGTTCCCCAG
MEF8_REV1	reverse primer used to generate megaprimer and cloning MEF8 variants into pCHF1 plant expression vector; SalI restriction site	TTGTGTCGACTCACCAATAATCTTTACAGGTGCAAG
pCHF1_FWD	forward primer for sequencing MEF8	CCTTCGCAAGACCCTTCC
pCHF1_REV	revesrse primer for sequencing MEF8	GTGCGCAATGAAACTGATGC
MEF8_FWD3	forward primer for sequencing MEF8	GGATACCAATCTTCCTGAGAA
MEF8_REV2	reverse primer for sequencing MEF8	CATAGCTGTGTTAACTTTAAGAGTC
SALK_T-DNA_LB	Salk left border primer to confirm T-DNA insertions in SALK lines	ATTTTGCCGATTTCGGAAC
MEF8-qRT-F1	Forward primer upstream of the T-DNA insertion used for MEF8 qRT-PCR	TTCTAGCGAAGATCAGAGCTTTAGT
MEF8-qRT-R1	Reverse primer downstream of the T-DNA insertion used for MEF8 qRT-PCR	CTTCGCTAACCGTAAAAGTCTACTC
ccmB-qRT-F1	Forward primer used for *ccmB* qRT-PCR	TTCGGATCCCTCCGTTGTTT
ccmB-qRT-R1	Reverse primer used for *ccmB* qRT-PCR	TAACCCGGTGACCCACCAA
ccmB-qRT-F2*	Forward primer used for *ccmB* qRT-PCR	TCTTGGAATCACATCCAGCA
ccmB-qRT-R2*	Reverse primer used for *ccmB* qRT-PCR	CGAGACCGAAATTGGAAAAA
ccmFc-qRT-F1	Forward primer used for *ccmFc* qRT-PCR	CTTCGGCCGAACGGGAATGAG
ccmFc-qRT-R1	Reverse primer used for *ccmFc* qRT-PCR	TCGGCTCCTTGGTAAGGCGAGAG
ccmFc-qRT-F2*	Forward primer used for *ccmFc* qRT-PCR	CACATGGAGGAGTGTGCATC
ccmFc-qRT-R2*	Reverse primer used for *ccmFc* qRT-PCR	GTGGGTCCATGTAAATGATCG
matR-qRT-F1*	Forward primer used for *matR* qRT-PCR	AATTTTTGCGAGAGCTGGAA
matR-qRT-R1*	Reverse primer used for *matR* qRT-PCR	TTGAACCCCGTCCTGTAGAC
matR-qRT-F2	Forward primer used for *matR* qRT-PCR	CGGCGGGGGAGGGAGGAG
matR-qRT-R2	Reverse primer used for *matR* qRT-PCR	CGATGCCCGCGGACCAATTTAC
nad5-qRT-F1*	Forward primer used for *nad5* qRT-PCR	CCATGGATCTCATCGGAAAT
nad5-qRT-R1*	Reverse primer used for *nad5* qRT-PCR	TGGACCAAGCTACTTATGGATG
nad5-qRT-F2	Forward primer used for *nad5* qRT-PCR	AACAGCTGGCGTTTTCATGATAGC
nad5-qRT-R2	Reverse primer used for *nad5* qRT-PCR	TGCCGCAAGCAAAGATCATATAGC
rpl16-qRT-F1*	Forward primer used for *rpl16* qRT-PCR	CGGACACTTTCATCGTGCTA
rpl16-qRT-R1*	Reverse primer used for *rpl16* qRT-PCR	GAGCATTTGCCAAACTCACA
rpl16-qRT-F2	Forward primer used for *rpl16* qRT-PCR	AAGCGGGCCGAGAATCTTATGT
rpl16-qRT-R2	Reverse primer used for *rpl16* qRT-PCR	GCAGCATAGGGACAATTCCTTGTC
rps3-qRT-F1*	Forward primer used for *rps3* qRT-PCR	CCGATTTCGGTAAGACTTGG
rps3-qRT-R1*	Reverse primer used for *rps3* qRT-PCR	AGCCGAAGGTGAGTCTCGTA
rps3-qRT-F2	Forward primer used for *rps3* qRT-PCR	GGGGGCAAGGAAAAGAGTCGAGT
rps3-qRT-R2	Reverse primer used for *rps3* qRT-PCR	CCCGGCGTATTTCGGATGCT
rps4-qRT-F1*	Forward primer used for *rps4* qRT-PCR	ACCCATCACAGAGATGCACA
rps4-qRT-R1*	Reverse primer used for *rps4* qRT-PCR	TCACACAAACCCTTCGATGA
rps4-qRT-F2	Forward primer used for *rps4* qRT-PCR	GGATCCGAAAAAGTATGCTTAGGA
rps4-qRT-R2	Reverse primer used for *rps4* qRT-PCR	GGGGGATGCGAAGCAATAG

Note: all editotyping RT-PCR primers were retrieved from Bentolila S, Oh J, Hanson MR, Bukowski R (Plos Genetics, 2013).
*Primers from Koprivova et al. (J. Bio.l Chem., 2010)

Figure S-5.1. Percent total signal of acylated galactosyldiacylglycerols.

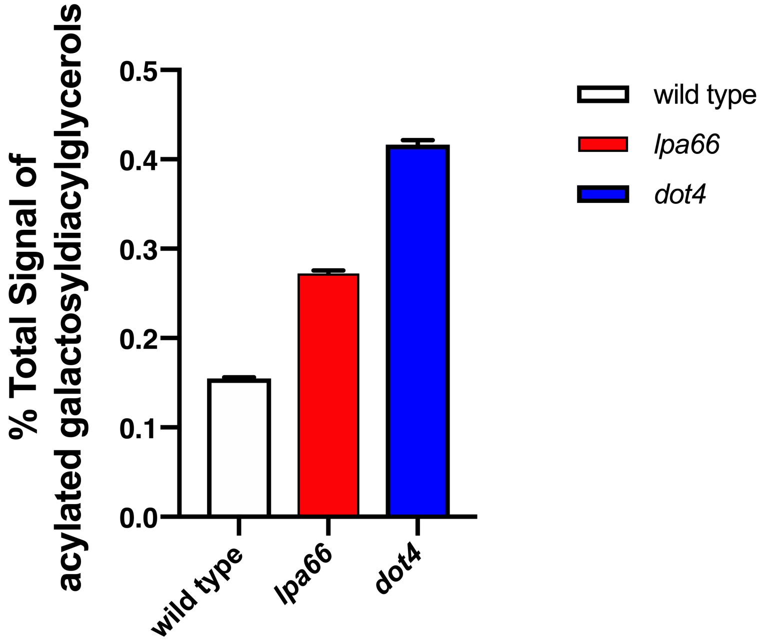


Figure S-5.2 Concentration and percent to total signal of mitochondria-derived cardiolipins.

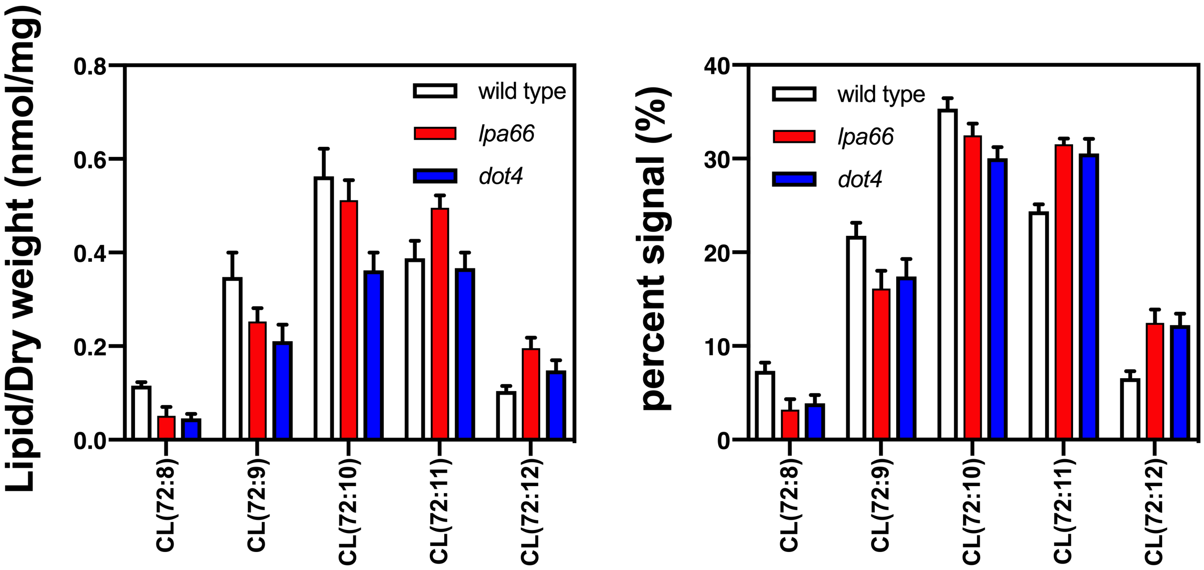


Table S-5.1 Differentially Expressed Genes between lpa66 (LP) and wild type (WT) Arabidopsis plants.

ID	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	WT4	WT2	WT1	LP3	LP2	LP1
AT1G01010	139.7108421	-1.273134844	0.30468703	-4.1785003	2.93E-05	0.00037534	220.386327	182.655542	190.291151	115.711057	58.0684893	71.1524862
AT1G01110	60.02612475	2.034278147	0.32234516	6.31086918	2.77E-10	1.38E-08	24.0231541	23.3393193	23.2803004	94.3490155	89.48259	105.682369
AT1G01190	39.875462	2.102203582	0.44152839	4.7611968	1.92E-06	3.62E-05	19.8452142	15.2212952	10.1218697	46.2844227	71.3956835	76.3842866
AT1G01200	32.37477189	1.331541757	0.49060662	2.71407216	0.00664617	0.03012533	14.6227894	27.3983314	13.1584307	31.1529768	61.876259	46.039844
AT1G01210	341.0707848	-1.227611911	0.23759603	-5.166803	2.38E-07	5.86E-06	577.600183	458.668362	397.789481	173.566585	249.408921	189.391176
AT1G01225	51.81646332	1.00058939	0.40094293	2.49559057	0.01257476	0.04888873	40.7349134	39.5753675	23.2803004	48.9546779	91.3864749	66.9670458
AT1G01600	19.20321454	1.961680611	0.68100639	2.88056125	0.00396968	0.02031099	6.26690976	5.07376507	12.1462437	12.4611907	44.741295	34.529883
AT1G01760	58.44821145	1.084382982	0.38004226	2.85332209	0.00432647	0.02166197	28.2010939	56.8261688	27.3290483	84.5580799	74.2515108	79.5233669
AT1G01900	209.8925722	1.258032196	0.48071674	2.61699268	0.00887082	0.03749904	68.9360074	214.112886	88.0602668	143.303693	296.054101	448.888479
AT1G02205	89.3053513	3.224973268	1.22791075	2.62639062	0.00862957	0.03673742	1.04448496	37.5458615	13.1584307	71.2068042	310.333238	102.543289
AT1G02220	248.3882082	-2.088537078	0.25855039	-8.0778724	6.59E-16	8.96E-14	448.084048	382.561886	376.533555	127.282162	74.2515108	81.6160871
AT1G02230	73.27725241	-6.522915508	0.77859713	-8.3777801	5.39E-17	8.35E-15	181.740383	168.449	85.0237059	4.45042526	0	0
AT1G02335	167.9353066	1.071620242	0.26979627	3.97196092	7.13E-05	0.00078918	83.5587968	130.903139	110.32838	202.049307	279.871079	200.901137
AT1G02340	68.70396182	2.025915408	0.62708666	3.23067852	0.00123497	0.0081296	44.9128533	21.3098133	15.1828046	225.191518	53.308777	52.3180045
AT1G02350	78.54752794	1.063608141	0.34536528	3.07966143	0.00207236	0.01222281	54.3132179	64.9441929	33.4021702	129.062333	103.761727	85.8015274
AT1G02370	229.3478753	-1.333043387	0.25772177	-5.1724127	2.31E-07	5.70E-06	348.857977	335.883248	300.619532	120.161482	173.253525	97.3114884
AT1G02390	38.40338993	1.729036235	0.470881	3.6719176	0.00024074	0.00213888	24.0231541	22.3245663	7.08530882	55.1852732	59.0204317	62.7816054
AT1G02450	25.3144596	-4.45667752	0.91362208	-4.8780317	1.07E-06	2.16E-05	81.4698269	54.7966627	9.10968277	3.56034021	1.90388489	1.04636009
AT1G02620	55.04335815	-1.669949717	0.49463648	-3.3761151	0.00073517	0.00536055	110.715406	60.8851808	79.962771	45.3943377	12.3752518	20.9272018
AT1G02660	2919.577378	-1.081262809	0.23195649	-4.6614898	3.14E-06	5.52E-05	4652.13601	3620.63875	3622.61718	2109.50157	1329.8636	2182.70715
AT1G02700	19.32065133	1.603406231	0.54459184	2.94423475	0.00323754	0.01723942	11.4893346	12.1770362	5.06093487	28.4827217	30.4621583	28.2517224
AT1G02710	11.88610764	2.423818318	0.8394227	2.88748245	0.00388338	0.01996883	0	5.07376507	6.07312185	13.3512758	23.7985612	23.019922
AT1G02730	196.7833525	1.382156831	0.43942635	3.14536633	0.00165879	0.01022625	61.6246126	158.30147	107.291819	132.622673	401.719713	319.139828
AT1G02816	446.4047926	-1.18259459	0.26614267	-4.443461	8.85E-06	0.00013349	641.313766	546.951874	671.079964	337.342235	175.15741	306.583507
AT1G02850	449.1950894	-3.473247804	0.90609389	-3.8332096	0.00012648	0.00127023	608.934732	538.83385	1324.95275	162.885565	21.8946763	37.6689633
AT1G02870	532.0785201	-1.586433126	0.16227752	-9.7760501	1.43E-22	5.90E-20	829.321058	794.55161	771.286475	258.124665	292.246331	246.940981
AT1G02930	2552.62829	1.265040877	0.37530957	3.37065982	0.00074988	0.00544281	1606.41787	1565.7639	1327.98931	4409.48135	1431.72144	4974.39587
AT1G03010	34.51235379	3.540517398	0.53530237	6.61405139	3.74E-11	2.17E-09	6.26690976	7.1032711	3.03656092	54.2951882	80.915108	55.4570848
AT1G03090	1549.951988	-1.001068493	0.29864649	-3.3520183	0.00080225	0.00576313	1739.06746	1954.4143	2508.19932	1496.23297	655.888346	945.909522
AT1G03340	112.2148985	-1.433231066	0.29183798	-4.9110506	9.06E-07	1.87E-05	158.761714	155.257211	177.132721	65.8662939	40.9335252	75.3379265
AT1G03360	241.1175096	-1.5063945	0.24724028	-6.0928361	1.11E-09	4.77E-08	368.703191	382.561886	318.838897	104.139951	164.686043	107.775089
AT1G03650	83.48845486	-1.825597265	0.32150973	-5.6782021	1.36E-08	4.58E-07	132.64959	102.490054	155.876794	45.3943377	35.2218705	29.2980825
AT1G03760	257.5076572	-1.739069407	0.22839407	-7.6143368	2.65E-14	2.76E-12	435.550228	359.222567	394.75292	145.973949	113.281151	96.2651283
AT1G03800	73.79749967	-1.489515415	0.34549932	-4.3111963	1.62E-05	0.00022523	105.492981	103.504807	117.413689	45.3943377	22.8466187	48.1325642
AT1G03820	88.59376019	2.030682886	0.47571181	4.26872502	1.97E-05	0.00026667	34.4680037	51.7524037	18.2193655	69.4266341	170.397698	187.298456
AT1G03850	443.2746859	-2.522434268	0.91078397	-2.7695198	0.0056139	0.02642545	1015.23938	499.258483	751.042735	293.728067	32.3660432	68.0134059
AT1G03860	2110.900067	-1.339512986	0.14465391	-9.260123	2.04E-20	6.48E-18	3117.78761	2840.29369	3120.57244	1229.20746	1275.60288	1081.93633
AT1G03990	65.79952144	1.641003321	0.40298643	4.07210566	4.66E-05	0.00055555	16.7117594	39.5753675	39.475292	114.820972	73.2995684	110.91417
AT1G04010	195.6939453	1.101501588	0.21955322	5.01701396	5.25E-07	1.17E-05	110.715406	116.696597	145.754924	247.443644	295.102158	258.450942
AT1G04090	17.0737636	1.914852055	0.58392957	3.27925175	0.00104083	0.00707934	7.31139472	5.07376507	9.10968277	26.7025516	33.3179856	20.9272018
AT1G04110	103.3743235	1.881393945	0.61726723	3.04794077	0.00230415	0.01325761	16.7117594	73.062217	42.5118529	42.7240825	205.619568	239.616461
AT1G04160	364.5745614	1.017493459	0.26046165	3.90650007	9.36E-05	0.00099116	191.140748	266.880043	265.192987	408.549039	644.465036	411.219516
AT1G04220	152.1434776	1.911082738	0.30897178	6.1852987	6.20E-10	2.89E-08	39.6904285	73.062217	78.950584	272.366026	254.168633	194.622977
AT1G04240	775.9996712	1.058269106	0.17508453	6.04433238	1.50E-09	6.21E-08	571.333273	444.46182	494.959431	1056.53096	1137.57122	951.141322
AT1G04480	4630.868605	-1.075124392	0.23971409	-4.4850279	7.29E-06	0.00011382	7077.43009	6286.39492	5477.95591	2056.09647	3722.09497	3165.23927
AT1G04540	108.1586936	1.491012389	0.29406578	5.07033619	3.97E-07	9.08E-06	75.2029171	49.7228977	45.5484139	184.247606	145.647194	148.583133
AT1G04680	4777.718712	1.312271758	0.25529037	5.1403105	2.74E-07	6.62E-06	3232.68095	3062.5246	1934.28931	5072.59471	7495.59483	7868.62788
AT1G04760	13.94158274	1.82308535	0.65831358	2.76932666	0.00561723	0.02643459	4.17793984	9.13277712	5.06093487	15.1314459	21.8946763	28.2517224
AT1G04770	318.3826993	2.668407663	0.44043318	6.05859822	1.37E-09	5.74E-08	41.7793984	61.8999338	155.876794	457.503717	776.785037	416.451316
AT1G04800	2765.279343	2.240802526	0.70948307	3.15835939	0.0015866	0.00988436	531.642845	1642.88513	722.7015	1775.71968	4772.08749	7146.63942
AT1G04900	313.5488578	-1.490973989	0.22839107	-6.5281624	6.66E-11	3.68E-09	423.016409	443.447067	521.276292	146.864034	207.523453	139.165892
AT1G04920	52.33109825	1.433477813	0.47768153	3.00090694	0.00269177	0.01492123	19.8452142	45.6638856	19.2315525	45.3943377	98.050072	85.8015274
AT1G04945	185.5528323	-1.137983577	0.23589738	-4.8240619	1.41E-06	2.74E-05	294.544759	256.732512	214.583639	126.392077	123.752518	97.3114884
AT1G05000	66.72204253	-1.323232542	0.41547235	-3.1848871	0.0014481	0.00923246	144.138924	70.0179579	71.8652752	43.6141676	25.7024461	44.9934839
AT1G05300	153.8066687	-1.559561928	0.31551705	-4.9428768	7.70E-07	1.63E-05	245.453966	165.404741	278.351418	98.7994408	54.2607195	80.569727
AT1G05370	26.01628173	1.44533429	0.50396956	2.86789997	0.00413206	0.02094759	9.40036464	21.3098133	11.1340567	29.3728067	40.9335252	43.9471238
AT1G05560	559.5114538	-1.174189457	0.19251352	-6.0992573	1.07E-09	4.63E-08	747.851231	675.825507	902.870782	386.296913	319.852662	324.371628
AT1G05630	581.3011006	1.240207149	0.26282586	4.71874092	2.37E-06	4.36E-05	275.744029	473.889657	287.461101	662.223279	862.459857	926.02868
AT1G05640	34.33349488	1.520389789	0.38859808	3.91249945	9.13E-05	0.00097009	17.7562443	18.2655542	17.2071786	48.9546779	50.4529497	53.3643646
AT1G05680	125.7130146	-4.097656555	0.34085421	-12.021728	2.73E-33	3.06E-30	226.653236	242.52597	242.924874	10.6810206	9.51942447	21.9735619
AT1G06080	153.7599877	4.595926646	1.24072591	3.70422396	0.00021204	0.00192708	3.13345488	32.4720964	1.01218697	217.180753	441.701295	227.06014
AT1G06180	38.34253405	-1.590553612	0.44747572	-3.5545026	0.00037869	0.00312801	51.179763	47.6933916	73.8896492	15.1314459	28.5582734	13.6026812
AT1G06360	337.2412754	3.159183316	1.15955379	2.7244819	0.00644025	0.02942721	29.2455789	136.991657	37.4509181	87.2283351	1342.23885	390.292314
AT1G06380	308.1888927	-1.03539241	0.18888295	-5.4816617	4.21E-08	1.24E-06	457.484413	391.694663	393.740733	192.258371	225.61036	188.344816
AT1G06420	9.912705606	2.265975892	0.83270389	2.72122649	0.00650402	0.02966163	3.13345488	2.02950603	5.06093487	8.90085052	25.7024461	14.6490413
AT1G06520	41.3321141	-1.173704812	0.37084231	-3.1649701	0.00155099	0.00973833	58.4911578	51.7524037	61.7434055	32.0430619	20.9427338	23.019922
AT1G06720	708.5222837	-1.502940488	0.21219517	-7.0828215	1.41E-12	1.07E-10	880.500821	1205.52658	1056.7232	372.945637	434.085756	301.351706
AT1G06850	150.987692	1.080877773	0.27611712	3.91456269	9.06E-05	0.000965	95.0481314	124.814621	70.8530882	202.049307	180.869065	232.29194
AT1G06950	6566.065991	-1.110691825	0.24288363	-4.5729381	4.81E-06	8.01E-05	7251.85908	10478.3396	9196.73085	3080.58437	5370.85928	4018.02275
AT1G07090	358.3227792	1.047619737	0.23552591	4.44800209	8.67E-06	0.00013133	273.65506	213.098133	214.583639	595.4669	471.211511	381.921433
AT1G07210	1018.011693	-1.178037334	0.18107978	-6.5056259	7.74E-11	4.27E-09	1582.39471	1183.20201	1470.70767	632.850472	674.927195	563.988089
AT1G07380	141.9710104	1.310552783	0.22098585	5.93048278	3.02E-09	1.17E-07	87.7367367	78.135982	78.950584	213.620413	190.388489	202.993858
AT1G07410	32.90383664	1.218941147	0.48702509	2.50283027	0.01232046	0.04814593	18.8007293	30.4425904	10.1218697	47.1745078	54.2607195	36.6226032
AT1G07450	190.6059677	-1.671554915	0.31564439	-5.2956902	1.19E-07	3.17E-06	351.991432	248.614488	269.241735	56.0753583	94.2423022	123.470491
AT1G07610	182.3310629	-3.097344403	0.49776471	-6.2225071	4.89E-10	2.36E-08	432.416773	289.204609	258.107679	64.9762088	9.51942447	39.7616834
AT1G07615	300.0364541	-1.729814214	0.19165355	-9.0257355	1.78E-19	4.35E-17	453.306473	450.550338	479.776626	145.083863	153.262734	118.23869
AT1G08070	34.76743763	-1.359723414	0.45147725	-3.0117208	0.00259771	0.01450084	47.0018232	47.6933916	55.6702836	30.2628918	13.3271943	14.6490413
AT1G08610	356.442124	-2.01675247	0.26533506	-7.6007766	2.94E-14	3.04E-12	523.286965	592.61576	599.214689	121.941652	198.004029	103.589649
AT1G08630	89.42861119	-2.373362356	0.51260805	-4.6299748	3.66E-06	6.33E-05	213.074932	87.2687592	149.803672	53.4051031	15.2310791	17.7881215
AT1G08650	365.5127193	1.960279011	0.31831701	6.1582603	7.35E-10	3.38E-08	144.138924	192.803073	111.340567	372.055552	781.544749	591.193451
AT1G09190	51.62798232	-1.215000124	0.34637143	-3.5077954	0.00045184	0.00360843	87.7367367	63.9294399	64.7799664	32.0430619	25.7024461	35.5762431

Table S-5.1 Differentially Expressed Genes between lpa66 (LP) and wild type (WT) Arabidopsis plants.

ID	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	WT4	WT2	WT1	LP3	LP2	LP1
AT1G09220	31.15078816	-1.292625719	0.46491179	-2.7803677	0.00542974	0.02582043	36.5569736	46.6786386	49.5971618	25.8124665	10.4713669	17.7881215
AT1G09240	198.5387675	-1.807340825	0.48298142	-3.7420504	0.00018252	0.00170862	530.59836	162.360482	233.815191	141.523523	47.5971223	75.3379265
AT1G09250	644.3923934	1.331478043	0.23749746	5.60628337	2.07E-08	6.62E-07	415.705014	271.953808	411.960099	1098.36495	765.361727	903.008758
AT1G09300	310.0514709	-1.524462286	0.19768943	-7.7114001	1.24E-14	1.39E-12	468.973747	429.240525	482.813187	185.137691	157.070504	137.073172
AT1G09350	77.56627173	1.201739565	0.36839502	3.26209499	0.00110592	0.00742129	41.7793984	65.9589459	33.4021702	134.402843	111.377266	78.4770068
AT1G09400	14.84661246	1.740127974	0.67813311	2.56605665	0.0102862	0.04204397	8.35587968	5.07376507	7.08530882	26.7025516	10.4713669	31.3908027
AT1G09420	54.88173604	1.050508164	0.34203772	3.07132251	0.00213113	0.01251388	30.2900638	38.5606145	38.463105	84.5580799	80.915108	56.5034449
AT1G09500	239.9357084	-4.412096598	0.350847	-12.575557	2.88E-36	4.98E-33	574.466728	281.086585	519.251918	17.801701	21.8946763	25.1126422
AT1G09680	42.75181006	-1.088455219	0.43353453	-2.510654	0.01205077	0.04734481	48.0463082	55.8114157	70.8530882	41.8339974	19.0388489	20.9272018
AT1G09750	2705.831533	1.334736419	0.32667327	4.08584517	4.39E-05	0.00052998	1214.73601	1764.65549	1629.62103	2024.94349	5405.12921	4195.90396
AT1G09890	37.70080312	1.295513468	0.41944561	3.08863276	0.0020108	0.01195112	16.7117594	27.3983314	21.2559265	38.2736572	61.876259	60.6888853
AT1G09932	103.6169042	1.263153535	0.39748027	3.1779025	0.00148345	0.00940049	49.0907931	76.106476	57.6946576	215.400583	79.0112231	144.397692
AT1G10050	359.473939	1.115606634	0.24829758	4.49302254	7.02E-06	0.00011026	196.363173	291.234115	193.327712	512.68899	395.056115	568.173529
AT1G10160	154.9691849	1.383879715	0.24868265	5.56484221	2.62E-08	8.16E-07	67.8915224	102.490054	87.0480798	198.488967	243.697266	230.19922
AT1G10230	196.0817286	-1.084098029	0.24263054	-4.4681021	7.89E-06	0.00012161	325.879308	240.496464	232.803004	105.920121	133.271943	138.119532
AT1G10380	235.8409166	1.098442993	0.20149463	5.45147533	5.00E-08	1.45E-06	145.183409	165.404741	139.681803	296.398322	308.429353	359.947871
AT1G10460	117.1399393	-1.155836554	0.40796781	-2.8331562	0.00460909	0.0227007	207.852507	102.490054	175.108347	83.6679949	97.0981296	36.6226032
AT1G10490	663.2759564	-1.035849108	0.22146744	-4.6772072	2.91E-06	5.18E-05	725.917047	1093.90375	855.297994	416.559804	510.241151	377.735993
AT1G10522	978.4289298	-2.852058771	0.17473392	-16.322296	6.85E-60	4.35E-56	1827.84868	1474.43613	1854.32654	235.872539	254.168633	223.921059
AT1G10640	129.8979666	3.110250012	1.03557174	3.00341337	0.0026697	0.01482117	26.112124	44.6491326	10.1218697	36.4934871	446.461008	215.550179
AT1G10990	37.0426665	1.561876345	0.38437772	4.06338936	4.84E-05	0.00057348	17.7562443	17.2508012	21.2559265	58.7456134	58.0684893	49.1789243
AT1G11000	214.4114203	1.884230925	0.24716014	7.62352257	2.47E-14	2.60E-12	80.4253419	101.475301	92.1090147	315.090108	279.871079	417.497676
AT1G11120	23.44838283	1.441000046	0.50623932	2.84647988	0.00442055	0.02202868	11.4893346	18.2655542	8.0974958	29.3728067	39.9815828	33.4835229
AT1G11160	18.81494816	1.625317342	0.60823396	2.67219103	0.00753577	0.03315415	7.31139472	13.1917892	7.08530882	16.0215309	39.9815828	29.2980825
AT1G11475	772.5606643	-1.118249734	0.1589669	-7.0344816	2.00E-12	1.45E-10	1178.17904	966.044869	1029.39415	503.788139	469.307626	488.650162
AT1G11545	441.3660389	2.025945746	0.3352307	6.0434374	1.51E-09	6.21E-08	135.783045	213.098133	173.083973	436.141676	1063.31971	626.769694
AT1G11700	560.3556987	1.194433974	0.29947897	3.98837346	6.65E-05	0.00074634	505.530721	307.470163	209.522704	761.02272	784.400576	794.187309
AT1G11730	29.01578252	1.564689786	0.49974514	3.13097549	0.00174227	0.01064433	10.4448496	17.2508012	16.1949916	25.8124665	55.2126619	49.1789243
AT1G11850	1061.70018	2.084564332	0.76002271	2.74276583	0.00609241	0.02814875	332.146217	611.896067	271.266109	448.602866	2629.26504	2077.02478
AT1G12010	167.056186	2.275194162	0.31472155	7.22922906	4.86E-13	3.97E-11	47.0018232	51.7524037	72.8774622	372.055552	207.523453	251.126422
AT1G12030	16.37590656	1.676960996	0.67114933	2.49864064	0.01246707	0.048619	3.13345488	9.13277712	11.1340567	24.0322964	36.173813	14.6490413
AT1G12200	202.6795492	1.156455594	0.29954837	3.86066399	0.00011308	0.00115887	128.47165	123.799868	124.498998	393.417593	188.484604	257.404582
AT1G12290	83.58145124	1.567945602	0.40101319	3.90996021	9.23E-05	0.00097816	31.3345488	42.6196266	52.6337227	187.807946	107.569496	79.5233669
AT1G12320	201.349266	1.035893949	0.30113629	3.43995061	0.00058182	0.00442021	121.160255	152.212952	122.474624	170.006245	339.843453	302.398066
AT1G12570	32.22661354	4.022409505	0.90616474	4.43893843	9.04E-06	0.00013579	1.04448496	6.08851808	4.0487479	15.1314459	140.887482	26.1590023
AT1G12780	4055.567029	-1.566510887	0.28728087	-5.4528896	4.96E-08	1.44E-06	7686.36482	4478.10505	6027.57344	2875.8648	1531.6754	1733.81867
AT1G12845	152.7206011	2.547111181	0.33644076	7.57075686	3.71E-14	3.70E-12	34.4680037	46.6786386	52.6337227	178.907095	359.834245	243.801901
AT1G13270	1083.035414	-1.232947533	0.26992666	-4.567713	4.93E-06	8.17E-05	1345.29663	1368.90182	1844.20467	430.801165	852.940432	656.067777
AT1G13448	42.41372153	1.682358936	0.49700361	3.38500346	0.00071177	0.00521427	25.067639	16.2360482	19.2315525	98.7994408	32.3660432	62.7816054
AT1G13530	54.67773645	-2.502961875	0.50870177	-4.9202932	8.64E-07	1.80E-05	115.937831	65.9589459	97.1699496	27.5926366	5.71165468	15.6954014
AT1G13609	48.86418442	2.512675686	0.66816588	3.7605567	0.00016954	0.00161	3.13345488	30.4425904	10.1218697	135.292928	61.876259	52.3180045
AT1G13630	77.68874428	-1.097921035	0.2975477	-3.6898993	0.00022434	0.00202153	85.6477667	105.534313	126.523372	47.1745078	55.2126619	46.039844
AT1G13670	37.79125424	3.320471397	0.71847318	4.62156625	3.81E-06	6.57E-05	13.5783045	7.1032711	0	36.4934871	83.7709353	85.8015274
AT1G13800	21.48147866	-1.433193348	0.55052115	-2.6033393	0.00923205	0.03868234	35.5124886	22.3245663	36.4387311	16.911616	11.4233094	6.27816054
AT1G13810	268.6884908	-1.597242174	0.23594095	-6.7696691	1.29E-11	8.30E-10	452.261988	352.119296	407.911351	160.215309	137.079712	102.543289
AT1G13920	83.27894678	1.082442323	0.36197759	2.9903573	0.00278651	0.0153222	32.3790338	58.8556748	68.8287143	85.448165	117.088921	137.073172
AT1G14040	66.69352747	-1.258531329	0.34316746	-3.667397	0.00024503	0.00216692	91.9146765	78.135982	112.352754	51.624933	29.5102158	36.6226032
AT1G14060	356.0800727	-1.627533848	0.20072575	-8.1082463	5.14E-16	7.13E-14	572.377758	490.125706	551.641901	155.764884	207.523453	159.046734
AT1G14090	110.1649558	-1.0694167	0.24660272	-4.3365973	1.45E-05	0.00020339	129.516135	154.242458	163.97429	75.6572294	68.5398562	69.059766
AT1G14190	52.09274452	1.22649125	0.40757543	3.00923749	0.00261904	0.01459532	44.9128533	29.4278374	19.2315525	56.0753583	77.1073382	85.8015274
AT1G14300	475.0443916	-1.73267978	0.20661609	-8.3859868	5.03E-17	7.91E-15	771.874386	666.69273	753.067109	236.762624	251.312806	170.556695
AT1G14390	13.70665861	2.378539479	0.75652374	3.14403813	0.00166634	0.01026613	2.08896992	7.1032711	4.0487479	15.1314459	37.1257554	16.7417614
AT1G14430	104.3644883	1.182428309	0.42635725	2.77332758	0.00554862	0.02619306	62.6690976	67.9884519	60.7312185	60.5257835	203.715684	170.556695
AT1G14640	41.12290148	1.357007371	0.50292418	2.69823448	0.00697083	0.03122926	10.4448496	33.4868494	25.3046744	76.5473145	37.1257554	63.8279655
AT1G14780	64.11000944	1.351363082	0.44110173	3.06360867	0.00218685	0.01276623	30.2900638	33.4868494	44.5362269	129.062333	44.741295	102.543289
AT1G14970	112.4315691	1.081697571	0.35725178	3.02782975	0.00246317	0.01393477	50.1352781	96.4015363	69.8409013	113.040802	212.283166	132.887732
AT1G14980	2650.338495	-1.8123429	0.20523717	-8.8304807	1.04E-18	2.23E-16	4923.7021	3551.63555	3901.98079	948.830666	1321.29612	1254.58575
AT1G15010	126.2654657	1.342019887	0.35365289	3.79473754	0.0001478	0.00144023	51.179763	71.032711	92.1090147	247.443644	118.992806	176.834855
AT1G15250	552.0436887	-1.226359378	0.28639104	-4.282115	1.85E-05	0.00025346	936.903009	764.109019	619.458429	238.542794	465.499856	287.749025
AT1G15380	396.4599938	-3.435194985	1.07828024	-3.1858091	0.0014435	0.00921566	884.678761	549.996133	742.94524	165.55582	10.4713669	25.1126422
AT1G15420	423.530463	-1.140749052	0.20973991	-5.4388744	5.36E-08	1.55E-06	597.445397	594.645266	556.702836	273.256111	315.09295	204.040218
AT1G15440	488.1737037	-1.247458934	0.24508343	-5.0899358	3.58E-07	8.34E-06	521.197995	829.053212	710.555256	238.542794	350.31482	279.378144
AT1G15510	379.7219873	-2.495941426	0.20474304	-12.190605	3.49E-34	4.43E-31	587.000548	621.028844	727.762435	127.282162	118.992806	96.2651283
AT1G15550	227.0111019	-1.957959222	0.28740378	-6.812573	9.59E-12	6.25E-10	416.749499	383.576639	283.412353	102.359781	114.233094	61.7352453
AT1G15570	160.2327884	1.507100784	0.43157504	3.49209438	0.00047925	0.00377508	58.4911578	116.696597	74.9018361	109.480461	356.978418	244.848261
AT1G15760	11.26283447	1.895374375	0.69886776	2.71206439	0.00668656	0.03025498	5.2224248	3.04425904	6.07312185	18.6917861	20.9427338	13.6026812
AT1G15870	32.50345929	-3.127560625	0.52402551	-5.9683366	2.40E-09	9.41E-08	61.6246126	50.7376507	62.7555924	5.34051031	11.4233094	3.13908027
AT1G15930	7460.983641	-1.210056359	0.24296023	-4.980471	6.34E-07	1.38E-05	10903.3785	10732.0279	9619.82501	3016.49824	5821.12806	4673.04416
AT1G16000	342.2242561	-1.018026156	0.2528026	-4.0269608	5.65E-05	0.00065527	514.931085	443.447067	416.008847	162.885565	293.198274	222.874699
AT1G16350	1603.251646	-1.217713678	0.21658514	-5.6223326	1.88E-08	6.11E-07	2340.6908	2257.82546	2128.62921	791.285611	1266.08345	834.995352
AT1G16445	158.326244	-1.186889847	0.22149055	-5.3586478	8.38E-08	2.31E-06	202.630082	227.304675	229.766443	83.6679949	100.905899	105.682369
AT1G16515	29.24392238	1.201584421	0.43511921	2.76150628	0.00575354	0.02691633	16.7117594	16.2360482	20.2437395	37.3835722	51.4048921	33.4835229
AT1G16640	34.41376285	1.790166389	0.52442218	3.41359778	0.00064111	0.00480633	22.9786691	15.2212952	8.0974958	31.1529768	59.9723741	69.059766
AT1G16830	43.43820724	-1.810199843	0.39694301	-4.5603519	5.11E-06	8.41E-05	67.8915224	65.9589459	68.8287143	12.4611907	26.6543885	18.8344816
AT1G17090	55.93961357	-1.216552384	0.32599205	-3.7318468	0.00019008	0.00176031	83.5587968	81.1802411	69.8409013	27.5926366	39.9815828	33.4835229
AT1G17170	61.33379715	-2.060860881	0.45676474	-4.5118651	6.43E-06	0.00010217	65.8025525	75.091723	155.876794	26.7025516	15.2310791	29.2980825
AT1G17255	29.14016875	1.277150588	0.44488183	2.87076367	0.00409482	0.02082486	14.6227894	13.1917892	23.2803004	46.2844227	41.8854677	35.5762431
AT1G17480	51.96414193	1.349231816	0.41356514	3.26244084	0.00110457	0.00741642	20.8896992	37.5458615	29.3534223	49.8447629	100.905899	73.2452063
AT1G17700	57.90793636	2.743995298	0.39027822	7.03086967	2.05E-12	1.49E-10	18.8007293	17.2508012	9.10968277	84.5580799	115.185036	102.543289
AT1G18250	101.2455913	1.302385489	0.43088409	3.02258895	0.00250622	0.01409592	61.6246126	69.0032049	44.5362269	64.9762088	210.379281	156.954014
AT1G18265	285.2966329	-1.435433384	0.33778837	-4.2495051	2.14E-05	0.00028647	484.641022	363.281579	401.838229	202.939392	78.0592806	181.020296

Table S-5.1 Differentially Expressed Genes between lpa66 (LP) and wild type (WT) Arabidopsis plants.

ID	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	WT4	WT2	WT1	LP3	LP2	LP1
AT1G18320	33.43735393	-1.217870886	0.39699552	-3.0677195	0.00215699	0.01263845	50.1352781	49.7228977	40.487479	18.6917861	23.7985612	17.7881215
AT1G18400	400.6726515	1.226964802	0.3133907	3.91512825	9.04E-05	0.00096388	306.034093	254.703006	158.913355	402.318444	756.794245	525.272765
AT1G18540	9333.83739	-1.047053929	0.23863814	-4.3876219	1.15E-05	0.00016648	13296.2935	12849.8174	11592.5774	4166.48813	7888.74706	6209.10078
AT1G18630	333.6334922	-1.302913922	0.19909378	-6.544222	5.98E-11	3.34E-09	528.50939	407.930711	487.874122	195.818711	171.34964	210.318378
AT1G18710	138.3829703	2.150712386	0.50955226	4.2207886	2.43E-05	0.00031865	19.8452142	49.7228977	82.9993319	343.57283	112.329209	221.828339
AT1G18800	1379.89024	-1.582898955	0.15589869	-10.153382	3.20E-24	1.60E-21	2267.57685	1922.95696	2017.28864	757.462379	666.359713	647.696896
AT1G18850	353.2686482	-1.257233627	0.2166683	-5.802573	6.53E-09	2.36E-07	472.107202	518.53879	504.069114	197.598882	259.880288	167.417614
AT1G18870	134.6127714	2.442650086	0.32210685	7.58335351	3.37E-14	3.45E-12	25.067639	45.6638856	54.6580966	267.025516	191.340432	223.921059
AT1G18880	81.44922771	1.434780359	0.33959623	4.2249596	2.39E-05	0.0003141	42.8238834	53.7819097	35.4265441	153.984714	87.5787051	115.09961
AT1G19300	291.0726077	1.315238488	0.25795517	5.09870952	3.42E-07	8.02E-06	126.38268	213.098133	160.937729	406.768869	347.458993	491.789243
AT1G19320	18.17953534	5.699909661	1.22626583	4.64818438	3.35E-06	5.85E-05	2.08896992	0	0	13.3512758	47.5971223	46.039844
AT1G19380	1718.922267	1.031080373	0.24909438	4.13931602	3.48E-05	0.00043272	1285.76099	964.015363	1138.71035	2272.38714	1629.72547	3022.9343
AT1G19620	43.70686102	1.270958941	0.41204754	3.08449586	0.00203897	0.01208086	21.9341842	28.4130844	26.3168613	40.9439124	60.9243166	83.7088072
AT1G19630	11.06486972	2.451250669	0.85315125	2.87317245	0.00406372	0.02069666	5.2224248	5.07376507	0	18.6917861	23.7985612	13.6026812
AT1G19850	256.5918736	1.381775414	0.25658273	5.38530167	7.23E-08	2.01E-06	105.492981	177.581777	143.73055	317.760364	435.037698	359.947871
AT1G19940	131.405454	1.16525833	0.30413835	3.83134293	0.00012745	0.00127721	65.8025525	69.0032049	108.304006	161.995479	228.466187	154.861293
AT1G19960	1117.389029	-2.990630024	0.87785981	-3.4067285	0.00065746	0.00489523	2838.91012	1944.26677	1172.11252	542.951882	74.2515108	131.841371
AT1G20030	262.3321591	-1.04850858	0.4074534	-2.5733214	0.01007276	0.0413589	344.680037	325.735717	390.704172	254.564325	64.7320864	193.576617
AT1G20160	432.330559	1.485422738	0.27219873	5.4571258	4.84E-08	1.41E-06	155.628259	223.245663	303.656092	733.430083	529.28	648.743256
AT1G20190	1454.592425	2.156924077	0.20892477	10.3239273	5.49E-25	3.07E-22	628.779946	528.68632	441.313521	2793.08689	1987.65583	2348.03204
AT1G20620	42394.85827	1.232268602	0.15819904	7.78935567	6.74E-15	7.81E-13	26659.4341	23258.1391	26028.3881	66406.5755	60485.4711	51531.1417
AT1G21140	39.56451968	-1.952579714	0.75391566	-2.589918	0.00959988	0.03989852	142.049955	29.4278374	17.2071786	22.2521263	7.61553957	18.8344816
AT1G21550	202.2150396	-1.412054932	0.4182752	-3.3758993	0.00073575	0.00536271	326.923793	235.422699	319.851084	185.137691	47.5971223	98.3578485
AT1G22030	71.11449331	1.531864998	0.34441244	4.44776328	8.68E-06	0.00013137	42.8238834	41.6048736	25.3046744	99.6895258	130.416115	86.8478875
AT1G22160	402.691476	1.659754751	0.29061005	5.71127793	1.12E-08	3.86E-07	254.85433	132.932645	193.327712	789.505441	546.414964	499.113763
AT1G22250	188.043471	1.832015241	0.32082341	5.71035398	1.13E-08	3.87E-07	106.537466	85.2392531	55.6702836	314.200023	205.619568	360.994231
AT1G22330	420.0516078	1.268130645	0.2157306	5.87830676	4.14E-09	1.56E-07	186.962808	276.01282	276.327044	573.214774	651.128634	556.663568
AT1G22500	208.1413266	-2.370790348	0.88219446	-2.6873784	0.00720153	0.03200662	306.034093	305.440657	435.240399	153.984714	20.9427338	27.2053624
AT1G22960	157.5935672	-1.055583178	0.25175267	-4.1929373	2.75E-05	0.00035457	181.740383	205.994862	251.02237	118.381312	104.713669	83.7088072
AT1G23010	53.07943558	-1.47075954	0.37694029	-3.9018369	9.55E-05	0.00100543	74.1584322	74.07697	86.0358929	40.0538273	19.0388489	25.1126422
AT1G23060	60.80466307	2.864507869	0.47235331	6.06433319	1.33E-09	5.55E-08	18.8007293	7.1032711	18.2193655	156.654969	76.1553957	87.8942476
AT1G23080	3642.376881	2.029651703	0.2540939	7.98780175	1.37E-15	1.77E-13	1723.40018	1629.69334	946.394822	4844.73294	6668.35684	6041.68316
AT1G23100	208.3237661	-1.925651644	0.21635381	-8.9004747	5.56E-19	1.28E-16	337.368642	308.484916	343.131384	76.5473145	81.8670504	102.543289
AT1G23200	129.4859696	1.366636648	0.38996606	3.50450148	0.00045746	0.00364267	38.6459435	75.091723	103.243071	215.400583	123.752518	220.781979
AT1G23280	908.4268184	-1.198820654	0.24343037	-4.9246962	8.45E-07	1.76E-05	1345.29663	1199.43806	1252.07529	461.954142	759.650073	432.146717
AT1G23340	73.01652271	1.52954277	0.36226605	4.2221532	2.42E-05	0.00031738	38.6459435	49.7228977	24.2924874	82.7779098	127.560288	115.09961
AT1G23410	83.3924248	-1.272271699	0.41770674	-3.0458491	0.00232024	0.01330818	103.404011	141.050669	109.316193	25.8124665	79.9631655	40.8080435
AT1G23450	13.27424792	-2.190168432	0.72125145	-3.0366226	0.00239245	0.01363602	17.7562443	12.1770362	35.4265441	5.34051031	4.75971223	4.18544036
AT1G23800	133.5112199	1.367708427	0.3385095	4.04038421	5.34E-05	0.00062535	56.4021878	93.3572773	73.8896492	139.743353	271.303597	166.371254
AT1G23870	1216.348695	-1.580433626	0.29680012	-5.3249089	1.01E-07	2.74E-06	1840.3825	1791.03907	1838.13155	862.492415	345.555108	620.491534
AT1G23965	19.790098	2.986424319	0.6308305	4.73411529	2.20E-06	4.08E-05	5.2224248	6.08851808	2.02437395	44.5042526	29.5102158	31.3908027
AT1G24020	574.6325978	2.279514666	0.89776445	2.53910106	0.01111377	0.04450888	165.028624	281.086585	142.718363	178.01701	1897.2213	783.723708
AT1G24070	81.20882254	1.833799967	0.53948228	3.39918483	0.00067587	0.00500486	7.31139472	45.6638856	53.6459097	105.920121	120.896691	153.814933
AT1G24090	65.21539746	-2.855220622	0.37643646	-7.5848674	3.33E-14	3.42E-12	96.0926163	121.770362	125.511185	11.5711057	13.3271943	23.019922
AT1G24580	39.57378015	-1.23779574	0.39816814	-3.1087262	0.00187896	0.01132672	53.268733	71.032711	42.5118529	23.1422114	27.606331	19.8808417
AT1G25260	1574.389962	-1.379975511	0.18802924	-7.3391538	2.15E-13	1.85E-11	2404.40438	2222.3091	2197.45792	731.649913	1068.07943	822.439031
AT1G25430	78.66225165	1.821295436	0.40893432	4.45376026	8.44E-06	0.00012826	27.156609	38.5606145	38.463105	191.368286	88.5306475	87.8942476
AT1G25450	523.918865	1.430585566	0.28904826	4.94929666	7.45E-07	1.59E-05	207.852507	321.676705	320.863271	506.458395	965.269641	821.392671
AT1G25530	50.98412158	2.659728998	0.5743396	4.63093437	3.64E-06	6.31E-05	5.2224248	23.3393193	13.1584307	45.3943377	136.12777	82.6624472
AT1G26200	23.32874446	1.324217112	0.46446442	2.85106252	0.00435734	0.0217764	13.5783045	13.1917892	13.1584307	28.4827217	38.0776979	33.4835229
AT1G26208	161.2196834	1.240338805	0.30958315	4.00648038	6.16E-05	0.00070011	63.7135826	95.3867833	128.547746	224.301433	272.25554	183.113016
AT1G26210	353.598373	1.275799908	0.33685333	3.78740478	0.00015223	0.00147434	128.47165	202.950603	288.473288	333.781895	620.666475	547.246327
AT1G26420	68.3926162	1.483285311	0.56602625	2.62052391	0.00877948	0.03719551	55.3577029	32.4720964	20.2437395	93.4589305	36.173813	172.649415
AT1G26500	68.32822097	-1.326557695	0.30151532	-4.3996361	1.08E-05	0.00015874	111.759891	83.2097471	98.1821366	41.8339974	35.2218705	39.7616834
AT1G26730	264.7450077	1.190529377	0.20202971	5.89284296	3.80E-09	1.45E-07	146.227894	158.30147	179.157095	342.682745	344.603166	417.497676
AT1G26740	377.968385	-1.110456701	0.20371671	-5.4509849	5.01E-08	1.45E-06	589.089518	476.933916	483.825374	205.609647	277.967194	234.38466
AT1G26930	127.5464553	-1.001716187	0.38154385	-2.6254287	0.00865399	0.03680919	167.117594	135.976904	207.49833	127.282162	44.741295	82.6624472
AT1G26945	331.1795089	1.148963796	0.34503642	3.32997834	0.00086853	0.00613789	246.498451	260.791525	110.32838	358.704276	601.627626	409.126795
AT1G27020	501.2844258	1.070729294	0.2841448	3.76825231	0.00016439	0.00156665	388.548405	299.352139	282.400166	931.91905	458.836259	646.650536
AT1G27045	94.80249972	1.217470428	0.41249708	2.95146433	0.00316271	0.01693572	96.0926163	40.5901205	34.4143571	117.491227	118.040863	162.185814
AT1G27470	457.8860258	-1.384616488	0.21777925	-6.3578899	2.05E-10	1.03E-08	550.443574	741.784453	694.360265	231.422114	307.47741	221.828339
AT1G28130	28.71149017	1.983173609	0.52301062	3.79184196	0.00014953	0.00145586	12.5338195	7.1032711	15.1828046	64.0861238	30.4621583	42.9007637
AT1G28210	142.0903433	-1.507166324	0.22753994	-6.623744	3.50E-11	2.06E-09	210.985962	204.980109	214.583639	64.9762088	83.7709353	73.2452063
AT1G28290	197.84391	2.472863125	0.34040524	7.26446855	3.75E-13	3.14E-11	58.4911578	83.2097471	39.475292	249.223815	452.172662	304.490786
AT1G28330	2410.042119	-1.34547992	0.36212489	-3.7155135	0.00020279	0.00185991	3856.23847	2622.12179	3898.94423	2295.52935	831.045756	956.373123
AT1G28390	78.03886781	1.537230953	0.32776524	4.69003654	2.73E-06	4.93E-05	45.9573382	46.6786386	27.3290483	95.2391006	128.51223	124.516851
AT1G28395	593.1805269	-1.365313912	0.2104416	-6.4878517	8.71E-11	4.76E-09	978.682408	799.625375	785.457093	272.366026	401.719713	321.232548
AT1G28400	806.7416874	1.325446068	0.27221034	4.86919817	1.12E-06	2.25E-05	402.12671	617.984585	360.338563	868.723011	1429.81756	1161.4597
AT1G28530	318.924326	-1.497671237	0.26991411	-5.5486955	2.88E-08	8.85E-07	426.149864	473.889657	513.178796	134.402843	235.129784	130.795011
AT1G28660	177.6171109	1.04565228	0.32091477	3.25834887	0.00112063	0.00751202	152.494804	84.2245001	111.340567	325.771129	205.619568	186.252096
AT1G28680	201.5942672	1.223627224	0.2878481	4.25094769	2.13E-05	0.00028489	123.249225	142.065422	97.1699496	193.148456	327.468202	326.464348
AT1G29030	174.4633948	-1.160584925	0.26219817	-4.4263655	9.58E-06	0.00014313	219.341842	258.762018	244.949248	80.1076547	138.983597	104.636009
AT1G29250	1494.501728	-1.383020767	0.200128	-6.9106808	4.82E-12	3.26E-10	2501.54148	2019.3585	1960.60617	672.014214	969.077411	844.412593
AT1G29290	12.61575131	2.368419832	0.72138993	3.28313403	0.0010266	0.00701263	5.2224248	4.05901205	3.03656092	30.2628918	14.2791367	18.8344816
AT1G29300	111.8818096	1.098098359	0.27910311	3.93438239	8.34E-05	0.00090142	58.4911578	71.032711	84.0115189	145.083863	128.51223	184.159376
AT1G29320	342.792473	-1.092442057	0.2754726	-3.9657013	7.32E-05	0.00080783	390.637375	580.438724	429.167277	187.807946	296.054101	172.649415
AT1G29395	1141.598528	3.132942389	0.34279439	9.13942136	6.28E-20	1.76E-17	229.786691	211.068627	260.132053	3316.4569	1195.63971	1636.50718
AT1G29560	65.04906563	1.591985006	0.31550989	5.04575311	4.52E-07	1.02E-05	29.2455789	40.5901205	27.3290483	91.6787604	99.9539569	101.496929
AT1G29600	264.6732463	-1.074641597	0.40521032	-2.6520588	0.00800026	0.03469757	336.324157	397.783181	343.131384	304.409088	92.3384173	114.05325
AT1G30160	43.91684394	1.023551243	0.39458324	2.59400585	0.00948649	0.03954504	30.2900638	24.3540723	32.3899832	73.8770593	62.8282015	39.7616834
AT1G30240	280.9530379	-1.25958745	0.24343328	-5.1742614	2.29E-07	5.66E-06	326.923793	453.594597	408.923538	173.566585	196.100144	126.609571

Table S-5.1 Differentially Expressed Genes between lpa66 (LP) and wild type (WT) Arabidopsis plants.

ID	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	WT4	WT2	WT1	LP3	LP2	LP1
AT1G30250	105.181147	-2.283998462	0.40208578	-5.6803762	1.34E-08	4.53E-07	173.384503	134.962151	215.595826	57.8555284	19.9907914	29.2980825
AT1G30282	15.96080104	1.526002764	0.60620827	2.51729124	0.0118261	0.04664722	13.5783045	5.07376507	6.07312185	24.0322964	21.8946763	25.1126422
AT1G30420	253.5221867	1.620777426	0.29954678	5.4107657	6.28E-08	1.77E-06	106.537466	175.552271	91.0968277	422.7904	295.102158	430.053997
AT1G30680	1343.021635	-1.801641382	0.18982933	-9.4908484	2.29E-21	7.93E-19	1924.98578	2036.6093	2300.70099	712.958127	496.913957	585.961651
AT1G30760	21.52621615	2.685698424	0.84694044	3.17105939	0.00151884	0.00958499	4.17793984	13.1917892	0	26.7025516	59.9723741	25.1126422
AT1G30820	1917.029776	-1.535372756	0.21898612	-7.0112789	2.36E-12	1.68E-10	3164.78943	2752.01017	2635.73488	1281.72248	801.53554	866.386155
AT1G30960	166.8709961	-1.784410587	0.30103034	-5.9276769	3.07E-09	1.18E-07	233.964631	260.791525	281.387979	63.1960387	108.521439	53.3643646
AT1G31010	156.2421001	-1.350392962	0.2282211	-5.9170381	3.28E-09	1.26E-07	259.03227	205.994862	208.510517	89.0085052	93.2903598	81.6160871
AT1G31290	113.1524782	-2.638601843	0.43490358	-6.0670962	1.30E-09	5.47E-08	255.898815	126.844127	202.437395	48.0645928	14.2791367	31.3908027
AT1G31660	834.4763196	-1.227908307	0.24255601	-5.0623701	4.14E-07	9.44E-06	1125.95479	1233.93966	1148.83222	373.835722	680.638849	443.656678
AT1G31710	233.5744128	1.074400146	0.33681878	3.1898463	0.00142348	0.00911826	109.670921	168.449	173.083973	243.883304	474.067338	232.29194
AT1G31790	85.19552845	-1.75091183	0.3455865	-5.0664937	4.05E-07	9.26E-06	148.316864	105.534313	140.69399	54.2951882	36.173813	26.1590023
AT1G31840	20.84894856	-1.904104463	0.63764847	-2.9861351	0.00282528	0.0154906	19.8452142	26.3835784	52.6337227	14.2413608	5.71165468	6.27816054
AT1G31970	3296.369367	-1.167547875	0.1939085	-6.021128	1.73E-09	6.95E-08	4694.9599	4621.18522	4369.61117	1751.68738	2558.8213	1781.95123
AT1G32580	1503.167509	-1.079727857	0.15968012	-6.7618175	1.36E-11	8.73E-10	1942.74203	1956.44381	2223.77478	1042.2896	1006.20317	847.551673
AT1G32860	158.5462494	1.046880983	0.28918826	3.62006733	0.00029453	0.00253511	68.9360074	128.873633	112.352754	194.038541	250.360863	196.715697
AT1G33055	84.73736377	-2.823663025	0.60564843	-4.6622147	3.13E-06	5.51E-05	239.187056	79.1507351	127.535559	43.6141676	9.51942447	9.41724082
AT1G33120	3391.379251	-1.054639071	0.22539224	-4.6791277	2.88E-06	5.16E-05	5018.75023	4668.87862	4047.73571	1603.93326	2763.48892	2245.48875
AT1G33340	201.5557411	-1.13803135	0.33240233	-3.4236564	0.00061785	0.00465673	334.235187	193.817826	303.656092	170.006245	79.9631655	127.655931
AT1G33350	38.59027935	-1.20700917	0.39287543	-3.072244	0.00212456	0.01247917	48.0463082	56.8261688	56.6824706	18.6917861	31.4141007	19.8808417
AT1G33760	54.55270085	1.517567913	0.42989867	3.5300596	0.00041547	0.0033804	21.9341842	17.2508012	45.5484139	98.7994408	69.4917986	74.2915664
AT1G33770	117.0491281	1.731475446	0.33324862	5.1957468	2.04E-07	5.11E-06	39.6904285	75.091723	47.5727878	146.864034	161.830216	231.24558
AT1G33800	64.46596861	1.339579976	0.37521273	3.57018802	0.00035673	0.00296845	33.4235187	38.5606145	37.4509181	56.9654433	119.944748	100.450569
AT1G33811	1025.042877	1.321288063	0.34491013	3.83081841	0.00012772	0.00127926	405.260165	794.55161	557.715023	798.406292	1771.56489	1822.75928
AT1G33930	69.11282973	2.029390177	0.58154932	3.48962696	0.0004837	0.00379909	13.5783045	45.6638856	22.2681134	40.0538273	178.013238	115.09961
AT1G34030	4173.892022	-1.038192289	0.22734818	-4.56653	4.96E-06	8.20E-05	6293.02188	5587.23009	4961.74055	2010.70213	3477.44576	2713.21171
AT1G34060	92.80844772	-2.614491674	0.58386474	-4.4779064	7.54E-06	0.0001173	166.073109	118.726103	194.339899	56.9654433	12.3752518	8.37088072
AT1G34180	38.9827187	-1.288843947	0.38260252	-3.3686238	0.00075544	0.00547899	62.6690976	44.6491326	58.7068445	25.8124665	19.0388489	23.019922
AT1G34245	11.3873454	2.496991647	0.82140152	3.03991604	0.00236644	0.01352425	4.17793984	4.05901205	2.02437395	8.01076547	22.8466187	27.2053624
AT1G35230	289.6953594	1.453050467	0.47802726	3.03968115	0.00236829	0.01353073	226.653236	163.375235	74.9018361	284.827217	236.081727	752.332905
AT1G36622	16.63476852	2.454538414	0.75943961	3.23203898	0.0012291	0.00810333	8.35587968	1.01475301	6.07312185	41.8339974	14.2791367	28.2517224
AT1G36675	10.5483727	2.756791082	0.83483881	3.30218368	0.00095935	0.00663907	1.04448496	5.07376507	2.02437395	24.0322964	13.3271943	17.7881215
AT1G36680	11.18352989	2.843363223	0.87012418	3.26776718	0.00108399	0.00730765	4.17793984	4.05901205	0	26.7025516	13.3271943	18.8344816
AT1G36940	55.52887275	2.790241095	0.46519355	5.99802193	2.00E-09	7.95E-08	18.8007293	19.2803073	4.0487479	97.0192707	90.4345324	103.589649
AT1G37130	10565.49102	-1.360537837	0.34416232	-3.9531864	7.71E-05	0.00084443	11843.415	17599.8763	16181.8332	8739.74513	2931.98274	6096.09389
AT1G42980	16.37047205	1.826258448	0.64233667	2.84314834	0.00446703	0.02220794	9.40036464	6.08851808	6.07312185	14.2413608	24.7505036	37.6689633
AT1G43980	23.82579747	-1.2876372	0.47126838	-2.7322801	0.00628976	0.02887829	32.3790338	29.4278374	39.475292	12.4611907	11.4233094	17.7881215
AT1G44800	229.8837404	2.110613708	0.2505949	8.42241301	3.69E-17	6.05E-15	105.492981	79.1507351	74.9018361	396.977933	424.566331	298.212626
AT1G44830	32.81042255	3.462864368	0.63091286	5.48865713	4.05E-08	1.21E-06	4.17793984	5.07376507	7.08530882	27.5926366	93.2903598	59.6425252
AT1G44890	83.18603891	-1.423171615	0.28563	-4.9825705	6.27E-07	1.37E-05	124.29371	100.460548	138.669616	42.7240825	43.7893526	49.1789243
AT1G45110	154.8740935	-1.507815151	0.22375513	-6.7386841	1.60E-11	1.01E-09	224.564266	221.216157	241.912687	91.6787604	71.3956835	78.4770068
AT1G45332	794.8693933	-1.167078261	0.17502622	-6.6680194	2.59E-11	1.55E-09	1011.06144	1063.46116	1225.75843	542.061797	497.8659	429.007637
AT1G45545	26.45582258	1.333617734	0.47061233	2.83379258	0.00459992	0.02267673	13.5783045	16.2360482	15.1828046	25.8124665	41.8854677	46.039844
AT1G46480	61.83278919	1.842205295	0.38373912	4.80067109	1.58E-06	3.04E-05	25.067639	37.5458615	18.2193655	91.6787604	77.1073382	121.377771
AT1G47510	52.22940153	1.221419063	0.33560148	3.63949245	0.00027318	0.00237932	27.156609	27.3983314	39.475292	75.6572294	70.4437411	73.2452063
AT1G47560	54.16493858	1.522204944	0.34125127	4.46065728	8.17E-06	0.0001249	24.0231541	34.5016025	25.3046744	73.8770593	75.2034533	92.079688
AT1G48120	228.9554352	1.036471561	0.29927473	3.46327796	0.00053364	0.00411827	146.227894	186.714555	117.413689	296.398322	409.335252	217.642899
AT1G48330	155.6395604	1.067081124	0.26322305	4.05390456	5.04E-05	0.00059355	127.427165	100.460548	73.8896492	194.038541	225.61036	212.411098
AT1G48460	605.215463	-2.316304326	0.19911483	-11.633007	2.80E-31	2.66E-28	1057.01878	957.926845	1009.15041	172.6765	250.360863	184.159376
AT1G48570	1110.219669	-2.337094073	0.19492908	-11.989458	4.04E-33	4.04E-30	1903.0516	1897.58814	1760.19315	315.090108	457.884317	327.510708
AT1G48630	2624.52075	-1.077992366	0.31016729	-3.4755191	0.00050987	0.0039589	3443.66691	4194.98896	3046.68279	992.444833	2499.80087	1569.54014
AT1G48650	2973.034161	-1.099025669	0.17106492	-6.4246118	1.32E-10	6.91E-09	3544.98195	4297.47901	4319.00182	1951.95652	2091.41756	1633.3681
AT1G48920	10236.52718	-1.233847237	0.21520836	-5.733268	9.85E-09	3.43E-07	13435.21	15747.952	13912.51	5016.51935	7992.50878	5314.4629
AT1G49000	313.3384811	1.18732563	0.45479162	2.61070252	0.00903565	0.03802684	303.945123	170.478506	99.1943235	404.098614	217.99482	684.319499
AT1G49210	51.87476837	1.599249997	0.47879347	3.34016671	0.00083728	0.00597014	43.8683683	22.3245663	11.1340567	86.3382501	62.8282015	84.7551673
AT1G49230	68.21056799	1.86391744	0.38358341	4.85922326	1.18E-06	2.34E-05	35.5124886	26.3835784	26.3168613	72.0968892	148.503022	100.450569
AT1G49450	89.94718664	2.760639423	0.34036722	8.11076764	5.03E-16	7.04E-14	14.6227894	27.3983314	27.3290483	182.467436	157.070504	130.795011
AT1G49620	113.6386591	-1.837882634	0.36520029	-5.0325333	4.84E-07	1.09E-05	223.519781	138.00641	171.059599	28.4827217	69.4917986	51.2716444
AT1G49650	653.7795068	-1.014953818	0.21103352	-4.8094436	1.51E-06	2.92E-05	749.940201	921.395736	952.467943	345.353	514.048921	439.471238
AT1G49790	17.52021925	1.880734894	0.57881614	3.24927859	0.00115698	0.00772037	5.2224248	10.1475301	7.08530882	29.3728067	32.3660432	20.9272018
AT1G50040	88.48442861	-1.667045268	0.28717779	-5.8049241	6.44E-09	2.34E-07	121.160255	121.770362	160.937729	42.7240825	46.6451799	37.6689633
AT1G50110	35.79318692	1.597611054	0.60926104	2.62221111	0.00873613	0.03705311	19.8452142	25.3688253	8.0974958	21.3620413	85.6748202	54.4107247
AT1G50750	86.15738775	1.911365915	0.47564192	4.0184976	5.86E-05	0.00067391	35.5124886	39.5753675	33.4021702	50.734848	201.811799	155.907653
AT1G51170	144.5902993	1.317067679	0.3494851	3.76859464	0.00016417	0.00156528	106.537466	100.460548	41.499666	197.598882	192.292374	229.15286
AT1G51310	781.9479441	-1.732739516	0.17830354	-9.71792	2.53E-22	1.00E-19	1077.90848	1215.67411	1312.80651	383.626657	310.333238	391.338674
AT1G51380	55.80401951	-2.410329801	0.36063591	-6.6835546	2.33E-11	1.41E-09	98.1815863	97.4162893	86.0358929	12.4611907	21.8946763	18.8344816
AT1G51790	235.9154613	1.010111711	0.38261112	2.64004794	0.00828943	0.03565111	174.428988	216.142392	78.950584	281.266876	229.41813	435.285798
AT1G51800	458.1493028	2.10656944	0.27967912	7.53209407	4.99E-14	4.80E-12	166.073109	203.965356	147.779298	574.994944	614.954821	1041.12829
AT1G51820	460.1323139	2.324330638	0.31186328	7.45304356	9.12E-14	8.51E-12	143.09444	160.330976	155.876794	471.745078	699.677698	1130.0689
AT1G51850	21.00884385	2.359131194	0.64500243	3.65755399	0.00025463	0.00223934	8.35587968	8.11802411	4.0487479	17.801701	33.3179856	54.4107247
AT1G51890	27.73724214	1.807948444	0.6156415	2.93669033	0.00331735	0.01758501	13.5783045	15.2212952	8.0974958	31.1529768	20.9427338	77.4306467
AT1G52000	1133.263914	1.707672109	0.65904383	2.59113587	0.00956597	0.03979235	212.030447	434.31429	947.407009	2394.32879	1192.78389	1618.71906
AT1G52030	26.10041337	1.818471707	0.7105428	2.55927118	0.01048919	0.04260827	2.08896992	18.2655542	14.1706176	19.5818711	63.7801439	38.7153234
AT1G52040	101.6277266	2.472311968	0.30841578	8.01616568	1.09E-15	1.42E-13	31.3345488	36.5311085	25.3046744	210.950157	146.599137	159.046734
AT1G52160	295.7225345	-1.56728309	0.20683177	-7.5775743	3.52E-14	3.53E-12	412.571559	499.258483	414.99666	142.413608	173.253525	131.841371
AT1G52190	4124.039253	1.90013227	0.27035778	7.02821369	2.09E-12	1.51E-10	2302.04485	1828.58493	1098.22287	7460.69291	6481.77612	5572.91384
AT1G52342	1505.296307	-1.182237113	0.35984229	-3.2854313	0.00101826	0.0069682	3064.51887	1352.66577	1852.30216	1352.03919	572.11741	838.134433
AT1G52400	4904.604032	1.362387812	0.40807215	3.33859539	0.00084203	0.00599502	947.347859	3279.68174	4013.32136	7511.42775	5919.17813	7756.66735
AT1G52720	928.6196305	1.029848045	0.29109141	3.53788534	0.00040335	0.00330011	428.238834	551.010886	852.261433	1303.9746	925.288058	1510.94397
AT1G52750	36.1509052	2.33933508	0.55483039	4.21630667	2.48E-05	0.00032415	10.4448496	12.1770362	13.1584307	35.6034021	104.713669	40.8080435
AT1G52800	48.68726591	2.8372505	0.40150601	7.06652062	1.59E-12	1.19E-10	14.6227894	13.1917892	8.0974958	94.3490155	77.1073382	84.7551673

Table S-5.1 Differentially Expressed Genes between lpa66 (LP) and wild type (WT) Arabidopsis plants.

ID	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	WT4	WT2	WT1	LP3	LP2	LP1
AT1G52830	52.25441355	2.898033759	0.50750146	5.71039497	1.13E-08	3.87E-07	22.9786691	10.1475301	4.0487479	80.9977397	87.5787051	107.775089
AT1G52910	88.46951688	1.538289668	0.52829756	2.91178642	0.00359368	0.01876307	34.4680037	66.9736989	34.4143571	43.6141676	202.763741	148.583133
AT1G52930	813.8890595	-1.898542306	0.22302562	-8.5126648	1.70E-17	2.84E-15	1374.54221	1319.17892	1156.92971	288.387557	450.268777	294.027185
AT1G53070	65.85657448	2.65197453	0.4344333	6.10444582	1.03E-09	4.50E-08	15.6672744	26.3835784	12.1462437	74.7671444	154.214676	111.96053
AT1G53460	428.0624645	-1.004226588	0.19733807	-5.088864	3.60E-07	8.38E-06	631.913401	462.727374	619.458429	287.497472	298.909928	267.868183
AT1G53480	70.5369245	6.678933535	0.77767103	8.58837895	8.82E-18	1.55E-15	0	3.04425904	1.01218697	137.963183	150.406907	130.795011
AT1G53490	44.41438495	2.038130754	0.37121886	5.49037496	4.01E-08	1.20E-06	16.7117594	20.2950603	15.1828046	70.3167191	78.0592806	65.9206857
AT1G53510	1690.009016	1.02761823	0.17672416	5.81481459	6.07E-09	2.22E-07	931.680584	1283.66256	1121.50317	2124.63302	2455.05957	2223.51519
AT1G53830	12.52734885	3.260775432	1.02422802	3.1836421	0.00145435	0.00925985	0	2.02950603	5.06093487	43.6141676	17.134964	7.32452063
AT1G54010	507.1853359	-1.305964491	0.3477638	-3.7553204	0.00017312	0.00163668	492.996901	580.438724	1093.16193	323.990959	189.436547	363.086951
AT1G54160	154.9591313	1.182190754	0.2388337	4.94984892	7.43E-07	1.59E-05	95.0481314	79.1507351	110.32838	237.652709	216.090935	191.483897
AT1G54200	130.8620407	1.258484886	0.31554903	3.98823884	6.66E-05	0.00074634	79.380857	88.2835122	63.7677794	135.292928	254.168633	164.278534
AT1G54570	496.0800171	-1.381793811	0.18457733	-7.4862598	7.09E-14	6.71E-12	675.781769	761.06476	714.604004	278.596621	314.141007	232.29194
AT1G54740	1774.079566	-1.007231727	0.29167132	-3.4533108	0.00055375	0.00424423	3042.58469	2021.388	2044.61769	1665.34913	805.34331	1065.19457
AT1G55040	117.4186204	-1.128418995	0.3443172	-3.2772658	0.00104818	0.00711407	112.804376	182.655542	188.266777	88.1184202	86.6267627	46.039844
AT1G55205	78.65433443	-1.088808862	0.38650135	-2.8170894	0.0048461	0.02362956	91.9146765	112.637585	116.401502	31.1529768	79.0112231	40.8080435
AT1G55265	272.5030644	1.274827422	0.31946659	3.99048748	6.59E-05	0.00074077	199.496627	179.611283	99.1943235	505.56831	292.246331	358.901511
AT1G55380	32.52512132	1.564689959	0.49904325	3.1353795	0.00171632	0.01051619	24.0231541	8.11802411	17.2071786	56.0753583	34.2699281	55.4570848
AT1G55500	1010.44008	-1.033380549	0.18173433	-5.6862154	1.30E-08	4.40E-07	1169.82316	1402.38866	1501.07328	740.550763	670.167483	578.63713
AT1G56110	2274.191747	-1.172897015	0.27836024	-4.213594	2.51E-05	0.00032739	3060.34093	3675.43542	2716.70984	938.149645	1990.51166	1264.00299
AT1G56150	210.565952	1.339602766	0.22908039	5.84774078	4.98E-09	1.86E-07	97.1371013	142.065422	118.425876	267.915601	320.804605	317.047107
AT1G56690	47.66029037	-1.327226181	0.379374	-3.4984637	0.00046795	0.00370908	69.9804923	55.8114157	78.950584	36.4934871	23.7985612	20.9272018
AT1G57660	5132.587168	-1.114385814	0.26244597	-4.2461533	2.17E-05	0.00028972	7538.04796	7356.95935	6170.2918	2101.49081	4370.36777	3258.36532
AT1G57770	3733.359224	-1.015415491	0.1711767	-5.9319726	2.99E-09	1.16E-07	4943.54732	5312.23203	4729.94973	2106.83132	2411.27022	2896.32473
AT1G58170	31.24759877	1.980740183	0.63089171	3.13958822	0.00169185	0.0103897	12.5338195	20.2950603	5.06093487	24.9223815	82.8189929	41.8544036
AT1G58225	44.08700131	2.614737321	0.55081288	4.74705189	2.06E-06	3.85E-05	24.0231541	9.13277712	4.0487479	70.3167191	62.8282015	94.1724082
AT1G58390	17.61509126	-1.936861838	0.63092359	-3.0698834	0.00214142	0.01256271	26.112124	30.4425904	27.3290483	5.34051031	13.3271943	3.13908027
AT1G58400	22.07534064	-1.463304432	0.47861713	-3.0573591	0.00223297	0.01292444	34.4680037	33.4868494	29.3534223	13.3512758	12.3752518	9.41724082
AT1G58561	296.8622361	1.373506921	0.30189313	4.54964619	5.37E-06	8.79E-05	114.893346	213.098133	168.023038	558.083328	317.948777	409.126795
AT1G59865	14.63811202	1.907015716	0.7569595	2.51931012	0.0117585	0.0463977	8.35587968	9.13277712	1.01218697	26.7025516	13.3271943	29.2980825
AT1G59930	46.48109865	1.648517548	0.43713652	3.77117329	0.00016248	0.00155076	22.9786691	18.2655542	26.3168613	105.030036	57.1165468	49.1789243
AT1G59990	1748.307824	-2.056836796	0.17828361	-11.536881	8.60E-31	7.44E-28	2763.7072	2598.78247	3095.26777	797.516207	592.108202	642.465096
AT1G60060	58.03240996	1.949566685	0.47426983	4.11066981	3.95E-05	0.00048407	21.9341842	37.5458615	12.1462437	78.3274846	132.32	65.9206857
AT1G60080	189.5834236	-1.189751265	0.24617514	-4.8329464	1.35E-06	2.64E-05	293.500274	226.289922	271.266109	109.480461	142.791367	94.1724082
AT1G60390	59.51797464	1.078480978	0.38888796	2.7732434	0.00555006	0.02619306	40.7349134	49.7228977	24.2924874	62.3059536	104.713669	75.3379265
AT1G60850	259.0058878	-1.139946911	0.19881076	-5.7338291	9.82E-09	3.42E-07	367.658706	357.193061	344.143571	145.973949	189.436547	149.629493
AT1G60960	193.0791547	-1.097677528	0.29057655	-3.7775847	0.00015836	0.00152323	261.12124	236.437452	292.522036	174.45667	101.857842	92.079688
AT1G61400	32.83170328	-1.320086607	0.50120462	-2.6338277	0.00844283	0.0361231	35.5124886	49.7228977	55.6702836	31.1529768	12.3752518	12.5563211
AT1G61500	121.7352846	1.11113062	0.23610964	4.70599438	2.53E-06	4.61E-05	66.8470374	78.135982	86.0358929	161.105394	165.637986	172.649415
AT1G61570	825.2693927	-1.27439781	0.229855	-5.5443555	2.95E-08	9.06E-07	1272.18268	1166.96597	1063.80851	345.353	596.867914	506.438284
AT1G61740	5137.05588	-1.337963687	0.21705739	-6.1641009	7.09E-10	3.27E-08	7576.6939	7038.3269	7470.95206	3630.65693	2104.74475	3000.96074
AT1G61870	835.7058947	-1.142916492	0.24417275	-4.68077	2.86E-06	5.12E-05	1087.30884	1082.74147	1281.42871	441.482186	711.101008	410.173155
AT1G62010	136.664837	-1.040630868	0.29908941	-3.4793304	0.00050267	0.00391419	199.496627	171.493259	181.181469	96.1291856	115.185036	56.5034449
AT1G62150	152.8739081	-1.157305835	0.3007703	-3.8478062	0.00011918	0.00120837	207.852507	219.186651	206.486143	83.6679949	135.175827	64.8743256
AT1G62290	81.20420087	1.415672612	0.32457029	4.3616827	1.29E-05	0.0001844	41.7793984	46.6786386	44.5362269	146.864034	124.704461	82.6624472
AT1G62350	62.91425475	-2.127789677	0.3943491	-5.3957006	6.83E-08	1.92E-06	114.893346	97.4162893	95.1455756	22.2521263	35.2218705	12.5563211
AT1G62720	33.14583279	-1.259141182	0.40366478	-3.1192743	0.00181297	0.01099161	45.9573382	48.7081447	45.5484139	21.3620413	14.2791367	23.019922
AT1G62730	139.1011572	-1.196770932	0.23865034	-5.0147464	5.31E-07	1.18E-05	196.363173	174.537518	210.534891	91.6787604	91.3864749	70.1061261
AT1G62770	35.198587	3.566131954	0.55313134	6.44717037	1.14E-10	6.06E-09	8.35587968	5.07376507	3.03656092	46.2844227	64.7320864	83.7088072
AT1G63040	18.00746659	-2.778399641	1.00131917	-2.7747393	0.0055246	0.02609798	9.40036464	20.2950603	64.7799664	11.5711057	0.95194245	1.04636009
AT1G63090	836.8154796	-1.220611553	0.33082935	-3.6895503	0.00022465	0.00202335	1283.67202	966.044869	1264.22153	805.526972	365.5459	335.881589
AT1G63100	22.31903828	1.687073683	0.60682667	2.78015743	0.00543326	0.0258307	8.35587968	15.2212952	8.0974958	16.0215309	48.5490648	37.6689633
AT1G63250	136.2226821	-1.121359264	0.27130922	-4.133141	3.58E-05	0.00044307	155.628259	203.965356	200.413021	75.6572294	109.473381	72.1988462
AT1G63300	186.1781582	1.408139314	0.29864127	4.71515303	2.42E-06	4.42E-05	85.6477667	109.593325	110.32838	182.467436	356.978418	272.053624
AT1G63660	1212.063773	-1.44827189	0.19012929	-7.6173002	2.59E-14	2.71E-12	1524.94804	1979.78313	1817.88781	712.068042	697.773813	539.921807
AT1G63780	688.141757	-1.566463775	0.17176604	-9.1197527	7.53E-20	1.99E-17	1087.30884	1050.26937	949.431382	340.01249	393.152231	308.676227
AT1G63810	496.6630787	-1.287633703	0.27127345	-4.7466263	2.07E-06	3.86E-05	539.998724	905.159688	669.05559	270.585856	371.257554	223.921059
AT1G63860	869.8253247	1.190110888	0.32370184	3.67656505	0.0002364	0.00210976	505.530721	613.925573	470.666943	1184.7032	666.359713	1777.76579
AT1G63930	15.06343061	-1.864696036	0.64310874	-2.8995035	0.00373754	0.01934907	28.2010939	23.3393193	19.2315525	2.67025516	8.56748202	8.37088072
AT1G64185	52.93860351	-1.458458804	0.35702311	-4.0850543	4.41E-05	0.00053145	91.9146765	74.07697	66.8043403	21.3620413	35.2218705	28.2517224
AT1G64220	29.18226803	-2.882845825	0.51998717	-5.5440711	2.96E-08	9.06E-07	44.9128533	52.7671567	56.6824706	7.12068042	10.4713669	3.13908027
AT1G64390	2869.167928	1.050737127	0.370044	2.83949241	0.00451854	0.02238799	1641.93036	2738.81838	1223.73405	2117.51234	5586.95022	3906.06222
AT1G64450	67.74343281	1.023963125	0.39553252	2.58882158	0.0096305	0.03999084	35.5124886	63.9294399	34.4143571	59.6356985	110.425324	102.543289
AT1G64600	219.9626314	-1.834608343	0.25761689	-7.1214599	1.07E-12	8.40E-11	294.544759	380.53238	356.289815	117.491227	101.857842	69.059766
AT1G64625	32.8170841	1.75374383	0.50649053	3.46254019	0.0005351	0.00412653	12.5338195	23.3393193	9.10968277	33.823232	64.7320864	53.3643646
AT1G64640	325.7472565	1.703954437	0.26794411	6.35936527	2.03E-10	1.03E-08	167.117594	159.316223	132.596494	371.165467	670.167483	454.120279
AT1G65010	2621.02443	1.057328532	0.20780914	5.08797899	3.62E-07	8.39E-06	1437.21131	1885.4111	1781.44908	3151.79117	4406.54159	3063.74235
AT1G65030	312.1043181	-1.217017286	0.27531425	-4.4204661	9.85E-06	0.00014678	329.012762	544.922368	435.240399	143.303693	237.033669	183.113016
AT1G65080	55.03542391	-1.348012034	0.38986141	-3.4576698	0.00054487	0.00418627	79.380857	81.1802411	76.9262101	46.2844227	27.606331	18.8344816
AT1G65310	63.74032763	1.567229699	0.34608024	4.52851546	5.94E-06	9.59E-05	42.8238834	25.3688253	28.3412353	79.2175696	110.425324	96.2651283
AT1G65390	910.417233	1.480198307	0.33314669	4.44308268	8.87E-06	0.00013362	475.240657	478.963422	486.861935	837.570034	1004.29928	2179.56807
AT1G65450	26.39341112	4.899836076	0.83989085	5.83389625	5.41E-09	2.00E-07	2.08896992	3.04425904	0	28.4827217	50.4529497	74.2915664
AT1G65486	348.9629263	1.053890054	0.36770912	2.86609713	0.00415567	0.02101688	283.055424	244.555476	152.840233	291.057812	384.584748	737.683864
AT1G65690	58.04248479	1.689058328	0.49844167	3.38867801	0.0007023	0.00516244	45.9573382	16.2360482	20.2437395	74.7671444	57.1165468	133.934092
AT1G65920	187.1992672	1.393162401	0.24961972	5.58113928	2.39E-08	7.57E-07	85.6477667	102.490054	121.462437	230.532028	324.612374	258.450942
AT1G65970	11.43079463	-2.044466349	0.71291476	-2.8677571	0.00413393	0.02095147	16.7117594	17.2508012	21.2559265	6.23059536	1.90388489	5.23180045
AT1G66350	456.1817192	1.575725137	0.2883029	5.46551946	4.62E-08	1.36E-06	185.918323	170.478506	330.985141	553.632902	730.139857	765.935586
AT1G66460	63.97086962	2.097809786	0.50005027	4.19519781	2.73E-05	0.00035129	19.8452142	38.5606145	14.1706176	65.8662939	79.0112231	166.371254
AT1G66520	454.8971835	-1.624727467	0.24220019	-6.7082007	1.97E-11	1.21E-09	750.984686	707.282851	602.25125	155.764884	259.880288	253.219142
AT1G66700	10.32836564	3.188321489	1.1636469	2.73993897	0.00614506	0.0283438	0	3.04425904	3.03656092	6.23059536	5.71165468	43.9471238
AT1G66760	6050.120196	-1.222563289	0.36298956	-3.3680398	0.00075705	0.00548852	6427.76044	6540.08317	12443.8267	5461.56188	2078.09036	3349.39865

Table S-5.1 Differentially Expressed Genes between lpa66 (LP) and wild type (WT) Arabidopsis plants.

ID	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	WT4	WT2	WT1	LP3	LP2	LP1
AT1G66920	468.8689579	1.333274345	0.27014476	4.93540703	8.00E-07	1.68E-05	263.21021	239.481711	296.570784	818.878248	431.229928	763.842866
AT1G66930	38.06617279	2.798501007	0.52476245	5.33289115	9.67E-08	2.63E-06	9.40036464	14.2065422	5.06093487	40.0538273	78.0592806	81.6160871
AT1G66940	1478.802594	2.421367335	0.25095752	9.64851461	4.99E-22	1.83E-19	512.842115	521.583049	361.35075	1769.48908	2999.57065	2707.97991
AT1G67120	1062.972178	-1.238592314	0.30453975	-4.0670958	4.76E-05	0.00056514	1000.61659	1780.89154	1698.44974	890.975137	534.991655	471.908401
AT1G67260	63.75247538	8.437533339	3.03662217	2.77859176	0.00545951	0.02591667	0	1.01475301	0	133.512758	0	247.987341
AT1G67400	87.95171212	1.467896861	0.38199586	3.8427036	0.00012169	0.00123182	38.6459435	63.9294399	37.4509181	82.7779098	175.15741	129.748651
AT1G67750	270.0371065	2.142139541	0.44810091	4.78048469	1.75E-06	3.32E-05	107.581951	142.065422	49.5971618	220.741093	691.110216	409.126795
AT1G68110	224.3000095	-1.473795426	0.29645551	-4.9713883	6.65E-07	1.44E-05	407.349134	243.540723	339.082637	159.325224	97.0981296	99.4042086
AT1G68238	41.65583757	-2.212096199	0.54287593	-4.0747731	4.61E-05	0.00055025	91.9146765	86.2540062	27.3290483	15.1314459	10.4713669	18.8344816
AT1G68330	48.47052117	1.77828881	0.36772835	4.83587627	1.33E-06	2.60E-05	25.067639	22.3245663	18.2193655	59.6356985	81.8670504	83.7088072
AT1G68500	26.96677087	1.816048394	0.5536994	3.27984532	0.00103864	0.00707204	8.35587968	15.2212952	12.1462437	22.2521263	60.9243166	42.9007637
AT1G68600	322.7378151	1.673732485	0.32518073	5.14708383	2.65E-07	6.42E-06	102.359526	153.227705	206.486143	649.762088	336.987626	487.603802
AT1G68810	309.3822948	1.125346457	0.21142802	5.32259839	1.02E-07	2.77E-06	183.829353	217.157145	182.193655	349.803425	438.845468	484.464722
AT1G68990	956.1372207	-1.484426416	0.26380815	-5.6269164	1.83E-08	5.98E-07	975.548953	1646.94414	1604.31636	629.290132	477.875108	402.848635
AT1G69070	832.7937113	-1.042170312	0.24314296	-4.286245	1.82E-05	0.00024916	951.525799	1227.85115	1184.25876	477.975673	728.235972	426.914917
AT1G69200	1626.404137	-2.792608996	0.20973463	-13.314964	1.89E-40	4.01E-37	2795.04175	2610.9595	3121.58463	334.67198	522.616403	373.550552
AT1G69210	77.38881497	-1.474372279	0.35718783	-4.1277226	3.66E-05	0.00045246	107.581951	79.1507351	154.864607	49.8447629	35.2218705	37.6689633
AT1G69690	539.5209963	1.485145582	0.2429563	6.11280951	9.79E-10	4.31E-08	296.633729	279.057079	276.327044	626.619877	1069.98331	688.50494
AT1G69790	67.14730293	-1.208097503	0.3460514	-3.4910927	0.00048105	0.00378456	90.8701915	85.2392531	105.267445	55.1852732	27.606331	38.7153234
AT1G70270	17.1822475	5.030776262	1.15131342	4.36959752	1.24E-05	0.00017889	0	0	3.03656092	13.3512758	64.7320864	21.9735619
AT1G70300	353.8650356	-1.31297045	0.31965123	-4.1075095	4.00E-05	0.00048917	491.952416	459.683115	562.775958	315.980193	138.983597	153.814933
AT1G70350	324.3267458	-1.159584875	0.20604146	-5.62792	1.82E-08	5.95E-07	515.97557	418.078242	409.935725	170.89633	221.80259	209.272018
AT1G70360	78.82527181	-1.475372592	0.33192986	-4.4448324	8.80E-06	0.00013275	149.361349	97.4162893	101.218697	50.734848	32.3660432	41.8544036
AT1G70710	292.7156635	1.857197191	0.44083051	4.21295063	2.52E-05	0.00032788	88.7812216	200.921097	90.0846408	208.279902	659.696116	508.531004
AT1G70810	630.7725458	-1.318389079	0.42819399	-3.0789528	0.0020773	0.01224691	694.582498	765.123772	1241.95342	602.58758	146.599137	333.788869
AT1G70940	3150.712911	1.095172426	0.26973244	4.06021775	4.90E-05	0.00058024	2241.46472	2584.57593	1201.46594	4497.59977	4252.32691	4126.8442
AT1G71100	1043.369948	-1.017769155	0.22298909	-4.5642105	5.01E-06	8.26E-05	1523.90356	1179.143	1487.91485	865.162671	540.70331	663.392297
AT1G71140	705.9123367	-1.503937575	0.26527912	-5.6692649	1.43E-08	4.79E-07	1073.73054	908.203947	1149.8444	502.898054	251.312806	349.48427
AT1G71210	365.583932	-1.001332076	0.20524554	-4.8787033	1.07E-06	2.16E-05	463.751322	565.217429	434.228212	265.245346	258.928346	206.132938
AT1G71260	869.5293124	-1.912587028	0.18866058	-10.137714	3.76E-24	1.83E-21	1504.05834	1208.57084	1409.97646	355.143936	425.518274	313.908027
AT1G71420	28.61959319	-1.541733173	0.47654126	-3.2352564	0.00121534	0.00802535	40.7349134	35.5163555	51.6215357	19.5818711	8.56748202	15.6954014
AT1G71830	96.320293	1.072374798	0.35384229	3.0306575	0.00244022	0.01385423	55.3577029	83.2097471	47.5727878	88.1184202	166.589928	137.073172
AT1G71850	197.2919036	-1.759994887	0.25225715	-6.9769872	3.02E-12	2.09E-10	275.744029	313.558681	324.912019	86.3382501	115.185036	68.0134059
AT1G71890	49.34445591	1.727463185	0.56457095	3.05978049	0.00221499	0.01288705	20.8896992	29.4278374	18.2193655	31.1529768	56.1646044	140.212252
AT1G72040	1784.401987	-1.405279537	0.19271592	-7.2919744	3.05E-13	2.57E-11	2163.12835	2746.93641	2862.46477	1020.03747	1096.6377	817.207231
AT1G72210	43.11673401	2.093375744	0.55323715	3.78386691	0.00015441	0.00149167	13.5783045	11.1622831	24.2924874	28.4827217	93.2903598	87.8942476
AT1G72230	182.1865118	1.729361922	0.35380918	4.88783795	1.02E-06	2.07E-05	95.0481314	108.578572	49.5971618	184.247606	331.275971	324.371628
AT1G72240	14.62992077	2.014884471	0.71902062	2.80226242	0.00507456	0.02445528	8.35587968	6.08851808	3.03656092	29.3728067	30.4621583	10.4636009
AT1G72360	93.43016423	1.158752827	0.3000897	3.86135485	0.00011276	0.00115684	77.2918871	44.6491326	51.6215357	130.842503	138.983597	117.19233
AT1G72416	638.8661808	1.497776729	0.24653087	6.07541247	1.24E-09	5.25E-08	310.212033	278.042326	413.984473	717.408552	1150.89842	962.651283
AT1G72440	1340.861113	-1.163930869	0.2480699	-4.6919471	2.71E-06	4.90E-05	1811.13692	2176.64521	1574.96293	700.496936	1118.53237	663.392297
AT1G72680	576.6370985	-1.705280437	0.29163831	-5.8472443	5.00E-09	1.86E-07	741.584322	696.120567	1210.57562	360.484446	231.322015	219.735619
AT1G72870	13.68681114	1.688709503	0.6561207	2.57377872	0.01005946	0.04133914	7.31139472	8.11802411	4.0487479	28.4827217	14.2791367	19.8808417
AT1G72900	2185.335716	-1.709166157	0.25351722	-6.7418147	1.56E-11	9.92E-10	2974.69317	2901.17887	4165.1494	1198.05448	707.293238	1165.64514
AT1G72970	1401.506497	1.021018657	0.37898265	2.69410394	0.00705782	0.03152988	699.804923	1154.78893	921.090147	835.789864	2827.26907	1970.29605
AT1G73330	12.23097859	-2.332711071	0.9119035	-2.5580679	0.01052555	0.04271041	18.8007293	13.1917892	29.3534223	8.90085052	0	3.13908027
AT1G73370	70.41145813	1.158194633	0.37636603	3.07730918	0.00208879	0.01230507	28.2010939	59.8704278	42.5118529	71.2068042	117.088921	103.589649
AT1G73550	25.63402585	3.403182468	0.68086367	4.99833168	5.78E-07	1.27E-05	1.04448496	6.08851808	6.07312185	26.7025516	43.7893526	70.1061261
AT1G73590	126.0233626	1.765446428	0.29155021	6.05537688	1.40E-09	5.85E-08	49.0907931	71.032711	51.6215357	151.314459	233.225899	199.854777
AT1G73620	18.66047226	1.756136267	0.63888904	2.74873438	0.00598258	0.02771533	6.26690976	10.1475301	9.10968277	13.3512758	43.7893526	29.2980825
AT1G73700	55.24930812	1.255825712	0.39803273	3.15508153	0.00160453	0.00996601	19.8452142	40.5901205	37.4509181	95.2391006	81.8670504	56.5034449
AT1G73805	434.4256824	-1.147764589	0.3958824	-2.8992564	0.00374049	0.01934907	641.313766	791.507351	363.375124	408.549039	137.079712	264.729103
AT1G74290	226.3818002	-1.447440585	0.29951312	-4.832645	1.35E-06	2.64E-05	368.703191	281.086585	344.143571	153.984714	73.2995684	137.073172
AT1G74310	183.0864766	1.069517789	0.28345792	3.77310958	0.00016123	0.00154263	90.8701915	147.139187	116.401502	202.049307	316.044892	226.01378
AT1G74400	16.17722587	-1.996610283	0.69584316	-2.8693395	0.0041133	0.02087472	16.7117594	16.2360482	44.5362269	4.45042526	5.71165468	9.41724082
AT1G74430	301.2237623	1.384232997	0.46962263	2.94754319	0.0032031	0.01711347	72.0694622	138.00641	290.497662	634.630642	249.408921	422.729477
AT1G74560	2968.719252	-1.536905119	0.16894784	-9.0969207	9.29E-20	2.42E-17	4820.29809	4031.61372	4395.92803	1749.90721	1478.36662	1336.20184
AT1G74670	4037.053961	2.734660183	0.33753697	8.10180944	5.41E-16	7.47E-14	1506.14731	1149.71516	508.117861	6433.53476	8240.96576	6383.84291
AT1G75030	323.0271889	1.128180629	0.38566604	2.92527862	0.00344148	0.01812252	201.585597	263.835784	142.718363	223.411348	436.941583	669.670458
AT1G75040	1185.852179	1.044921129	0.34144001	3.06033592	0.00221089	0.0128671	862.744577	908.203947	551.641901	1578.1208	875.787051	2338.6148
AT1G75200	829.1211629	-1.143578184	0.19421658	-5.8881593	3.91E-09	1.48E-07	1067.46363	1224.80689	1132.63722	490.436864	628.282015	431.100357
AT1G75240	213.1281025	1.037730603	0.28900633	3.59068472	0.00032981	0.00278096	146.227894	126.844127	145.754924	204.719562	398.863885	256.358222
AT1G75300	18.50148092	1.975381863	0.58963371	3.35018475	0.00080758	0.00579088	8.35587968	4.05901205	10.1218697	29.3728067	37.1257554	21.9735619
AT1G75310	679.2403718	1.043212917	0.22877826	4.55993031	5.12E-06	8.42E-05	340.502097	461.712621	529.373788	1077.00291	896.729785	770.121027
AT1G75500	5511.850392	1.011672663	0.16801474	6.02133292	1.73E-09	6.95E-08	3658.83082	4153.38408	3151.95024	6612.44185	7817.35137	7677.14398
AT1G75590	23.26743436	3.245894947	0.58303278	5.56725975	2.59E-08	8.06E-07	5.2224248	5.07376507	3.03656092	40.0538273	48.5490648	37.6689633
AT1G75670	207.0364495	-1.173556758	0.25408506	-4.6187554	3.86E-06	6.64E-05	288.277849	299.352139	273.290483	117.491227	167.541871	96.2651283
AT1G75750	12114.83082	-1.595907461	0.29854955	-5.3455363	9.01E-08	2.46E-06	20831.208	12911.7173	20877.3685	8386.38136	3921.05094	5761.25866
AT1G75780	223.8190907	3.023349018	0.45066393	6.70865546	1.96E-11	1.21E-09	35.5124886	70.0179579	41.499666	205.609647	692.062159	298.212626
AT1G76040	210.5304627	1.152254846	0.23620148	4.87827108	1.07E-06	2.16E-05	127.427165	138.00641	126.523372	329.331469	222.754533	319.139828
AT1G76240	460.5368514	1.766341799	0.21687107	8.14466314	3.80E-16	5.53E-14	178.606928	243.540723	205.473956	615.938856	851.036547	668.624098
AT1G76300	724.9756364	-1.19678906	0.16993305	-7.0427093	1.89E-12	1.37E-10	1092.53127	951.838327	983.84574	381.846487	473.115396	466.6766
AT1G76590	488.253878	-1.167747441	0.46251296	-2.5247886	0.01157679	0.04589	612.068187	594.645266	820.883637	584.785879	125.656403	191.483897
AT1G76610	31.77825989	2.376106943	0.47557958	4.99623414	5.85E-07	1.28E-05	15.6672744	7.1032711	8.0974958	58.7456134	46.6451799	54.4107247
AT1G76780	65.06439628	1.078348835	0.40207139	2.68198349	0.00731871	0.03241385	22.9786691	52.7671567	49.5971618	65.8662939	112.329209	86.8478875
AT1G77030	595.902756	-1.134398829	0.25892622	-4.3811663	1.18E-05	0.00017058	670.559344	989.384188	796.591149	317.760364	499.769785	301.351706
AT1G77110	81.55739737	1.317024222	0.35719368	3.6871431	0.00022679	0.00203775	37.6014586	64.9441929	37.4509181	83.6679949	127.560288	138.119532
AT1G77270	116.9848841	1.065486679	0.34646744	3.07528662	0.002103	0.01236805	58.4911578	101.475301	66.8043403	103.249866	196.100144	175.788495
AT1G77380	18.40366126	-2.282120444	0.72064144	-3.1667905	0.00154131	0.00968397	17.7562443	27.3983314	46.5606008	11.5711057	1.90388489	5.23180045
AT1G77405	21.42750405	-1.515142204	0.50575045	-2.9958297	0.00273699	0.01510226	37.6014586	24.3540723	33.4021702	12.4611907	12.3752518	8.37088072
AT1G77460	487.3569037	1.208093584	0.27476891	4.3967623	1.10E-05	0.00016061	249.631905	402.856946	230.77863	561.643668	847.228778	632.001495

Table S-5.1 Differentially Expressed Genes between lpa66 (LP) and wild type (WT) Arabidopsis plants.

ID	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	WT4	WT2	WT1	LP3	LP2	LP1
AT1G77570	50.15543727	-1.478111897	0.40399125	-3.6587721	0.00025343	0.00222976	96.0926163	56.8261688	68.8287143	32.9331469	29.5102158	16.7417614
AT1G77580	557.5168474	1.252127517	0.18208874	6.87646883	6.14E-12	4.08E-10	301.856153	382.561886	304.668279	755.682209	860.555972	739.776584
AT1G77750	729.4344107	-1.369333197	0.19766092	-6.9276882	4.28E-12	2.91E-10	1161.46728	1004.60548	988.906674	328.441384	478.827051	414.358596
AT1G77760	1982.476585	-2.590352018	0.38079528	-6.8024793	1.03E-11	6.66E-10	2379.33674	3517.13395	4304.8312	874.063521	261.784173	557.709928
AT1G77765	115.2403427	1.980479551	0.51901442	3.81584685	0.00013572	0.00134382	25.067639	78.135982	36.4387311	78.3274846	184.676835	288.795385
AT1G77855	30.06082189	1.813755469	0.5017	3.61521921	0.00030009	0.002566	10.4448496	19.2803073	10.1218697	32.0430619	45.6932374	62.7816054
AT1G78000	57.16652989	1.135483781	0.36119464	3.14368946	0.00166832	0.01027504	34.4680037	28.4130844	44.5362269	99.6895258	75.2034533	60.6888853
AT1G78060	709.4089033	1.432557195	0.22618948	6.33343861	2.40E-10	1.20E-08	382.281495	428.225772	340.094824	835.789864	1324.15194	945.909522
AT1G78090	55.23436645	1.074277792	0.35804017	3.00043933	0.0026959	0.01493617	47.0018232	35.5163555	24.2924874	83.6679949	66.6359713	74.2915664
AT1G78120	22.30170544	1.511063547	0.56270353	2.68536353	0.0072451	0.03216268	8.35587968	19.2803073	7.08530882	25.8124665	41.8854677	31.3908027
AT1G78130	195.0185635	1.316308121	0.21930282	6.00223997	1.95E-09	7.76E-08	96.0926163	111.622831	127.535559	307.969428	257.976403	268.914543
AT1G78210	873.7938654	1.264553039	0.1466514	8.62284998	6.53E-18	1.20E-15	481.507567	546.951874	512.166609	1182.92303	1228.00576	1291.20835
AT1G78260	128.8067703	1.027446309	0.2994582	3.43101746	0.00060132	0.00454298	63.7135826	88.2835122	102.230884	135.292928	217.99482	165.324894
AT1G78320	40.8706058	1.619177971	0.53374292	3.03362894	0.00241631	0.01375146	10.4448496	37.5458615	12.1462437	45.3943377	68.5398562	71.1524862
AT1G78580	1141.709777	1.044060499	0.24478918	4.26514158	2.00E-05	0.00027022	549.399089	877.761357	809.74958	1191.82388	1825.82561	1595.69914
AT1G78930	134.2893382	-2.674001324	0.25618426	-10.437805	1.67E-25	9.91E-23	253.809845	223.245663	219.644574	34.713317	41.8854677	32.4371628
AT1G78940	32.85496099	1.887410182	0.48356781	3.90309312	9.50E-05	0.00100299	11.4893346	19.2803073	11.1340567	35.6034021	70.4437411	49.1789243
AT1G78970	205.3810928	2.858226019	0.27096335	10.5483861	5.17E-26	3.28E-23	45.9573382	47.6933916	55.6702836	425.460655	270.351655	387.153234
AT1G78990	68.08555374	1.413239094	0.47226207	2.99248911	0.00276713	0.01523374	32.3790338	63.9294399	15.1828046	83.6679949	117.088921	96.2651283
AT1G79150	742.8330189	-1.350517804	0.25729867	-5.2488332	1.53E-07	3.94E-06	972.415498	1249.16096	979.796992	305.299173	567.357698	382.967793
AT1G79245	20071.98695	1.12026424	0.33037644	3.39087204	0.00069671	0.00513318	7807.52508	13798.6115	16338.7221	38331.5128	17457.6725	26697.8777
AT1G79330	12.79718197	2.113751091	0.76830879	2.75117389	0.00593821	0.02757638	6.26690976	3.04425904	5.06093487	12.4611907	13.3271943	36.6226032
AT1G79420	43.74309256	1.360570059	0.47386394	2.87122517	0.00408884	0.02080052	15.6672744	26.3835784	31.3777962	33.823232	80.915108	74.2915664
AT1G79460	301.5939648	1.444993332	0.24099479	5.99595263	2.02E-09	8.04E-08	115.937831	192.803073	177.132721	393.417593	463.595972	466.6766
AT1G79470	245.345113	-1.952676436	0.21370502	-9.1372512	6.41E-20	1.77E-17	434.505743	382.561886	353.253254	115.711057	97.0981296	88.9406077
AT1G79490	257.8120731	-1.402756587	0.22664225	-6.1892988	6.04E-10	2.83E-08	297.678214	408.945464	416.008847	151.314459	149.454964	123.470491
AT1G79560	1963.304728	-1.21092023	0.23153549	-5.2299551	1.70E-07	4.32E-06	1973.03209	3018.89022	3233.93738	992.444833	1328.91166	1232.61219
AT1G79760	33.63947589	2.928234382	0.77066808	3.79960514	0.00014493	0.00141297	2.08896992	20.2950603	1.01218697	53.4051031	58.0684893	66.9670458
AT1G80080	137.4803366	1.874581792	0.59317114	3.16027138	0.00157622	0.00984156	43.8683683	94.3720303	38.463105	56.9654433	411.239137	179.973936
AT1G80120	106.7531901	1.83463132	0.51898897	3.53501023	0.00040776	0.00332765	12.5338195	44.6491326	82.9993319	206.499732	128.51223	165.324894
AT1G80150	151.7694305	-1.667053728	0.2941912	-5.6665655	1.46E-08	4.86E-07	186.962808	226.289922	279.363605	62.3059536	97.0981296	58.5961651
AT1G80160	12.5969149	-3.208145137	0.97310287	-3.2968201	0.00097786	0.00673775	17.7562443	13.1917892	37.4509181	6.23059536	0.95194245	0
AT1G80190	392.7698206	-1.011356237	0.21661289	-4.6689569	3.03E-06	5.36E-05	472.107202	503.317495	600.226876	319.540534	232.273957	229.15286
AT1G80245	185.6814681	-1.912414022	0.20966103	-9.1214569	7.41E-20	1.99E-17	294.544759	269.924302	315.802336	78.3274846	78.0592806	77.4306467
AT1G80270	545.503583	-1.228701748	0.29551927	-4.157772	3.21E-05	0.000404	663.24795	922.410489	708.530882	250.1139	480.730936	247.987341
AT1G80280	118.6078753	2.274903296	0.45365973	5.01455854	5.32E-07	1.18E-05	39.6904285	61.8999338	20.2437395	110.370546	282.726907	196.715697
AT1G80720	155.8605917	-1.673307373	0.27686784	-6.0437044	1.51E-09	6.21E-08	237.098086	238.466958	235.839565	48.9546779	83.7709353	91.0333279
AT1G80750	1180.464532	-1.189679415	0.22943737	-5.1852034	2.16E-07	5.40E-06	1712.95533	1686.51951	1524.35358	526.040266	932.903598	700.014901
AT1G80820	37.02566123	1.294969599	0.48008401	2.69738125	0.00698872	0.03128731	19.8452142	17.2508012	27.3290483	81.8878248	37.1257554	38.7153234
AT1G80830	505.8026648	-1.120821309	0.27947407	-4.0104662	6.06E-05	0.00069099	710.249773	651.471435	717.640565	460.173972	217.99482	277.285424
AT2G01150	99.38535748	1.572573664	0.33759971	4.65810141	3.19E-06	5.60E-05	75.2029171	39.5753675	35.4265441	161.105394	143.743309	141.258612
AT2G01610	12.27005652	3.219010904	0.82645896	3.89494346	9.82E-05	0.00102933	0	3.04425904	4.0487479	20.4719562	20.9427338	25.1126422
AT2G01740	82.05082946	-1.518995188	0.28049288	-5.41545	6.11E-08	1.74E-06	107.581951	119.740856	137.657429	45.3943377	39.0296403	42.9007637
AT2G01830	581.2626609	-1.037968905	0.25941454	-4.0011979	6.30E-05	0.00071303	822.009664	867.613827	655.89716	321.320704	523.568346	297.166266
AT2G01850	7911.805508	-1.301852267	0.28107751	-4.6316486	3.63E-06	6.29E-05	12590.2217	9540.70783	11642.1746	6707.68095	3182.3436	3807.70437
AT2G01918	408.0820563	-1.013576608	0.22189095	-4.5679042	4.93E-06	8.17E-05	595.356427	498.24373	543.544406	206.499732	326.516259	278.331784
AT2G01950	308.7815324	1.509025206	0.26414428	5.71288236	1.11E-08	3.84E-07	138.9165	216.142392	126.523372	380.956402	524.520288	465.63024
AT2G02150	76.64422644	-1.180753874	0.325455	-3.6280096	0.00028561	0.0024707	91.9146765	109.593325	117.413689	32.9331469	60.9243166	47.0862041
AT2G02710	3708.63065	-1.29438087	0.27895823	-4.6400526	3.48E-06	6.06E-05	5802.11395	4373.58549	5631.80833	3051.21156	1416.49036	1976.57421
AT2G02740	719.4925921	-1.755811277	0.2005808	-8.7536358	2.07E-18	4.01E-16	1134.31067	1110.1398	1086.07662	266.135431	407.431367	312.861667
AT2G02750	68.3105673	-1.346070294	0.35066989	-3.8385683	0.00012375	0.00124744	87.7367367	79.1507351	127.535559	48.0645928	38.0776979	29.2980825
AT2G02880	198.9928762	-1.283762472	0.20793114	-6.173979	6.66E-10	3.08E-08	287.233364	270.939055	288.473288	117.491227	130.416115	99.4042086
AT2G02955	129.3535231	-1.467710136	0.2845373	-5.1582346	2.49E-07	6.09E-06	156.672744	220.201404	193.327712	64.9762088	87.5787051	53.3643646
AT2G03380	32.09643515	-1.386279354	0.44462023	-3.1178954	0.00182147	0.01103964	54.3132179	36.5311085	48.5849748	24.0322964	12.3752518	16.7417614
AT2G03500	80.25941143	1.071017387	0.32981648	3.2473131	0.001165	0.00775766	39.6904285	74.07697	41.499666	110.370546	112.329209	103.589649
AT2G03590	159.3521864	2.155604276	0.30753217	7.00936186	2.39E-12	1.69E-10	67.8915224	53.7819097	53.6459097	318.650449	172.301583	289.841745
AT2G03820	2924.679714	-1.121744614	0.12751916	-8.796675	1.41E-18	2.95E-16	4045.29025	4012.33342	3965.74857	1846.92648	1942.91453	1734.86503
AT2G04030	14468.42082	-2.801506157	0.16281753	-17.206416	2.38E-66	2.26E-62	24710.4252	24107.4873	27103.3306	3612.85523	4156.18072	3120.24579
AT2G04040	15.46020863	-2.808826482	0.72144124	-3.8933545	9.89E-05	0.00103268	34.4680037	33.4868494	13.1584307	3.56034021	2.85582734	5.23180045
AT2G04050	59.91119747	-4.824358411	0.65324665	-7.3852019	1.52E-13	1.34E-11	91.9146765	188.744061	66.8043403	5.34051031	6.66359713	0
AT2G04100	21.83214466	-1.238968504	0.48303523	-2.5649651	0.01031862	0.04211315	31.3345488	26.3835784	34.4143571	16.0215309	12.3752518	10.4636009
AT2G04530	651.0872769	-2.245088559	0.16770338	-13.387259	7.18E-41	1.71E-37	1077.90848	1043.1661	1105.30818	255.45441	201.811799	222.874699
AT2G04570	480.7063118	1.525771701	0.39809347	3.83269718	0.00012675	0.00127221	146.227894	344.001272	253.046744	346.243085	926.240001	868.478875
AT2G04790	592.3733066	-1.013535671	0.2352998	-4.3074225	1.65E-05	0.0002286	1024.63975	668.722236	683.226208	349.803425	367.449784	460.39844
AT2G05185	54.38928379	-1.092318221	0.32394206	-3.3719555	0.00074637	0.00541933	77.2918871	83.2097471	61.7434055	37.3835722	34.2699281	32.4371628
AT2G05440	66.46378476	2.409465587	0.58252818	4.13622151	3.53E-05	0.00043802	11.4893346	17.2508012	34.4143571	91.6787604	198.955971	44.9934839
AT2G05540	1439.763699	-2.428474237	0.33017671	-7.3550742	1.91E-13	1.66E-11	3293.26108	1846.85048	2145.83639	680.02498	371.257554	301.351706
AT2G05914	54.19033497	-2.872280797	0.51024921	-5.6291725	1.81E-08	5.93E-07	77.2918871	138.00641	70.8530882	19.5818711	4.75971223	14.6490413
AT2G06950	1216.698375	-2.386914082	0.25136439	-9.4958321	2.18E-21	7.70E-19	1657.59763	2039.65356	2431.27311	319.540534	523.568346	328.557068
AT2G07674	15.56758106	-1.985072682	0.62270131	-3.1878409	0.00143339	0.00916853	26.112124	26.3835784	22.2681134	9.79093557	5.71165468	3.13908027
AT2G07677	26.96072174	-1.854569882	0.69385066	-2.6728661	0.00752063	0.03310781	45.9573382	29.4278374	51.6215357	25.8124665	4.75971223	4.18544036
AT2G07698	72.23904452	-1.033584056	0.39361456	-2.6258786	0.00864256	0.03677921	121.160255	79.1507351	91.0968277	69.4266341	27.606331	44.9934839
AT2G07739	45.83502223	-2.039847662	0.42544477	-4.7946239	1.63E-06	3.12E-05	89.8257066	61.8999338	69.8409013	26.7025516	15.2310791	11.509961
AT2G07774	58.3532647	-1.77823733	0.40707624	-4.3683152	1.25E-05	0.0001797	125.338195	63.9294399	81.987145	34.713317	19.0388489	25.1126422
AT2G07779	12.16243558	-2.411708591	0.71014444	-3.3960818	0.00068358	0.00505015	19.8452142	17.2508012	24.2924874	4.45042526	1.90388489	5.23180045
AT2G07787	13.95543405	-1.855622278	0.61656935	-3.0095922	0.00261599	0.01458256	27.156609	19.2803073	19.2315525	7.12068042	5.71165468	5.23180045
AT2G07811	338.3236775	-1.366184032	0.34474198	-3.9629176	7.40E-05	0.00081684	637.135826	362.266826	463.581635	284.827217	119.944748	162.185814
AT2G12400	357.579957	1.348044858	0.2090566	6.44822909	1.13E-10	6.05E-09	215.163902	164.389988	225.717695	583.005709	476.923166	480.279282
AT2G12460	43.12077403	1.142505528	0.43292138	2.63906005	0.00831363	0.03571481	16.7117594	38.5606145	25.3046744	45.3943377	75.2034533	57.549805
AT2G12462	108.4150651	1.822220673	0.35226693	5.17284058	2.31E-07	5.70E-06	49.0907931	50.7376507	43.5240399	105.920121	237.985612	163.232174
AT2G13610	305.0879681	1.676525667	0.33831196	4.95556138	7.21E-07	1.55E-05	107.581951	196.862085	131.584307	279.486706	605.435396	509.577364

Table S-5.1 Differentially Expressed Genes between lpa66 (LP) and wild type (WT) Arabidopsis plants.

ID	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	WT4	WT2	WT1	LP3	LP2	LP1
AT2G13820	239.3740355	1.37775946	0.33385469	4.12682374	3.68E-05	0.00045365	123.249225	153.227705	122.474624	189.588116	462.644029	385.060513
AT2G14060	28.69325775	-3.038741267	0.63109066	-4.815063	1.47E-06	2.85E-05	73.1139472	43.6343796	36.4387311	3.56034021	2.85582734	12.5563211
AT2G14880	2113.639585	-1.093340473	0.2502229	-4.3694661	1.25E-05	0.00017889	3149.12215	2958.00503	2527.43088	906.996668	1749.67022	1390.61256
AT2G14890	1710.630128	1.218969773	0.2526822	4.82412202	1.41E-06	2.74E-05	842.899363	1274.52979	966.638561	1754.35764	3049.07166	2376.28377
AT2G15000	419.3410392	-1.564190252	0.21096454	-7.4144699	1.22E-13	1.11E-11	763.518506	600.733784	516.215357	221.631178	215.138993	198.808417
AT2G15220	43.23975209	1.943050248	0.61517802	3.15851702	0.00158574	0.00988436	27.156609	20.2950603	6.07312185	53.4051031	34.2699281	118.23869
AT2G15390	619.9859379	1.133497747	0.43581528	2.60086739	0.00929884	0.03889367	451.217503	382.561886	330.985141	1303.9746	277.015252	974.161244
AT2G15620	10110.10983	-2.227942142	0.23924819	-9.3122633	1.25E-20	4.04E-18	15320.5054	19850.5985	14818.4173	4006.27282	2473.14648	4191.71852
AT2G15690	623.5001195	-1.323849731	0.1968759	-6.7242853	1.76E-11	1.10E-09	803.208934	946.764562	923.114521	307.079343	431.229928	329.603429
AT2G15800	18.60959309	4.388979047	0.93765826	4.68078749	2.86E-06	5.12E-05	0	3.04425904	2.02437395	60.5257835	31.4141007	14.6490413
AT2G15810	20.94794656	7.8009568	1.37075017	5.69101284	1.26E-08	4.28E-07	0	0	0	77.4373995	30.4621583	17.7881215
AT2G15830	143.4902391	1.035103794	0.25624379	4.03952738	5.36E-05	0.00062686	81.4698269	104.51956	96.1577626	190.478201	157.070504	231.24558
AT2G15890	5551.443205	-1.378273309	0.38800082	-3.5522433	0.00038196	0.00314705	8887.52253	6599.9536	8568.16274	5434.85933	1529.77151	2288.38952
AT2G16060	44.83627068	1.239174283	0.49448345	2.50599749	0.01221065	0.04782483	29.2455789	37.5458615	13.1584307	45.3943377	49.5010072	94.1724082
AT2G16367	33.48451999	2.646474493	0.54516648	4.85443366	1.21E-06	2.39E-05	8.35587968	15.2212952	4.0487479	48.0645928	45.6932374	79.5233669
AT2G16630	220.0946361	1.127010703	0.39079646	2.88388157	0.00392806	0.02013331	99.2260712	193.817826	121.462437	153.094629	341.747338	411.219516
AT2G16650	292.8527154	-1.218984751	0.2587565	-4.7109338	2.47E-06	4.50E-05	313.345488	444.46182	471.67913	194.928626	200.859856	131.841371
AT2G16660	464.1713065	2.496093263	0.94241978	2.64860025	0.00808259	0.03498288	59.5356427	175.552271	184.218029	179.797181	1644.95655	540.968167
AT2G16720	48.65767865	1.166266339	0.36486199	3.1964589	0.00139126	0.00894038	31.3345488	28.4130844	30.3656092	88.1184202	56.1646044	57.549805
AT2G16850	187.2225424	1.081327434	0.28067645	3.8525763	0.00011688	0.00119014	120.11577	125.829374	114.377128	169.11616	310.333238	283.563585
AT2G16890	110.3986694	1.669558509	0.38466898	4.34024731	1.42E-05	0.00020034	38.6459435	60.8851808	58.7068445	90.7886753	199.907914	213.457458
AT2G17280	253.9123171	-1.363882968	0.28290797	-4.8209422	1.43E-06	2.77E-05	371.836646	260.791525	464.593821	123.721822	178.013238	124.516851
AT2G17670	421.7264772	-1.824715236	0.18541483	-9.8412586	7.48E-23	3.16E-20	705.027348	613.925573	654.884973	196.708797	201.811799	158.000374
AT2G18010	10.33490219	2.022729602	0.76791034	2.63407002	0.00843681	0.03610544	4.17793984	4.05901205	4.0487479	21.3620413	19.9907914	8.37088072
AT2G18120	107.692111	-1.604250953	0.35318446	-4.5422467	5.57E-06	9.08E-05	238.142571	133.947398	114.377128	60.5257835	55.2126619	43.9471238
AT2G18193	44.17807769	-2.066555323	0.6180852	-3.3434797	0.00082735	0.00591288	73.1139472	116.696597	24.2924874	26.7025516	8.56748202	15.6954014
AT2G18220	498.5217928	-1.079945688	0.25994556	-4.1545072	3.26E-05	0.00040923	628.779946	773.241796	628.568111	250.1139	443.60518	266.821823
AT2G18328	1051.796587	1.227781535	0.25242215	4.86400075	1.15E-06	2.30E-05	700.849408	420.107748	767.237727	1251.45958	1523.10791	1648.01714
AT2G18330	562.1466526	-1.551530706	0.2116972	-7.3290092	2.32E-13	1.99E-11	769.785416	853.407284	891.736725	242.993219	361.73813	253.219142
AT2G18480	41.58150224	-2.454809145	0.7965418	-3.0818334	0.0020573	0.01215537	82.5143119	79.1507351	49.5971618	32.0430619	0.95194245	5.23180045
AT2G18700	11024.07929	-1.14582072	0.30815203	-3.7183618	0.00020052	0.0018453	15516.8686	16017.8763	14021.8262	10361.4801	3931.52231	6294.9023
AT2G18900	427.1831804	-1.453139113	0.29754672	-4.8837342	1.04E-06	2.11E-05	488.818961	784.40408	604.275624	184.247606	325.564317	175.788495
AT2G18969	17.37644585	3.560612399	0.77790705	4.57716945	4.71E-06	7.89E-05	0	2.02950603	6.07312185	33.823232	36.173813	26.1590023
AT2G19190	9.81688708	2.846491644	0.85334442	3.33568905	0.00085088	0.00603876	4.17793984	2.02950603	1.01218697	20.4719562	12.3752518	18.8344816
AT2G19385	374.0278828	-1.742084832	0.21096155	-8.2578311	1.48E-16	2.24E-14	606.845762	572.3207	548.60534	149.534289	215.138993	151.722213
AT2G19480	6782.576894	-1.045395902	0.15472618	-6.7564256	1.41E-11	9.03E-10	9773.24577	8584.8105	9055.02468	3888.78159	4932.96576	4460.63307
AT2G19540	2728.098379	-1.132589283	0.15685467	-7.2206282	5.17E-13	4.21E-11	3621.22936	3657.16986	3963.72419	1948.39618	1653.52403	1524.54665
AT2G19670	279.3790131	-1.615896594	0.25835821	-6.2544813	3.99E-10	1.95E-08	410.482589	418.078242	435.240399	101.469696	187.532662	123.470491
AT2G19730	7733.622	-1.127397318	0.22717797	-4.9626173	6.95E-07	1.50E-05	11842.3705	10742.1754	9246.32802	3478.45238	5950.59223	5141.81348
AT2G19870	1115.840501	-1.131716786	0.25633118	-4.4150571	1.01E-05	0.00014991	1491.52452	1591.13273	1514.23171	482.426098	969.077411	646.650536
AT2G19930	16.46234685	1.516405958	0.56666091	2.67603772	0.00744983	0.03286454	7.31139472	9.13277712	9.10968277	18.6917861	30.4621583	24.0662821
AT2G20020	1662.825094	-1.239280687	0.15081301	-8.2173325	2.08E-16	3.07E-14	2182.97357	2519.63173	2305.76193	939.929815	1089.02216	939.631361
AT2G20060	968.7060838	-1.291716248	0.16899448	-7.6435409	2.11E-14	2.27E-12	1548.9712	1213.6446	1364.42804	581.225539	590.204317	513.762804
AT2G20390	541.6713937	-1.352285153	0.18209706	-7.4261778	1.12E-13	1.02E-11	899.301551	675.825507	760.152418	304.409088	292.246331	318.093468
AT2G20450	2406.658478	-1.138410937	0.26936328	-4.2263034	2.38E-05	0.00031266	3496.93565	3487.70611	2944.45191	942.60007	2023.82964	1544.42749
AT2G20490	895.336293	-1.567838624	0.17701501	-8.8570941	8.21E-19	1.82E-16	1537.48186	1201.46757	1278.39215	449.492951	495.010072	410.173155
AT2G20530	1409.209496	-1.357944162	0.14806247	-9.1714271	4.67E-20	1.33E-17	2240.42024	1846.85048	1995.02053	785.055016	785.352519	802.558189
AT2G20570	4756.100853	1.706355998	0.2038462	8.37080108	5.72E-17	8.78E-15	1874.8505	2641.40209	2177.21418	8677.43917	6178.10648	6987.59268
AT2G20585	284.1817761	-1.270741337	0.22797222	-5.574106	2.49E-08	7.81E-07	382.281495	374.443862	448.39883	128.172248	197.052086	174.742135
AT2G20880	65.48610997	-1.684393018	0.44189898	-3.8117151	0.00013801	0.00136121	52.224248	158.30147	89.0724538	29.3728067	30.4621583	33.4835229
AT2G20940	182.140135	-1.400694919	0.25072891	-5.5864915	2.32E-08	7.35E-07	303.945123	266.880043	221.668948	80.9977397	119.944748	99.4042086
AT2G21050	348.2615948	2.095710592	0.35073476	5.97520071	2.30E-09	9.04E-08	126.38268	199.906344	69.8409013	439.702016	652.080576	601.657052
AT2G21140	499.6257376	1.51203824	0.42825915	3.53066186	0.00041452	0.00337559	152.494804	392.709416	232.803004	327.551299	892.922015	999.273886
AT2G21350	43.96903537	-1.456443132	0.35975313	-4.0484516	5.16E-05	0.00060642	67.8915224	61.8999338	63.7677794	25.8124665	26.6543885	17.7881215
AT2G21430	45.53063014	-1.621428508	0.39788399	-4.0751288	4.60E-05	0.0005498	85.6477667	56.8261688	63.7677794	18.6917861	30.4621583	17.7881215
AT2G22240	1920.246347	1.074148946	0.25174904	4.26674492	1.98E-05	0.00026868	1118.64339	935.602279	1655.93789	3150.90108	2437.92461	2222.46883
AT2G22360	2852.691691	-1.203413049	0.20639646	-5.8305897	5.52E-09	2.03E-07	4392.05926	3912.88762	3628.69031	1344.02843	2126.63943	1711.84511
AT2G22390	49.26052358	1.047374796	0.33230858	3.15181393	0.0016226	0.01004895	36.5569736	31.4573434	28.3412353	64.0861238	61.876259	73.2452063
AT2G22410	50.67737038	-1.227392976	0.36539454	-3.3590895	0.000782	0.00564496	67.8915224	76.106476	68.8287143	19.5818711	37.1257554	34.529883
AT2G22620	22.79373509	1.848451024	0.52610618	3.51345621	0.00044232	0.00355329	10.4448496	13.1917892	6.07312185	27.5926366	42.8374101	36.6226032
AT2G22760	25.29531318	3.275988442	0.94171198	3.47875837	0.00050374	0.00392095	0	2.02950603	12.1462437	88.1184202	18.0869065	31.3908027
AT2G22810	25.284363	1.855347116	0.51120991	3.62932544	0.00028416	0.00246261	15.6672744	10.1475301	7.08530882	33.823232	50.4529497	34.529883
AT2G22830	249.6309331	1.094467822	0.19633313	5.57454465	2.48E-08	7.81E-07	145.183409	184.685048	147.779298	335.562065	345.555108	339.020669
AT2G22860	87.71941141	-1.252816627	0.49470481	-2.5324529	0.01132676	0.04510557	72.0694622	69.0032049	229.766443	67.646464	42.8374101	44.9934839
AT2G22870	605.9495592	-1.736112764	0.20641019	-8.4109839	4.07E-17	6.56E-15	977.637923	912.262959	906.91953	279.486706	341.747338	217.642899
AT2G23170	26.86565148	4.423326225	0.73110344	6.05020574	1.45E-09	6.01E-08	3.13345488	1.01475301	3.03656092	31.1529768	69.4917986	53.3643646
AT2G23300	66.29008488	2.314881518	0.36237238	6.38812897	1.68E-10	8.55E-09	19.8452142	27.3983314	19.2315525	80.9977397	124.704461	125.563211
AT2G23470	261.6180328	-1.274775413	0.18972482	-6.7190755	1.83E-11	1.13E-09	370.792161	404.886452	335.033889	149.534289	160.878274	148.583133
AT2G23550	12.82472981	2.133575523	0.68530313	3.11333108	0.00184988	0.01117623	3.13345488	6.08851808	5.06093487	21.3620413	26.6543885	14.6490413
AT2G23950	406.1294304	1.152522936	0.23908095	4.82063898	1.43E-06	2.78E-05	198.452142	335.883248	221.668948	562.533753	594.012087	524.226405
AT2G24110	23.79469347	-1.550987009	0.49924053	-3.1066929	0.00189193	0.01139408	35.5124886	46.6786386	24.2924874	13.3512758	11.4233094	11.509961
AT2G24120	1020.039535	-2.146875205	0.36085878	-5.94935	2.69E-09	1.05E-07	1121.77685	2146.20262	1724.76661	222.521263	592.108202	312.861667
AT2G24170	208.3608853	1.225896475	0.33737526	3.63362879	0.00027946	0.0024252	111.759891	159.316223	103.243071	182.467436	415.046907	278.331784
AT2G24210	29.15283305	2.927575199	0.83661952	3.49929106	0.0004665	0.00370067	0	3.04425904	17.2071786	33.823232	47.5971223	73.2452063
AT2G24300	62.62171054	1.223755114	0.308405	3.96801324	7.25E-05	0.0008005	40.7349134	41.6048736	30.3656092	88.1184202	93.2903598	81.6160871
AT2G24440	82.08012497	1.044901691	0.33320917	3.13587315	0.00171343	0.01050649	53.268733	55.8114157	51.6215357	76.5473145	148.503022	106.728729
AT2G24610	44.42065001	1.522391439	0.47106701	3.23179377	0.00123016	0.00810635	27.156609	20.2950603	21.2559265	45.3943377	45.6932374	106.728729
AT2G24692	18.05346621	2.098761615	0.64944642	3.23161628	0.00123092	0.00810858	6.26690976	8.11802411	6.07312185	13.3512758	39.9815828	34.529883
AT2G24762	504.5858159	1.716390699	0.36012979	4.76603371	1.88E-06	3.54E-05	338.413127	263.835784	104.255258	818.878248	816.766619	685.365859
AT2G25060	93.84898119	1.311710683	0.45785209	2.86492233	0.00417112	0.0210782	48.0463082	67.9884519	45.5484139	53.4051031	193.244317	154.861293
AT2G25090	21.17552924	-2.629408492	0.732825	-3.5880442	0.00033317	0.0028043	39.6904285	31.4573434	38.463105	13.3512758	0.95194245	3.13908027

Table S-5.1 Differentially Expressed Genes between lpa66 (LP) and wild type (WT) Arabidopsis plants.

ID	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	WT4	WT2	WT1	LP3	LP2	LP1
AT2G25355	186.2806293	-1.332237901	0.20987113	-6.3478856	2.18E-10	1.09E-08	254.85433	271.953808	273.290483	101.469696	120.896691	95.2187682
AT2G25460	172.8782013	1.15395626	0.41474625	2.78231875	0.0053972	0.02567853	78.336372	69.0032049	174.09616	214.510498	157.070504	344.25247
AT2G26360	54.39118147	1.089594666	0.34180543	3.18776287	0.00143378	0.00916853	29.2455789	44.6491326	30.3656092	64.9762088	82.8189929	74.2915664
AT2G26750	48.78645919	2.75065828	0.41789925	6.58210874	4.64E-11	2.63E-09	9.40036464	15.2212952	13.1584307	63.1960387	92.3384173	99.4042086
AT2G26790	40.93250849	-1.346375311	0.46080793	-2.9217712	0.00348047	0.01828592	36.5569736	55.8114157	84.0115189	31.1529768	17.134964	20.9272018
AT2G26980	1135.890841	-1.49628377	0.19150131	-7.813439	5.56E-15	6.54E-13	1848.73838	1746.38994	1437.3055	696.936596	571.165468	514.809165
AT2G27530	10709.29526	-1.085988647	0.24638175	-4.4077479	1.04E-05	0.000154	15751.8777	14888.4562	13038.9926	4632.00261	8988.24058	6956.20188
AT2G27610	19.31062394	-1.442861841	0.56102683	-2.5718232	0.01011645	0.04149272	26.112124	21.3098133	37.4509181	14.2413608	10.4713669	6.27816054
AT2G27660	76.10591266	1.825902929	0.40886573	4.46577641	7.98E-06	0.00012254	34.4680037	40.5901205	25.3046744	104.139951	74.2515108	177.881215
AT2G27710	9253.507916	-1.252173115	0.25565029	-4.8979922	9.68E-07	1.98E-05	14451.4939	13115.6827	11536.9071	3589.71302	7206.20432	5621.04641
AT2G27775	269.7975739	-1.738626142	0.22250786	-7.8137739	5.55E-15	6.54E-13	476.285142	399.812687	369.448246	108.590376	148.503022	116.14597
AT2G28000	20584.01667	-1.385382338	0.31826533	-4.3529163	1.34E-05	0.00019054	25978.4299	34803.9989	28532.5386	6068.59989	16398.1606	11722.3721
AT2G28120	362.3583235	-1.168407346	0.33633544	-3.4739346	0.00051289	0.0039791	526.42042	316.60294	661.970282	312.419853	158.974389	197.762057
AT2G28410	272.7212511	1.081492912	0.31240397	3.46184111	0.00053649	0.00413361	163.984139	237.452205	123.486811	255.45441	421.710504	434.239438
AT2G28460	33.24256107	1.274758653	0.41248156	3.09046216	0.00199845	0.01190005	17.7562443	24.3540723	16.1949916	40.9439124	55.2126619	44.9934839
AT2G28500	26.05299418	1.916033714	0.62074221	3.08668184	0.00202404	0.01201108	7.31139472	19.2803073	6.07312185	21.3620413	44.741295	57.549805
AT2G28790	93.1372111	1.566495916	0.35099115	4.46306383	8.08E-06	0.0001239	33.4235187	66.9736989	40.487479	105.920121	145.647194	166.371254
AT2G28950	3929.201683	1.074948569	0.23768526	4.52257143	6.11E-06	9.79E-05	2727.15023	2698.22826	2163.04357	3657.35948	6254.26188	6075.16669
AT2G29110	78.90839599	1.218216476	0.37438398	3.25392253	0.00113823	0.00760861	45.9573382	63.9294399	32.3899832	121.941652	74.2515108	134.980452
AT2G29130	34.33662691	2.697048571	0.53966984	4.99758995	5.81E-07	1.28E-05	3.13345488	11.1622831	13.1584307	46.2844227	79.9631655	52.3180045
AT2G29200	382.8687594	-1.058394092	0.27302719	-3.8765154	0.00010596	0.00109657	414.660529	625.087856	512.166609	190.478201	335.083741	219.735619
AT2G29260	47.5146529	-1.504850174	0.43688716	-3.4444825	0.00057215	0.00436419	81.4698269	51.7524037	77.9383971	37.3835722	21.8946763	14.6490413
AT2G29300	2271.834831	-1.01675265	0.18875747	-5.3865559	7.18E-08	2.00E-06	3358.01915	3170.08841	2594.23522	1605.71343	1241.33295	1661.61982
AT2G29490	185.3140589	-1.27986242	0.36671845	-3.490041	0.00048295	0.00379635	223.519781	200.921097	363.375124	160.215309	67.5879137	96.2651283
AT2G29540	210.3420649	-1.517262234	0.23679894	-6.4073861	1.48E-10	7.61E-09	380.192525	274.998067	280.375792	110.370546	120.896691	95.2187682
AT2G29680	273.4166807	-1.410951904	0.22923168	-6.1551348	7.50E-10	3.43E-08	310.212033	478.963422	402.850416	140.633438	156.118561	151.722213
AT2G29750	16.40801117	2.10377434	0.75972471	2.76912719	0.00562067	0.02644424	11.4893346	2.02950603	5.06093487	18.6917861	16.1830216	44.9934839
AT2G29760	200.8380852	-1.437860676	0.23288985	-6.1739946	6.66E-10	3.08E-08	264.254695	257.747265	358.314189	113.930887	111.377266	99.4042086
AT2G29890	134.6216131	1.008518853	0.277896	3.62912332	0.00028439	0.00246342	84.6032818	107.563819	75.9140231	140.633438	217.99482	181.020296
AT2G30540	61.26917015	1.324714236	0.44784216	2.95799362	0.00309649	0.01665296	14.6227894	36.5311085	53.6459097	77.4373995	103.761727	81.6160871
AT2G30600	4827.419334	-1.113682025	0.3173069	-3.5097945	0.00044845	0.00358744	4952.94768	5833.81508	9023.64688	4461.99637	2107.60058	2584.50942
AT2G30770	143.9730256	1.553124226	0.47764248	3.25164593	0.00114739	0.00766443	19.8452142	86.2540062	113.364941	227.861773	210.379281	206.132938
AT2G30900	29.82320159	-2.025425335	0.70013816	-2.8928938	0.0038171	0.01967054	54.3132179	46.6786386	42.5118529	0.89008505	20.9427338	13.6026812
AT2G31010	220.1668762	1.299363257	0.40792704	3.18528344	0.00144612	0.009226	53.268733	146.124434	182.193655	280.376791	413.143022	245.894621
AT2G31060	1135.742669	-1.389532137	0.17401539	-7.9851107	1.40E-15	1.79E-13	1463.32343	1768.7145	1700.47412	670.234044	674.927195	536.782726
AT2G31141	49.30517295	1.43730001	0.49489436	2.90425622	0.00368127	0.01910505	28.2010939	33.4868494	18.2193655	121.051567	45.6932374	49.1789243
AT2G31160	41.49062531	-1.062431255	0.40250451	-2.6395512	0.00830159	0.0356792	71.0249773	60.8851808	36.4387311	27.5926366	24.7505036	28.2517224
AT2G31170	1362.374272	-1.010985435	0.2424834	-4.1692976	3.06E-05	0.00038817	1650.28624	1885.4111	1927.204	614.158686	1147.09065	950.094962
AT2G31240	363.2341271	-1.036129344	0.19584704	-5.2905029	1.22E-07	3.24E-06	502.397266	496.214224	466.618195	223.411348	284.630792	206.132938
AT2G31340	274.1224004	-1.004384316	0.22196343	-4.5249991	6.04E-06	9.69E-05	351.991432	387.635651	358.314189	180.687266	222.754533	143.351332
AT2G31830	51.88956471	-1.082291219	0.41106188	-2.6329156	0.00846554	0.03619584	55.3577029	76.106476	79.962771	22.2521263	50.4529497	27.2053624
AT2G31840	1719.419789	-1.705915065	0.15721105	-10.851114	1.97E-27	1.44E-24	2790.86381	2288.26805	2816.91635	818.878248	763.457842	838.134433
AT2G31890	1150.555243	-1.524058228	0.15473925	-9.8492026	6.91E-23	3.06E-20	1593.88405	1608.38353	1920.11869	599.917325	604.483454	576.54441
AT2G31945	70.02702852	-2.435137173	0.47452801	-5.1317038	2.87E-07	6.89E-06	174.428988	61.8999338	118.425876	31.1529768	13.3271943	20.9272018
AT2G32179	38.56292715	-1.486454042	0.46090235	-3.2250954	0.00125931	0.00825848	48.0463082	51.7524037	70.8530882	17.801701	31.4141007	11.509961
AT2G32180	339.6166747	-1.967910052	0.295324	-6.6635629	2.67E-11	1.59E-09	559.843939	437.358549	625.53155	94.3490155	196.100144	124.516851
AT2G32220	260.004459	-1.035691414	0.25996137	-3.9840205	6.78E-05	0.00075765	396.904285	360.23732	291.509849	142.413608	225.61036	143.351332
AT2G32530	1252.729037	-2.578400913	0.3650943	-7.0622875	1.64E-12	1.22E-10	2249.8206	1901.64715	2287.54256	614.158686	193.244317	269.960903
AT2G32650	516.0557926	-1.557941233	0.20387942	-7.6414835	2.15E-14	2.30E-12	831.410028	672.781248	806.713019	210.950157	295.102158	279.378144
AT2G32680	257.3308877	2.015386224	0.51093782	3.9444843	8.00E-05	0.00086919	108.626436	112.637585	85.0237059	833.119609	151.358849	253.219142
AT2G32880	1102.392028	-1.055167868	0.2574593	-4.098387	4.16E-05	0.00050689	1469.59034	1335.41497	1659.98664	724.529232	477.875108	946.955882
AT2G32930	285.1031515	1.452728018	0.26329585	5.51747408	3.44E-08	1.04E-06	113.848861	185.699801	157.901168	323.100874	444.557123	485.511082
AT2G32990	583.4459113	1.247654532	0.33615062	3.71159377	0.00020596	0.0018808	313.345488	484.037188	239.888313	516.24933	1119.48432	827.670832
AT2G33210	1452.605281	-1.266640442	0.17105669	-7.404799	1.31E-13	1.18E-11	1919.76336	2272.032	1964.65492	743.221018	965.269641	850.690754
AT2G33385	19.62889388	1.437719359	0.51144563	2.81108933	0.00493741	0.02397036	9.40036464	12.1770362	10.1218697	24.0322964	28.5582734	33.4835229
AT2G33430	3399.855375	-1.078367732	0.22523884	-4.7876634	1.69E-06	3.23E-05	4472.4846	4707.43923	4663.14539	1566.54969	2812.03799	2177.47535
AT2G33750	31.85766621	1.222605997	0.41980358	2.91232863	0.00358745	0.01874081	20.8896992	21.3098133	15.1828046	41.8339974	54.2607195	37.6689633
AT2G33760	11.01246929	-2.313690365	0.9031918	-2.5616822	0.01041666	0.04239509	16.7117594	13.1917892	25.3046744	8.01076547	2.85582734	0
AT2G33847	56.87634453	-1.310754472	0.35944797	-3.6465764	0.00026576	0.00232856	99.2260712	88.2835122	55.6702836	29.3728067	35.2218705	33.4835229
AT2G34080	30.07555068	-2.260660997	0.81459579	-2.7751936	0.00551689	0.02609265	19.8452142	51.7524037	77.9383971	24.9223815	2.85582734	3.13908027
AT2G34150	144.7308627	1.532426764	0.40545659	3.77950888	0.00015714	0.00151341	66.8470374	105.534313	50.6093487	115.711057	303.669641	226.01378
AT2G34170	579.9087635	1.278795187	0.25838879	4.94911255	7.46E-07	1.59E-05	334.235187	416.048736	265.192987	656.882768	1065.2236	741.869304
AT2G34180	48.61208391	1.971987568	0.47273853	4.17141287	3.03E-05	0.00038537	12.5338195	24.3540723	22.2681134	43.6141676	110.425324	78.4770068
AT2G34260	308.3983893	-1.510640197	0.22835278	-6.615379	3.71E-11	2.16E-09	531.642845	435.329043	402.850416	143.303693	197.052086	140.212252
AT2G34360	62.10380664	-1.918721238	0.4093971	-4.6866996	2.78E-06	5.00E-05	67.8915224	85.2392531	141.706176	33.823232	20.9427338	23.019922
AT2G34400	53.22760364	-1.312881481	0.38477489	-3.4120769	0.0006447	0.00481904	68.9360074	64.9441929	94.1333887	42.7240825	26.6543885	21.9735619
AT2G34640	1195.188631	-1.249150575	0.20707479	-6.0323643	1.62E-09	6.58E-08	1447.65615	1730.15389	1869.50934	568.764348	852.940432	702.107621
AT2G34650	92.66060679	1.073100996	0.37352755	2.8728831	0.00406745	0.02070828	54.3132179	85.2392531	39.475292	88.1184202	158.022446	130.795011
AT2G34680	1338.739704	1.201473093	0.23184369	5.18225496	2.19E-07	5.46E-06	598.489882	1004.60548	831.005506	1640.42675	2188.51569	1769.39491
AT2G34850	25.39150206	2.311385917	0.70068688	3.29874296	0.00097119	0.00670634	5.2224248	12.1770362	8.0974958	12.4611907	70.4437411	43.9471238
AT2G35035	37.40599623	1.218684651	0.39984393	3.04790081	0.00230446	0.01325761	15.6672744	27.3983314	24.2924874	44.5042526	57.1165468	55.4570848
AT2G35150	20.22246285	3.018596149	0.60923271	4.95475063	7.24E-07	1.55E-05	5.2224248	4.05901205	4.0487479	27.5926366	43.7893526	36.6226032
AT2G35190	445.9324758	1.002793285	0.28768259	3.48576286	0.00049074	0.0038354	268.432635	290.219362	331.997328	415.669719	858.652087	510.623724
AT2G35240	875.2644627	-1.388496631	0.17188125	-8.0782321	6.57E-16	8.96E-14	1323.36244	1206.54133	1270.29465	442.372271	566.405756	442.610318
AT2G35290	59.0128192	1.086632327	0.38127041	2.85003056	0.0043715	0.02181853	26.112124	32.4720964	54.6580966	64.9762088	94.2423022	81.6160871
AT2G35340	250.5760748	1.287480078	0.17994773	7.1547446	8.38E-13	6.68E-11	139.960985	146.124434	150.815859	355.143936	359.834245	351.57699
AT2G35637	12.28184036	3.213928535	0.94152165	3.41354715	0.00064123	0.00480633	1.04448496	5.07376507	1.01218697	8.90085052	19.9907914	37.6689633
AT2G35790	965.8304638	-1.345539531	0.15084464	-8.9200354	4.66E-19	1.08E-16	1494.65798	1303.95762	1360.37929	566.094093	564.501871	505.391924
AT2G35880	1285.945396	1.245243539	0.22512375	5.5313734	3.18E-08	9.66E-07	612.068187	680.899272	995.991983	1627.96556	2031.44518	1767.30219
AT2G36026	38.05851481	1.686078542	0.52395155	3.21800468	0.00129086	0.00840161	11.4893346	26.3835784	16.1949916	31.1529768	86.6267627	56.5034449
AT2G36080	248.5520332	-1.389048142	0.41443316	-3.351682	0.00080322	0.00576617	259.03227	218.171898	602.25125	196.708797	99.0020145	116.14597

Table S-5.1 Differentially Expressed Genes between lpa66 (LP) and wild type (WT) Arabidopsis plants.

ID	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	WT4	WT2	WT1	LP3	LP2	LP1
AT2G36170	2983.553357	-1.012600829	0.26826891	-3.7745739	0.00016028	0.00153718	4465.1732	4019.43669	3483.94757	1238.10831	2588.33151	2106.32286
AT2G36490	1296.223258	1.254196042	0.19026675	6.59177736	4.35E-11	2.48E-09	766.651961	905.159688	625.53155	1691.1616	2004.79079	1784.04395
AT2G36570	415.7476258	1.680835168	0.38171281	4.40340261	1.07E-05	0.00015673	169.206564	265.86529	157.901168	322.210789	977.644893	601.657052
AT2G36750	44.88248217	-3.556811916	0.46990499	-7.569215	3.75E-14	3.72E-12	65.8025525	75.091723	107.291819	7.12068042	6.66359713	7.32452063
AT2G36800	1122.099405	-1.245771012	0.24036891	-5.1827459	2.19E-07	5.45E-06	1971.9876	1329.32645	1434.26894	735.210253	496.913957	764.889226
AT2G36885	1732.491586	-1.335748232	0.34114238	-3.9155153	9.02E-05	0.00096332	2940.22516	2084.30269	2420.13906	475.305418	1093.78187	1381.19532
AT2G37020	813.7825319	-1.397140594	0.15181468	-9.2029345	3.48E-20	1.02E-17	1254.42644	1096.94801	1187.29532	430.801165	435.037698	478.186561
AT2G37030	13.93563574	2.148510078	0.7119419	3.01781659	0.00254603	0.01429306	5.2224248	6.08851808	4.0487479	10.6810206	31.4141007	26.1590023
AT2G37060	117.157371	-1.448293017	0.26026893	-5.5646021	2.63E-08	8.16E-07	177.562443	160.330976	176.120534	48.9546779	65.6840288	74.2915664
AT2G37190	5360.958098	-1.243734818	0.24160788	-5.1477411	2.64E-07	6.41E-06	8300.52198	7425.96255	6888.94455	2243.01433	4235.19195	3072.11323
AT2G37230	689.8911237	-1.107632982	0.20930375	-5.2919882	1.21E-07	3.22E-06	873.189427	1011.70875	942.346074	362.264616	551.174677	398.663195
AT2G37310	56.35259153	-1.415137829	0.37163146	-3.8079065	0.00014015	0.00137673	98.1815863	74.07697	73.8896492	31.1529768	40.9335252	19.8808417
AT2G37380	62.81737207	1.362554758	0.38927735	3.50021584	0.00046488	0.00369073	38.6459435	43.6343796	23.2803004	71.2068042	123.752518	76.3842866
AT2G37400	522.1056014	-1.315936057	0.2115326	-6.2209611	4.94E-10	2.37E-08	772.918871	682.928778	779.383971	279.486706	374.113382	243.801901
AT2G37510	69.26078848	-1.557706695	0.34375554	-4.5314374	5.86E-06	9.48E-05	97.1371013	100.460548	112.352754	22.2521263	45.6932374	37.6689633
AT2G37600	1558.360695	-1.215777965	0.24811475	-4.9000633	9.58E-07	1.96E-05	2553.76573	2080.24368	1901.89933	672.014214	1230.86158	911.379639
AT2G37690	855.7852207	-2.714797134	0.18945575	-14.329453	1.43E-46	5.45E-43	1426.76646	1434.86076	1595.20667	270.585856	218.946763	188.344816
AT2G37760	1198.799518	-2.61861158	0.42942824	-6.0979026	1.07E-09	4.65E-08	2232.06436	1395.28539	2558.80867	615.938856	164.686043	226.01378
AT2G37770	287.9195653	-3.28908388	0.80861152	-4.0675699	4.75E-05	0.00056435	278.877484	380.53238	907.931716	101.469696	19.9907914	38.7153234
AT2G38010	528.1139904	1.019788274	0.24120379	4.22791157	2.36E-05	0.00031124	319.612398	409.960218	316.814523	518.919585	861.507914	741.869304
AT2G38080	175.166027	1.036327243	0.40216374	2.57687886	0.00996969	0.0410545	55.3577029	165.404741	123.486811	156.654969	245.601151	304.490786
AT2G38110	110.5448493	1.678204532	0.51534617	3.2564607	0.00112811	0.00755171	60.5801277	55.8114157	41.499666	56.0753583	301.765756	147.536773
AT2G38230	15756.9593	-1.07857056	0.21085154	-5.115308	3.13E-07	7.41E-06	26192.5493	17131.0604	20837.8933	11108.2615	8385.66101	10886.3304
AT2G38530	34.70436638	1.940013137	0.51848273	3.74171214	0.00018277	0.00171008	19.8452142	7.1032711	16.1949916	80.1076547	39.9815828	44.9934839
AT2G39120	51.10682178	-1.323259881	0.33970853	-3.8952801	9.81E-05	0.00102887	71.0249773	69.0032049	78.950584	23.1422114	35.2218705	29.2980825
AT2G39180	94.53998553	1.218542263	0.34451437	3.53698529	0.00040472	0.00330569	34.4680037	74.07697	61.7434055	114.820972	119.944748	162.185814
AT2G39230	18.13755852	-2.093225504	0.65917399	-3.1755281	0.00149564	0.00946261	26.112124	25.3688253	36.4387311	1.7801701	7.61553957	11.509961
AT2G39250	317.810353	1.448249908	0.29332433	4.93736718	7.92E-07	1.67E-05	111.759891	225.275169	174.09616	366.715041	470.259569	558.756288
AT2G39430	12.50571516	2.207791873	0.75165926	2.93722435	0.00331164	0.01756885	6.26690976	6.08851808	1.01218697	15.1314459	26.6543885	19.8808417
AT2G39460	9202.991573	-1.236522087	0.23363561	-5.292524	1.21E-07	3.22E-06	13317.1832	13189.7597	12258.5965	3781.0813	7058.65324	5612.67553
AT2G39620	14.843633	-2.920984005	0.70730406	-4.129743	3.63E-05	0.00044909	27.156609	22.3245663	29.3534223	6.23059536	1.90388489	2.09272018
AT2G39670	2690.024849	-1.351561713	0.2008724	-6.7284591	1.71E-11	1.07E-09	3678.67603	3900.71058	4016.35792	1183.81312	1881.03827	1479.55317
AT2G39690	73.32240062	2.1110824	0.60556288	3.48614893	0.00049003	0.0038321	16.7117594	44.6491326	21.2559265	32.0430619	191.340432	133.934092
AT2G39700	501.3454508	1.606517362	0.27736632	5.79204196	6.95E-09	2.50E-07	255.898815	292.248868	195.352086	502.007969	923.384173	839.180793
AT2G39795	305.2458637	-1.459948823	0.18533582	-7.8773159	3.34E-15	4.08E-13	487.774476	447.506079	407.911351	153.984714	174.205468	160.093094
AT2G40180	55.28196722	2.166760108	0.56305841	3.84819772	0.00011899	0.00120709	16.7117594	33.4868494	10.1218697	48.0645928	69.4917986	153.814933
AT2G40240	140.7526158	-1.403636799	0.23338448	-6.0142678	1.81E-09	7.24E-08	207.852507	190.773567	214.583639	89.8985903	72.347626	69.059766
AT2G40260	89.06539228	1.054794016	0.30647256	3.4417242	0.00057802	0.00440187	41.7793984	57.8409218	73.8896492	104.139951	133.271943	123.470491
AT2G40320	65.05268209	1.177014769	0.35856706	3.2825513	0.00102872	0.00701958	31.3345488	48.7081447	39.475292	62.3059536	102.809784	105.682369
AT2G40330	183.8065842	1.702829141	0.42863596	3.97266979	7.11E-05	0.00078729	126.38268	61.8999338	70.8530882	126.392077	363.642015	353.669711
AT2G40360	1516.50793	-1.318907074	0.22661084	-5.8201412	5.88E-09	2.16E-07	1882.1619	2332.91718	2280.45725	742.330933	1142.33094	718.849382
AT2G40475	542.0632853	1.677212269	0.27761728	6.04145497	1.53E-09	6.26E-08	209.941477	349.075037	215.595826	637.300897	1045.23281	795.233669
AT2G40530	98.85786612	1.146851465	0.2880411	3.98155494	6.85E-05	0.00076421	75.2029171	64.9441929	44.5362269	149.534289	132.32	126.609571
AT2G40610	1651.470101	2.549881496	0.79056713	3.22538265	0.00125804	0.00825828	912.879855	427.211019	105.267445	2614.1798	2868.20259	2981.0799
AT2G40700	283.2860145	-1.018232963	0.2704739	-3.7646256	0.0001668	0.00158717	293.500274	484.037188	360.338563	158.435139	237.033669	166.371254
AT2G40750	873.5363015	-3.195445155	0.89198734	-3.5823885	0.00034047	0.00285312	1563.59399	1967.60609	1194.38063	387.186998	44.741295	83.7088072
AT2G40820	223.762843	1.009906727	0.3011292	3.3537323	0.00079729	0.00574094	148.316864	160.330976	136.645242	181.577351	379.825036	335.881589
AT2G40850	60.75211997	1.201403092	0.38286653	3.13791619	0.00170154	0.01044241	27.156609	47.6933916	35.4265441	67.646464	70.4437411	116.14597
AT2G41070	54.26379924	-1.379021708	0.40562814	-3.399719	0.00067455	0.00499704	101.315041	75.091723	58.7068445	34.713317	18.0869065	37.6689633
AT2G41170	392.4897613	1.686224676	0.2496107	6.75541815	1.42E-11	9.07E-10	195.318688	234.407946	128.547746	534.941116	645.416979	616.306093
AT2G41540	752.3047324	1.176213713	0.25985078	4.52649677	6.00E-06	9.64E-05	344.680037	527.671567	512.166609	801.966632	1347.9505	979.393045
AT2G41640	1045.204058	-1.387081758	0.1723362	-8.0486967	8.37E-16	1.12E-13	1608.50684	1462.25909	1466.65893	635.520727	615.906763	482.372002
AT2G41670	153.3782859	-1.347566556	0.22203172	-6.0692525	1.29E-09	5.42E-08	209.941477	230.348934	220.656761	90.7886753	94.2423022	74.2915664
AT2G41820	501.1327763	1.949646793	0.31678024	6.15457193	7.53E-10	3.44E-08	165.028624	297.322633	155.876794	573.214774	1045.23281	770.121027
AT2G41905	291.4285557	-2.07861722	0.29297817	-7.0947854	1.30E-12	1.01E-10	636.091341	379.517627	397.789481	91.6787604	98.050072	145.444053
AT2G41990	88.11788915	1.594322434	0.54291155	2.93661541	0.00331815	0.01758501	60.5801277	40.5901205	30.3656092	43.6141676	233.225899	120.33141
AT2G42200	123.0094011	1.001417214	0.32469842	3.08414561	0.00204138	0.01208693	81.4698269	98.4310423	65.7921534	105.920121	197.052086	189.391176
AT2G42270	834.1234274	1.327403461	0.30628723	4.33385178	1.47E-05	0.00020549	263.21021	682.928778	479.776626	1190.04371	1203.25525	1185.52598
AT2G42360	64.31977098	1.132537154	0.29980967	3.7775204	0.0001584	0.00152323	40.7349134	40.5901205	39.475292	75.6572294	94.2423022	95.2187682
AT2G42380	329.4529433	2.184949366	0.28602717	7.63895733	2.19E-14	2.33E-12	118.0268	142.065422	96.1577626	359.594361	653.984461	606.888853
AT2G42540	3874.353355	1.265689554	0.37120637	3.40966547	0.00065043	0.00485041	1707.73291	2003.12245	3117.53588	9032.58311	4146.6613	3238.48448
AT2G42650	120.3897294	-1.747784802	0.26068763	-6.7045176	2.02E-11	1.23E-09	179.651413	183.670295	193.327712	48.0645928	69.4917986	48.1325642
AT2G42710	683.568535	-1.476107666	0.22465743	-6.5704822	5.02E-11	2.83E-09	1040.30702	1018.81203	957.528878	267.025516	458.836259	358.901511
AT2G42870	232.5575875	1.475505876	0.29369986	5.02385631	5.06E-07	1.13E-05	115.937831	113.652338	139.681803	469.074822	323.660432	233.3383
AT2G43290	1222.16988	1.183945517	0.22992058	5.14936741	2.61E-07	6.37E-06	817.831724	787.448339	635.65342	1230.98763	1835.34504	2025.75314
AT2G43620	28.34514295	2.065232224	0.52926231	3.90209576	9.54E-05	0.00100543	9.40036464	10.1475301	13.1584307	26.7025516	44.741295	65.9206857
AT2G43650	923.2753212	-1.212492924	0.24612801	-4.9262695	8.38E-07	1.75E-05	1306.65069	1392.24113	1171.10033	482.426098	763.457842	423.775837
AT2G43780	532.260124	-1.090089911	0.1981746	-5.5006539	3.78E-08	1.13E-06	807.386874	625.087856	739.908679	303.519003	317.948777	399.709555
AT2G43820	4151.877538	-1.942429111	0.34186158	-5.681917	1.33E-08	4.49E-07	6840.332	5072.75032	7855.58311	2790.41664	1108.06101	1244.12215
AT2G43920	1147.367991	-1.349401783	0.20962704	-6.437155	1.22E-10	6.38E-09	2002.27767	1493.71644	1447.42737	560.753583	613.050936	766.981946
AT2G44040	1499.090804	-1.17245597	0.21018454	-5.5782216	2.43E-08	7.67E-07	1983.47694	2103.583	2142.79983	679.134895	1106.15712	979.393045
AT2G44120	5310.5926	-1.256172306	0.26847156	-4.6789773	2.88E-06	5.16E-05	7713.52143	8036.84387	6709.78746	2000.9112	4319.91482	3082.57683
AT2G44300	101.5781765	1.081884901	0.37939553	2.85160159	0.00434996	0.02175093	61.6246126	80.1654881	53.6459097	77.4373995	193.244317	143.351332
AT2G44510	119.9295732	-1.46511391	0.26998144	-5.4267208	5.74E-08	1.65E-06	181.740383	180.626036	165.998664	56.0753583	82.8189929	52.3180045
AT2G44640	1430.214996	-1.086704449	0.26079433	-4.1669022	3.09E-05	0.00039096	1934.38615	1866.13079	2033.48363	594.576815	1241.33295	911.379639
AT2G44740	136.59783	1.341332976	0.32850874	4.08309682	4.44E-05	0.00053493	99.2260712	89.2982652	43.5240399	194.038541	220.850648	172.649415
AT2G44860	1509.867026	-1.058745219	0.18808882	-5.628964	1.81E-08	5.93E-07	2194.4629	2009.21097	1917.08213	818.878248	1185.16835	934.399561
AT2G44940	369.3301682	1.088803622	0.24719784	4.40458382	1.06E-05	0.00015612	214.119417	208.024368	286.448914	410.329209	638.753382	458.30572
AT2G45030	1097.82826	-1.46353602	0.17013882	-8.6020109	7.83E-18	1.41E-15	1488.39107	1626.64908	1719.70567	634.630642	621.618418	495.974683
AT2G45040	10.88156363	1.832773344	0.69364647	2.64222976	0.00823622	0.03547256	3.13345488	6.08851808	5.06093487	15.1314459	18.0869065	17.7881215
AT2G45050	49.80117122	1.482939593	0.4226376	3.50877349	0.00045018	0.00359821	25.067639	36.5311085	17.2071786	77.4373995	92.3384173	50.2252843

Table S-5.1 Differentially Expressed Genes between lpa66 (LP) and wild type (WT) Arabidopsis plants.

ID	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	WT4	WT2	WT1	LP3	LP2	LP1
AT2G45080	35.63354736	1.943743871	0.57945606	3.3544284	0.00079529	0.00572869	17.7562443	10.1475301	16.1949916	23.1422114	94.2423022	52.3180045
AT2G45400	190.9999649	1.234879256	0.20283065	6.08822805	1.14E-09	4.87E-08	109.670921	106.549066	125.511185	266.135431	281.774964	256.358222
AT2G45540	2028.755971	1.043509501	0.23892337	4.36754897	1.26E-05	0.0001802	921.235735	1705.79982	1349.24524	2771.72485	2962.44489	2462.08529
AT2G46140	86.72853798	1.587201301	0.46527461	3.41132153	0.00064649	0.00483051	35.5124886	58.8556748	35.4265441	54.2951882	154.214676	182.066656
AT2G46150	34.19390178	2.868156039	0.59176477	4.84678401	1.25E-06	2.47E-05	14.6227894	2.02950603	8.0974958	45.3943377	52.3568346	82.6624472
AT2G46240	110.9929767	1.148044013	0.34355578	3.34165246	0.00083281	0.00594496	44.9128533	56.8261688	105.267445	158.435139	156.118561	144.397692
AT2G46310	221.7438753	-1.096060969	0.26810177	-4.0882273	4.35E-05	0.0005259	395.8598	226.289922	284.42454	134.402843	161.830216	127.655931
AT2G46530	362.0379617	1.086846497	0.20490462	5.30415814	1.13E-07	3.04E-06	283.055424	215.127639	197.37646	515.359245	498.817842	462.49116
AT2G46535	112.1868978	1.841629389	0.45418507	4.05479951	5.02E-05	0.00059165	62.6690976	62.9146868	21.2559265	101.469696	242.745324	182.066656
AT2G46590	140.6185397	1.254833613	0.2981874	4.2082047	2.57E-05	0.00033393	59.5356427	95.3867833	94.1333887	165.55582	252.264748	176.834855
AT2G46630	165.7880849	1.94826142	0.4112976	4.73686552	2.17E-06	4.03E-05	27.156609	100.460548	76.9262101	206.499732	265.591943	318.093468
AT2G46710	1355.0332	1.355101886	0.17011293	7.96589605	1.64E-15	2.08E-13	803.208934	830.067965	651.848412	1940.38541	2123.7836	1780.90487
AT2G46970	20.09191127	3.006791689	0.74908473	4.01395404	5.97E-05	0.00068331	7.31139472	5.07376507	1.01218697	40.0538273	51.4048921	15.6954014
AT2G47010	19.06357381	1.801457501	0.59054381	3.05050609	0.00228456	0.01317644	4.17793984	14.2065422	7.08530882	28.4827217	34.2699281	26.1590023
AT2G47050	9.930373496	3.407466885	0.96745017	3.522111	0.00042812	0.00345825	2.08896992	2.02950603	1.01218697	8.01076547	27.606331	18.8344816
AT2G47060	2038.87319	1.271724283	0.22549131	5.63979295	1.70E-08	5.62E-07	1209.51358	1359.76904	1013.19916	2607.05912	2332.25899	3711.43924
AT2G47140	28.77734975	2.589201182	0.6750744	3.83543084	0.00012534	0.00126013	7.31139472	10.1475301	7.08530882	14.2413608	53.308777	80.569727
AT2G47240	1986.456601	2.019314948	0.3759833	5.37075705	7.84E-08	2.17E-06	867.967002	927.484254	562.775958	1376.96158	4061.93842	4121.6124
AT2G47260	212.6207771	1.120031934	0.22532401	4.97076152	6.67E-07	1.44E-05	158.761714	134.962151	108.304006	265.245346	311.28518	297.166266
AT2G47270	96.4740465	-1.68322225	0.3648482	-4.6134866	3.96E-06	6.78E-05	200.541112	106.549066	134.620868	63.1960387	35.2218705	38.7153234
AT2G47420	1050.489973	-1.327259079	0.15060676	-8.8127458	1.22E-18	2.58E-16	1459.14549	1615.4868	1432.24457	571.434603	650.176691	574.45169
AT2G47440	1094.748272	1.18173475	0.20265085	5.83138315	5.50E-09	2.02E-07	530.59836	838.185989	640.714355	1507.80408	1540.24288	1510.94397
AT2G47630	419.7718847	1.130657041	0.41000079	2.75769477	0.00582105	0.02717909	336.324157	319.647199	133.608681	293.728067	772.977267	662.345937
AT2G47860	90.59472505	1.608640048	0.29439224	5.46427462	4.65E-08	1.36E-06	45.9573382	50.7376507	37.4509181	109.480461	151.358849	148.583133
AT2G47990	395.8665598	-1.308167088	0.24110321	-5.4257555	5.77E-08	1.65E-06	448.084048	717.430381	526.337227	201.159222	265.591943	216.596539
AT3G01080	36.03007107	-1.237287223	0.45637344	-2.7111289	0.00670545	0.03031152	67.8915224	41.6048736	42.5118529	31.1529768	15.2310791	17.7881215
AT3G01490	894.0136358	1.959871243	0.21171284	9.25721495	2.10E-20	6.55E-18	423.016409	377.488121	296.570784	1652.88794	1188.97612	1425.14244
AT3G01600	11.42074477	-4.521887359	1.04973677	-4.3076393	1.65E-05	0.00022855	29.2455789	18.2655542	18.2193655	0.89008505	1.90388489	0
AT3G01790	930.4056811	-1.080203517	0.14374174	-7.5148911	5.70E-14	5.45E-12	1351.56354	1202.48232	1235.8803	578.555284	620.666475	593.286171
AT3G01800	440.4363101	-1.679174943	0.19180921	-8.754402	2.05E-18	4.01E-16	768.740931	608.851808	636.665607	224.301433	219.898705	184.159376
AT3G01860	428.175146	1.018134906	0.2721344	3.74129444	0.00018307	0.00171209	292.455789	339.94226	216.608013	398.758103	667.311655	653.975057
AT3G01970	63.58007911	-1.783223923	0.51349854	-3.4726952	0.00051526	0.00399426	65.8025525	80.1654881	149.803672	47.1745078	12.3752518	26.1590023
AT3G02060	946.8791766	-1.09124204	0.19654477	-5.5521297	2.82E-08	8.70E-07	1055.97429	1516.041	1294.58714	587.456134	676.83108	550.385408
AT3G02080	7851.617412	-1.105986188	0.2178264	-5.0773744	3.83E-07	8.79E-06	11826.7032	10361.643	9977.12701	3599.50395	6022.93986	5321.78742
AT3G02170	2340.175472	1.642638647	0.20430147	8.04026834	8.96E-16	1.19E-13	940.036464	1332.37071	1133.64941	4187.85017	3011.9459	3435.20018
AT3G02330	32.57239154	-1.343075111	0.40547846	-3.3123217	0.00092525	0.00644526	50.1352781	40.5901205	49.5971618	20.4719562	19.9907914	14.6490413
AT3G02560	5265.319497	-1.072682671	0.24375735	-4.4006167	1.08E-05	0.00015814	7448.22225	7313.32497	6650.06843	2285.73841	4443.66734	3450.89558
AT3G02640	80.92704577	1.313150531	0.38774513	3.3866332	0.00070756	0.00519104	47.0018232	54.7966627	37.4509181	65.8662939	158.022446	122.424131
AT3G02650	521.4612687	-1.149886001	0.18576315	-6.190065	6.01E-10	2.83E-08	736.361897	676.84026	743.957427	319.540534	377.921151	274.146344
AT3G02832	49.02140709	-1.478761773	0.47913784	-3.0862972	0.00202666	0.01201913	94.0036464	75.091723	47.5727878	24.9223815	39.9815828	12.5563211
AT3G03030	132.8217786	1.040568387	0.35910521	2.89767002	0.00375946	0.0194285	67.8915224	109.593325	82.9993319	101.469696	224.658417	210.318378
AT3G03060	190.5800366	-1.356749576	0.32404179	-4.1869586	2.83E-05	0.00036232	243.364996	351.104543	227.742069	70.3167191	149.454964	101.496929
AT3G03480	348.485376	-1.924546726	0.25394658	-7.5785496	3.49E-14	3.52E-12	512.842115	449.535585	692.335891	151.314459	113.281151	171.603055
AT3G03630	915.7438753	-2.297142654	0.19868073	-11.56198	6.42E-31	5.82E-28	1441.38924	1480.52465	1642.77946	241.213049	326.516259	362.040591
AT3G03680	180.9570035	1.188040744	0.319523	3.71816973	0.00020067	0.00184581	84.6032818	159.316223	87.0480798	206.499732	232.273957	316.000747
AT3G03820	137.4742336	1.419581476	0.25824117	5.49711533	3.86E-08	1.16E-06	86.6922517	76.106476	61.7434055	184.247606	236.081727	179.973936
AT3G03840	43.67967562	1.549302255	0.40874754	3.79036475	0.00015043	0.00146134	28.2010939	25.3688253	13.1584307	55.1852732	63.7801439	76.3842866
AT3G03910	28.46319766	1.917438182	0.62699222	3.05815309	0.00222706	0.0129091	6.26690976	24.3540723	5.06093487	32.0430619	47.5971223	55.4570848
AT3G03920	2330.638412	-1.548462368	0.15731655	-9.842972	7.35E-23	3.16E-20	3563.78268	3442.04222	3415.11885	1048.52019	1361.2777	1153.08882
AT3G04000	285.5946496	-1.287424399	0.36672387	-3.5106098	0.00044708	0.00357796	300.811669	243.540723	671.079964	155.764884	156.118561	186.252096
AT3G04030	121.7910977	2.212692216	0.38151226	5.79979327	6.64E-09	2.40E-07	30.2900638	71.032711	28.3412353	242.993219	187.532662	170.556695
AT3G04060	53.27915608	-1.472739391	0.4143863	-3.5540253	0.00037938	0.00313121	76.2474021	79.1507351	79.962771	45.3943377	19.0388489	19.8808417
AT3G04070	47.5695894	-1.574239219	0.49741763	-3.1648239	0.00155177	0.00974001	76.2474021	56.8261688	80.974958	42.7240825	17.134964	11.509961
AT3G04290	853.1136522	2.548343963	1.01583289	2.50862517	0.0121202	0.04758243	134.73856	464.75688	147.779298	270.585856	3005.2823	1095.53901
AT3G04440	30.74648234	1.230769812	0.43401872	2.83575285	0.00457178	0.02260208	11.4893346	20.2950603	23.2803004	42.7240825	43.7893526	42.9007637
AT3G04620	34.40760074	-1.020776109	0.39200794	-2.6039679	0.00921514	0.03864997	48.0463082	51.7524037	38.463105	24.0322964	19.0388489	25.1126422
AT3G04690	102.4938792	1.071914516	0.2870033	3.73485081	0.00018783	0.00174367	56.4021878	84.2245001	57.6946576	159.325224	138.031655	119.28505
AT3G04950	126.3289214	-1.77121291	0.26377769	-6.7147941	1.88E-11	1.16E-09	194.274203	198.891591	193.327712	55.1852732	72.347626	43.9471238
AT3G05030	417.5532008	1.179580054	0.22387763	5.26886071	1.37E-07	3.60E-06	201.585597	327.765223	237.863939	571.434603	612.098993	554.570848
AT3G05400	18.88496439	1.428785258	0.56218878	2.54146883	0.01103878	0.04428735	11.4893346	8.11802411	11.1340567	26.7025516	38.0776979	17.7881215
AT3G05470	31.11239004	2.348917212	0.73297792	3.20462205	0.0013524	0.00874236	6.26690976	14.2065422	10.1218697	12.4611907	102.809784	40.8080435
AT3G05560	7181.687227	-1.165582816	0.2374009	-4.9097657	9.12E-07	1.88E-05	10527.3639	10085.6302	9190.65773	3052.99173	5748.78044	4484.69935
AT3G05600	18.53625023	3.868014397	1.11979588	3.4542138	0.0005519	0.00423346	0	5.07376507	2.02437395	2.67025516	63.7801439	37.6689633
AT3G05660	134.9931852	1.14563562	0.27498393	4.16619109	3.10E-05	0.00039192	102.359526	84.2245001	65.7921534	222.521263	177.061295	158.000374
AT3G05690	404.918931	1.3126595	0.24678975	5.31893842	1.04E-07	2.82E-06	213.074932	174.537518	309.729214	577.665199	629.233957	525.272765
AT3G05936	421.7701028	-1.335445341	0.44029316	-3.0330822	0.0024207	0.01376949	754.118141	379.517627	679.17746	429.020995	116.136979	172.649415
AT3G05937	182.259043	-1.793355668	0.44039964	-4.0721097	4.66E-05	0.00055555	341.546582	188.744061	318.838897	145.083863	42.8374101	56.5034449
AT3G06320	272.1520933	-1.517041019	0.20015546	-7.5793138	3.47E-14	3.52E-12	441.817138	347.045531	421.069782	130.842503	145.647194	146.490413
AT3G06370	73.80685668	1.361876298	0.35731673	3.81139813	0.00013818	0.00136186	45.9573382	51.7524037	26.3168613	83.6679949	129.464173	105.682369
AT3G06530	781.6695932	-1.484887803	0.25637302	-5.7919036	6.96E-09	2.50E-07	931.680584	1373.97558	1149.8444	338.23232	553.078562	343.20611
AT3G06690	47.94890685	1.328960391	0.43569279	3.05022353	0.00228671	0.01317941	26.112124	30.4425904	25.3046744	40.0538273	100.905899	64.8743256
AT3G06790	705.1391416	-1.312331216	0.17137082	-7.6578451	1.89E-14	2.06E-12	1041.35151	916.321971	1058.74758	445.932611	354.12259	414.358596
AT3G06880	748.0729008	1.081935698	0.37607575	2.87690896	0.00401591	0.02049527	364.525251	574.350206	501.032553	485.096353	1594.5036	968.929444
AT3G06890	31.98810516	2.068564409	0.45602513	4.53607551	5.73E-06	9.31E-05	16.7117594	8.11802411	12.1462437	43.6141676	59.0204317	52.3180045
AT3G06920	146.4895158	-1.203854437	0.25297645	-4.7587609	1.95E-06	3.66E-05	175.473473	211.068627	226.729882	105.030036	89.48259	71.1524862
AT3G07010	1395.453674	2.45260182	0.25722492	9.53485307	1.50E-21	5.39E-19	506.575206	514.479778	272.278296	2140.65455	2321.78763	2616.94659
AT3G07050	1384.303785	-1.10542647	0.25674986	-4.3054609	1.67E-05	0.00023047	1823.67074	2145.18787	1701.4863	646.201748	1222.2941	766.981946
AT3G07110	4724.713019	-1.134931951	0.28578315	-3.9713046	7.15E-05	0.00079043	6671.12544	7200.68738	5606.50365	1795.30155	4143.80547	2930.85461
AT3G07290	32.34009301	-1.735399335	0.41282695	-4.2036968	2.63E-05	0.00033996	45.9573382	55.8114157	47.5727878	16.911616	15.2310791	12.5563211
AT3G07430	3425.211241	-1.306622863	0.26626394	-4.9072469	9.24E-07	1.90E-05	4712.71614	5328.46807	4593.30449	1227.42729	2620.69756	2068.6539
AT3G07540	303.5351649	1.529930975	0.3008995	5.08452475	3.69E-07	8.53E-06	102.359526	214.112886	151.828046	362.264616	551.174677	439.471238

Table S-5.1 Differentially Expressed Genes between lpa66 (LP) and wild type (WT) Arabidopsis plants.

ID	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	WT4	WT2	WT1	LP3	LP2	LP1
AT3G07650	64.89705932	-1.544843194	0.33094097	-4.6680325	3.04E-06	5.37E-05	101.315041	83.2097471	105.267445	24.0322964	39.9815828	35.5762431
AT3G07750	220.6218886	-2.532907375	0.39824091	-6.360239	2.01E-10	1.02E-08	456.439928	320.661952	352.241067	99.6895258	68.5398562	26.1590023
AT3G07860	133.3425431	-1.617429676	0.26341344	-6.1402702	8.24E-10	3.67E-08	200.541112	183.670295	219.644574	74.7671444	73.2995684	48.1325642
AT3G07960	46.81018754	1.03089312	0.39704857	2.59639048	0.00942089	0.03933111	31.3345488	38.5606145	22.2681134	45.3943377	63.7801439	79.5233669
AT3G08030	4357.870366	1.095869467	0.17430873	6.28694554	3.24E-10	1.59E-08	2674.92598	3038.17052	2620.55208	4903.47855	6297.09929	6612.99577
AT3G08660	169.9011952	1.248691163	0.23673581	5.27461879	1.33E-07	3.50E-06	107.581951	102.490054	92.1090147	274.146196	248.456979	194.622977
AT3G08670	764.8405293	1.315781605	0.22260616	5.91080499	3.40E-09	1.31E-07	333.190702	468.815892	513.178796	1270.15137	1055.70417	948.002242
AT3G08770	29.91987675	2.460774562	0.84092418	2.926274	0.00343049	0.01807964	6.26690976	19.2803073	2.02437395	11.5711057	93.2903598	47.0862041
AT3G08980	112.7183772	-1.150926963	0.25817576	-4.4579203	8.28E-06	0.0001261	131.605105	160.330976	174.09616	64.9762088	64.7320864	80.569727
AT3G09070	158.0798221	1.224817318	0.28044715	4.36737304	1.26E-05	0.00018021	76.2474021	110.608078	97.1699496	164.665735	267.495828	232.29194
AT3G09162	175.4342112	-1.029567813	0.23645424	-4.3541947	1.34E-05	0.00018982	246.498451	188.744061	271.266109	121.051567	104.713669	120.33141
AT3G09200	18359.69367	-1.26042565	0.23988494	-5.2542926	1.49E-07	3.85E-06	26616.6102	26061.9016	25038.4692	7314.71896	14144.9128	10981.5492
AT3G09260	104.0101902	-6.321626844	0.72476605	-8.7222998	2.73E-18	5.14E-16	285.144394	61.8999338	269.241735	1.7801701	2.85582734	3.13908027
AT3G09430	22.64750643	-1.236243919	0.48915359	-2.5273124	0.01149392	0.04560902	35.5124886	36.5311085	23.2803004	10.6810206	15.2310791	14.6490413
AT3G09450	216.8459899	1.414114272	0.28410034	4.97751696	6.44E-07	1.40E-05	108.626436	147.139187	99.1943235	246.553559	415.998849	283.563585
AT3G09500	9470.523034	-1.090938334	0.24098546	-4.5269882	5.98E-06	9.62E-05	15102.208	12466.2408	11100.6546	4187.85017	7359.46706	6606.71761
AT3G09520	158.037743	2.223715771	0.44697967	4.97498188	6.53E-07	1.42E-05	63.7135826	66.9736989	36.4387311	110.370546	274.159425	396.570474
AT3G09720	298.8202373	-1.279992882	0.23929741	-5.3489624	8.85E-08	2.42E-06	413.616044	439.388055	417.021034	145.083863	231.322015	146.490413
AT3G09730	46.46616383	1.296116541	0.38667737	3.35193274	0.0008025	0.00576313	17.7562443	28.4130844	34.4143571	55.1852732	77.1073382	65.9206857
AT3G10050	2722.792189	-1.247577089	0.14534475	-8.583572	9.20E-18	1.61E-15	3594.07275	3891.57781	4010.28479	1783.73044	1544.05065	1513.03669
AT3G10110	121.7556796	-1.660349106	0.26559844	-6.2513511	4.07E-10	1.99E-08	190.096263	183.670295	181.181469	48.0645928	75.2034533	52.3180045
AT3G10530	433.7402154	-1.466165855	0.30142733	-4.8640774	1.15E-06	2.30E-05	553.577029	762.079513	595.165941	164.665735	341.747338	185.205736
AT3G10690	998.479857	-1.046724945	0.25228227	-4.1490229	3.34E-05	0.00041668	936.903009	1685.50476	1414.0252	530.490691	708.24518	715.710302
AT3G10870	111.4675599	1.553718897	0.44137645	3.52016722	0.00043127	0.00348076	53.268733	66.9736989	49.5971618	68.536549	249.408921	181.020296
AT3G11050	70.6759609	-3.758017194	0.58520361	-6.421726	1.35E-10	7.01E-09	220.386327	73.062217	101.218697	9.79093557	2.85582734	16.7417614
AT3G11460	39.44274225	-1.974791609	0.5520998	-3.5768743	0.00034773	0.002905	47.0018232	59.8704278	81.987145	28.4827217	5.71165468	13.6026812
AT3G11510	8943.092852	-1.017461836	0.23556431	-4.3192529	1.57E-05	0.0002178	13133.3539	12163.8444	10618.8536	4107.74252	7472.74821	6162.01457
AT3G12080	2753.018595	-1.05196172	0.18416393	-5.7120941	1.12E-08	3.85E-07	3096.89791	3858.09096	4188.4297	1640.42675	2048.58015	1685.68611
AT3G12220	30.33485053	-1.856955448	0.58856012	-3.155082	0.00160453	0.00996601	57.4466728	55.8114157	29.3534223	17.801701	3.80776979	17.7881215
AT3G12270	420.5768753	-1.321945372	0.2125559	-6.2192834	4.99E-10	2.39E-08	569.244303	627.117362	606.299998	217.180753	302.717698	200.901137
AT3G12340	165.7291371	-1.116896438	0.21221718	-5.2629878	1.42E-07	3.69E-06	226.653236	240.496464	213.571452	103.249866	115.185036	95.2187682
AT3G12520	94.37630332	2.018535309	0.47231012	4.27374988	1.92E-05	0.00026129	20.8896992	25.3688253	65.7921534	132.622673	217.99482	103.589649
AT3G12580	220.3989262	-1.180909429	0.29710228	-3.9747571	7.05E-05	0.00078269	271.56609	317.617693	328.960767	196.708797	101.857842	105.682369
AT3G12610	1467.0374	2.038445962	0.2702071	7.5440134	4.56E-14	4.40E-12	756.207111	583.482983	383.618863	1875.4092	2764.44087	2439.06537
AT3G12700	107.6480863	1.634984061	0.51300481	3.18707354	0.0014372	0.0091814	36.5569736	82.1949941	38.463105	60.5257835	251.312806	176.834855
AT3G12710	266.6103628	3.200556532	0.39395749	8.12411654	4.51E-16	6.40E-14	62.6690976	75.091723	19.2315525	428.13091	574.021295	440.517598
AT3G12770	31.17640371	-1.246496393	0.47674687	-2.6145875	0.00893353	0.03770513	38.6459435	39.5753675	53.6459097	27.5926366	17.134964	10.4636009
AT3G12820	30.12808816	1.302392537	0.46286653	2.81375396	0.00489667	0.02382857	18.8007293	19.2803073	14.1706176	48.9546779	52.3568346	27.2053624
AT3G12920	746.0549662	1.35987868	0.18432031	7.37780181	1.61E-13	1.40E-11	394.815315	394.738922	465.606008	1075.22274	1225.14993	920.79688
AT3G12930	2810.603287	-1.115549173	0.23607302	-4.7254412	2.30E-06	4.23E-05	4013.9557	3823.58936	3700.55558	1222.08678	2293.22935	1810.20296
AT3G12965	1347.96746	-1.145765959	0.28034034	-4.0870535	4.37E-05	0.0005279	2341.73528	1726.09488	1502.08547	537.611371	1017.62648	962.651283
AT3G13000	272.613372	1.389081894	0.2258421	6.15067732	7.72E-10	3.50E-08	161.895169	156.271964	133.608681	315.980193	406.479425	461.4448
AT3G13150	152.9854481	-1.879849504	0.31187868	-6.0275025	1.67E-09	6.74E-08	217.252872	289.204609	215.595826	60.5257835	91.3864749	43.9471238
AT3G13160	278.8904085	-1.055840908	0.19085469	-5.5321717	3.16E-08	9.63E-07	383.32598	336.898001	409.935725	194.038541	182.77295	166.371254
AT3G13175	25.93128775	1.85407456	0.50519759	3.66999885	0.00024255	0.00214998	7.31139472	17.2508012	9.10968277	35.6034021	47.5971223	38.7153234
AT3G13230	605.8592035	-1.412253705	0.25637657	-5.5085132	3.62E-08	1.09E-06	959.881678	914.292465	768.249914	260.79492	458.836259	273.099984
AT3G13310	854.1703167	1.091939588	0.24563457	4.44538243	8.77E-06	0.00013262	629.824431	587.541995	419.045408	858.04199	1307.96892	1322.59915
AT3G13380	209.7645821	-1.225586518	0.29160673	-4.2028746	2.64E-05	0.00034073	244.409481	262.821031	374.509181	113.040802	167.541871	96.2651283
AT3G13600	36.75288752	1.480579103	0.44908573	3.29687409	0.00097767	0.00673775	13.5783045	15.2212952	29.3534223	50.734848	66.6359713	44.9934839
AT3G13880	42.80163448	-1.36799899	0.35135231	-3.8935249	9.88E-05	0.00103268	58.4911578	58.8556748	67.8165273	24.9223815	24.7505036	21.9735619
AT3G13940	394.9847165	-1.159064779	0.21375777	-5.4223281	5.88E-08	1.68E-06	554.621514	590.586254	491.92287	226.971688	301.765756	204.040218
AT3G13980	156.3873161	1.553915066	0.26506924	5.86229871	4.57E-09	1.71E-07	76.2474021	98.4310423	63.7677794	227.861773	273.207482	198.808417
AT3G14060	17.11387293	-1.969919836	0.59220226	-3.3264308	0.00087966	0.00620259	28.2010939	27.3983314	26.3168613	10.6810206	3.80776979	6.27816054
AT3G14200	576.6785256	1.223630371	0.2176587	5.62178475	1.89E-08	6.12E-07	283.055424	390.67991	363.375124	647.091833	905.297267	870.571595
AT3G14390	2052.316314	-1.026269175	0.17039113	-6.0230199	1.71E-09	6.90E-08	2805.4866	2699.24302	2754.16076	1182.03295	1606.87885	1266.09571
AT3G14440	165.5698004	2.841903885	0.3697927	7.68512702	1.53E-14	1.68E-12	34.4680037	46.6786386	40.487479	446.822696	188.484604	236.47738
AT3G14460	46.93687673	1.451803568	0.43319308	3.35140065	0.00080404	0.00576986	13.5783045	33.4868494	28.3412353	88.1184202	64.7320864	53.3643646
AT3G14470	150.6596835	1.126448849	0.24136207	4.66705003	3.06E-06	5.39E-05	74.1584322	108.578572	101.218697	222.521263	201.811799	195.669337
AT3G14560	148.2031464	1.320173135	0.24168057	5.46247104	4.70E-08	1.37E-06	101.315041	86.2540062	66.8043403	207.389817	216.090935	211.364738
AT3G14580	24.03040808	-1.300130276	0.4767719	-2.726944	0.00639239	0.02926474	35.5124886	27.3983314	39.475292	10.6810206	13.3271943	17.7881215
AT3G14770	1272.868744	-1.409478729	0.19686961	-7.1594531	8.10E-13	6.48E-11	2305.17831	1697.68179	1545.60951	674.684469	702.533526	711.524862
AT3G14850	75.51945995	1.0410864	0.34903099	2.98279069	0.00285633	0.01563384	35.5124886	55.8114157	56.6824706	71.2068042	120.896691	113.00689
AT3G14900	857.3209475	-3.601718965	0.17155749	-20.99424	7.40E-98	1.41E-93	1552.10465	1479.50989	1720.71786	121.051567	141.839425	128.702291
AT3G15080	227.6849089	-1.22275211	0.19862225	-6.1561687	7.45E-10	3.42E-08	338.413127	325.735717	292.522036	142.413608	145.647194	121.377771
AT3G15140	141.6554179	-1.350977912	0.2346423	-5.7576059	8.53E-09	3.02E-07	190.096263	183.670295	236.851752	82.7779098	78.0592806	78.4770068
AT3G15270	80.40157085	1.554945219	0.35468014	4.38407747	1.16E-05	0.00016869	28.2010939	35.5163555	58.7068445	136.183013	96.1461871	127.655931
AT3G15310	169.7607946	1.868669334	0.28835811	6.48037726	9.15E-11	4.99E-09	71.0249773	74.07697	73.8896492	228.751858	363.642015	207.179298
AT3G15352	210.4079382	-1.170048831	0.20452295	-5.7208681	1.06E-08	3.67E-07	307.078578	295.293127	271.266109	115.711057	126.608345	146.490413
AT3G15357	32.62440127	-3.362454583	0.51932479	-6.474666	9.50E-11	5.15E-09	64.7580675	66.9736989	46.5606008	3.56034021	7.61553957	6.27816054
AT3G15450	29979.39935	-1.388899999	0.33292749	-4.1717793	3.02E-05	0.00038537	51897.3242	33982.0489	44291.2776	25962.0008	9655.55224	14088.1923
AT3G15530	1594.401628	1.189773981	0.18452387	6.44780537	1.13E-10	6.05E-09	969.282043	1017.79727	928.175456	2087.24945	1881.03827	2682.86727
AT3G15540	252.674353	3.134254274	0.34543449	9.07336812	1.15E-19	2.96E-17	66.8470374	61.8999338	26.3168613	335.562065	495.962015	529.458206
AT3G15550	64.01133028	1.033839548	0.32369852	3.19383468	0.00140396	0.00899928	41.7793984	48.7081447	35.4265441	67.646464	94.2423022	96.2651283
AT3G15590	942.6112205	-1.287139055	0.15060342	-8.5465462	1.27E-17	2.17E-15	1263.8268	1321.20842	1427.18363	587.456134	546.414964	509.577364
AT3G15620	185.4582238	-1.276829545	0.25784115	-4.9520006	7.35E-07	1.57E-05	266.343665	230.348934	291.509849	139.743353	99.0020145	85.8015274
AT3G15930	19.3317133	-1.449221217	0.57637945	-2.5143527	0.01192511	0.04696747	33.4235187	19.2803073	32.3899832	14.2413608	11.4233094	5.23180045
AT3G15950	880.7077881	-4.05933547	0.45059824	-9.0087689	2.08E-19	5.02E-17	1135.35515	1196.3938	2653.95425	177.126925	52.3568346	69.059766
AT3G16070	14.72694828	2.035217366	0.80620212	2.52445053	0.01158793	0.04590548	2.08896992	12.1770362	3.03656092	14.2413608	39.0296403	17.7881215
AT3G16080	3286.949566	-1.148667649	0.26942695	-4.2633733	2.01E-05	0.00027217	4866.25543	4731.7933	3993.07762	1297.74401	2788.23943	2044.58762
AT3G16420	2508.559441	-2.504967141	0.82852464	-3.0234069	0.00249946	0.01408973	3627.49627	3282.726	5886.87945	1544.29757	195.148202	514.809165
AT3G16460	1035.083692	-2.253657414	0.41688469	-5.4059491	6.45E-08	1.82E-06	967.193073	1579.97044	2587.14991	585.675964	202.763741	287.749025

Table S-5.1 Differentially Expressed Genes between lpa66 (LP) and wild type (WT) Arabidopsis plants.

ID	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	WT4	WT2	WT1	LP3	LP2	LP1
AT3G16510	169.5828489	1.282151601	0.2598229	4.93471366	8.03E-07	1.68E-05	80.4253419	100.460548	115.389315	240.322964	194.196259	286.702665
AT3G16670	7357.290823	1.224033744	0.36121184	3.38868669	0.00070228	0.00516244	3306.83938	6826.24352	3099.31652	5912.835	12976.8794	12021.6311
AT3G16700	136.228918	1.057287925	0.2380104	4.44219214	8.90E-06	0.00013397	87.7367367	96.4015363	80.974958	160.215309	182.77295	209.272018
AT3G16800	661.349127	1.967567904	0.23413905	8.40341625	4.34E-17	6.88E-15	288.277849	277.027573	242.924874	1384.08226	916.720576	859.061634
AT3G16810	571.9545694	-1.122985318	0.25027159	-4.4870666	7.22E-06	0.00011292	768.740931	851.377778	731.811183	285.717302	496.913957	297.166266
AT3G16860	104.9634042	1.061287185	0.34149393	3.10777761	0.001885	0.01135594	44.9128533	73.062217	86.0358929	179.797181	104.713669	141.258612
AT3G17120	592.8605188	1.030552691	0.28810237	3.57703655	0.00034751	0.002905	256.9433	367.340591	544.556593	648.872003	924.336116	815.114511
AT3G17130	58.6491513	1.700158475	0.44843776	3.79129197	0.00014987	0.00145738	19.8452142	32.4720964	30.3656092	45.3943377	117.088921	106.728729
AT3G17170	1538.734696	-1.588196941	0.33779702	-4.701631	2.58E-06	4.70E-05	2288.46655	2268.98774	2370.5419	398.758103	1210.87079	694.7831
AT3G17220	21.96829834	1.361362946	0.49658194	2.74146688	0.00611655	0.02824594	13.5783045	9.13277712	14.1706176	26.7025516	29.5102158	38.7153234
AT3G17390	16598.27796	1.12797979	0.22097922	5.10446086	3.32E-07	7.80E-06	10347.7125	9452.42432	11463.0175	17977.9379	29899.5603	20449.0152
AT3G17465	956.4038237	-1.520053064	0.17123071	-8.8772223	6.86E-19	1.55E-16	1492.56901	1408.47718	1354.30617	494.887289	565.453813	422.729477
AT3G17820	547.005053	1.181153433	0.28984577	4.07511012	4.60E-05	0.0005498	302.900638	372.414356	328.960767	473.525248	1051.8964	752.332905
AT3G17830	269.708418	-2.173519551	0.21959309	-9.8979416	4.25E-23	1.93E-20	376.014586	433.299537	515.20317	89.8985903	107.569496	96.2651283
AT3G18070	70.26759615	1.105948402	0.40659379	2.7200327	0.00652755	0.02969776	27.156609	71.032711	35.4265441	76.5473145	104.713669	106.728729
AT3G18080	3902.211197	1.308749994	0.27152353	4.82002427	1.44E-06	2.78E-05	1445.56718	2332.91718	2954.57378	6051.68827	4456.04259	6172.47817
AT3G18130	2907.604501	-1.017756795	0.33404925	-3.0467268	0.00231348	0.01328941	3822.81495	4573.49183	3281.51017	1007.57628	2897.71281	1862.52096
AT3G18217	33.28520695	1.868549162	0.43796419	4.26644275	1.99E-05	0.00026884	12.5338195	10.1475301	20.2437395	56.9654433	48.5490648	51.2716444
AT3G18580	295.681552	-1.554447396	0.20108674	-7.7302331	1.07E-14	1.22E-12	455.395443	468.815892	399.813855	167.33599	156.118561	126.609571
AT3G18600	611.4172532	-1.424773635	0.26626643	-5.3509323	8.75E-08	2.40E-06	788.586145	1033.01857	851.249246	247.443644	463.595972	284.609945
AT3G18680	2641.411656	-1.119687846	0.20401745	-5.4881964	4.06E-08	1.21E-06	3242.08132	3857.0762	3754.20149	1303.08452	2041.91655	1650.10986
AT3G18740	6361.64867	-1.046457554	0.23083382	-4.5333805	5.80E-06	9.40E-05	9926.78506	8448.83359	7342.40432	3068.12317	5243.299	4140.44688
AT3G18760	416.5258283	-1.25016921	0.20997641	-5.9538554	2.62E-09	1.02E-07	623.557521	527.671567	608.324372	216.290668	304.621583	218.689259
AT3G18850	189.4973787	1.421020584	0.36265713	3.91835832	8.92E-05	0.00095266	100.270556	109.593325	99.1943235	143.303693	408.38331	276.239064
AT3G19050	57.49649957	1.394661784	0.51822799	2.69121277	0.00711928	0.03173094	22.9786691	41.6048736	30.3656092	31.1529768	124.704461	94.1724082
AT3G19230	24.37159136	1.909975784	0.50994526	3.74545253	0.00018007	0.00169062	10.4448496	11.1622831	9.10968277	42.7240825	25.7024461	47.0862041
AT3G19270	138.1745555	-2.011626832	0.48051103	-4.1864322	2.83E-05	0.00036291	240.231541	190.773567	233.815191	107.700291	31.4141007	25.1126422
AT3G19380	737.6563082	1.041105896	0.27026901	3.85210981	0.0001171	0.00119142	574.466728	534.774838	338.07045	927.468624	777.736979	1273.42023
AT3G19440	155.560136	-1.873616789	0.2514506	-7.4512321	9.25E-14	8.58E-12	233.964631	256.732512	242.924874	67.646464	81.8670504	50.2252843
AT3G19620	129.6844482	1.191946468	0.31844099	3.74306859	0.00018179	0.00170423	54.3132179	75.091723	107.291819	139.743353	201.811799	199.854777
AT3G19930	2604.687773	1.028729493	0.20085892	5.12165208	3.03E-07	7.20E-06	1908.27402	1625.63433	1606.34073	3344.93963	2832.98072	4309.95721
AT3G20080	130.1359119	1.220512304	0.28921284	4.22011795	2.44E-05	0.00031915	80.4253419	92.3425242	61.7434055	160.215309	232.273957	153.814933
AT3G20130	28.57583764	1.53490276	0.42684408	3.59593307	0.00032323	0.00273639	13.5783045	13.1917892	17.2071786	41.8339974	43.7893526	41.8544036
AT3G20240	470.9678135	-1.256584617	0.2055716	-6.1126373	9.80E-10	4.31E-08	701.893893	649.441929	640.714355	234.982454	345.555108	253.219142
AT3G20260	88.08092529	1.431156333	0.47345746	3.022777	0.00250467	0.01409592	33.4235187	59.8704278	49.5971618	59.6356985	216.090935	109.86781
AT3G20370	12.94504823	-3.907774861	0.86629826	-4.5108885	6.46E-06	0.00010255	25.067639	19.2803073	28.3412353	0.89008505	0.95194245	3.13908027
AT3G20395	30.62520538	-1.803492534	0.52445622	-3.4387857	0.00058433	0.00443396	71.0249773	25.3688253	46.5606008	16.911616	12.3752518	11.509961
AT3G20440	313.2269268	-3.071164391	0.29955637	-10.252376	1.15E-24	6.10E-22	362.436281	614.940326	702.457761	74.7671444	71.3956835	53.3643646
AT3G20460	17.54069425	2.667127429	0.78314394	3.40566693	0.00066003	0.00491238	3.13345488	10.1475301	1.01218697	16.911616	44.741295	29.2980825
AT3G20470	203.406876	1.308832826	0.23949533	5.46496182	4.63E-08	1.36E-06	148.316864	108.578572	94.1333887	267.915601	297.006043	304.490786
AT3G20540	847.9031497	-1.039653362	0.17646336	-5.8916102	3.82E-09	1.45E-07	1068.50811	1203.49707	1150.85659	542.951882	644.465036	477.140201
AT3G20660	144.3616823	-1.123369306	0.37554172	-2.9913302	0.00277765	0.01528671	180.695898	153.227705	260.132053	142.413608	63.7801439	65.9206857
AT3G20830	99.68878139	1.039947385	0.32809983	3.16960658	0.00152645	0.00962056	80.4253419	61.8999338	53.6459097	181.577351	118.040863	102.543289
AT3G21010	101.3215993	-1.048962369	0.3445032	-3.0448552	0.00232792	0.01334821	121.160255	150.183446	138.669616	56.9654433	98.050072	42.9007637
AT3G21030	22.06501842	-1.450557497	0.51185751	-2.8339088	0.00459825	0.02267665	20.8896992	38.5606145	37.4509181	12.4611907	10.4713669	12.5563211
AT3G21090	13.28684028	-3.691216046	0.87431165	-4.2218539	2.42E-05	0.00031758	36.5569736	12.1770362	25.3046744	1.7801701	2.85582734	1.04636009
AT3G21110	1314.823446	-1.085863488	0.16302485	-6.6607236	2.72E-11	1.62E-09	1675.35388	1874.24882	1812.82687	752.121869	962.413814	811.97543
AT3G21230	303.8940223	1.1841359	0.30566575	3.87395671	0.00010708	0.00110634	171.295533	182.655542	203.449582	623.949622	289.390504	352.623351
AT3G21300	461.8023887	-2.294954012	0.31789453	-7.2192309	5.23E-13	4.23E-11	686.226619	812.817164	802.664271	98.7994408	243.697266	126.609571
AT3G21310	19.64336343	1.701384585	0.59847845	2.84285023	0.00447121	0.02222292	11.4893346	8.11802411	8.0974958	16.0215309	43.7893526	30.3444426
AT3G21460	495.6274395	-1.239130879	0.3230043	-3.8362674	0.00012492	0.00125718	871.100457	513.465025	704.482135	399.648188	173.253525	311.815307
AT3G21470	24.44898749	-1.505892878	0.52757452	-2.85437	0.00431223	0.021602	37.6014586	30.4425904	40.487479	17.801701	5.71165468	14.6490413
AT3G21530	217.5697563	-1.114814852	0.23433552	-4.7573448	1.96E-06	3.68E-05	324.834823	244.555476	323.899832	161.105394	117.088921	133.934092
AT3G21540	421.6308606	-1.211773421	0.27024224	-4.4840267	7.32E-06	0.00011417	456.439928	742.799206	567.836893	230.532028	331.275971	200.901137
AT3G21670	6334.010101	-1.070933986	0.24844199	-4.3105997	1.63E-05	0.00022567	8625.3568	7133.71369	9989.27326	5543.4497	3155.68921	3556.57795
AT3G21690	2715.965178	-1.296241096	0.23280474	-5.5679327	2.58E-08	8.04E-07	3249.39271	3647.02233	4684.40132	2006.25171	1258.46791	1450.25509
AT3G21950	427.9631105	1.932579167	0.28071083	6.88459078	5.80E-12	3.88E-10	159.806199	242.52597	130.57212	518.0295	773.929209	742.915664
AT3G22230	6277.884799	-1.192040055	0.23654065	-5.0394723	4.67E-07	1.05E-05	10056.3012	8402.15495	7741.20598	2693.39737	4805.40547	3968.84382
AT3G22235	6802.837822	-3.578191202	1.02722487	-3.4833572	0.00049517	0.00386368	15342.4396	15460.7769	6860.60332	2468.20585	277.967194	407.034075
AT3G22240	33.77836091	-1.904557382	0.51402977	-3.70515	0.00021127	0.00192097	65.8025525	60.8851808	33.4021702	21.3620413	7.61553957	13.6026812
AT3G22310	763.725508	-1.560697868	0.22897559	-6.8160011	9.36E-12	6.14E-10	934.814039	1349.62151	1137.69816	319.540534	480.730936	359.947871
AT3G22410	39.15626782	1.373663485	0.45311703	3.03158651	0.00243272	0.0138283	15.6672744	19.2803073	30.3656092	36.4934871	71.3956835	61.7352453
AT3G22450	50.13577666	-1.987069412	0.41652073	-4.7706375	1.84E-06	3.47E-05	79.380857	64.9441929	96.1577626	30.2628918	13.3271943	16.7417614
AT3G22540	36.41112287	2.290790316	0.52921067	4.32869257	1.50E-05	0.0002099	20.8896992	11.1622831	5.06093487	55.1852732	46.6451799	79.5233669
AT3G22750	421.7247999	-1.054221579	0.22270802	-4.733649	2.21E-06	4.09E-05	681.004194	480.992928	545.568779	222.521263	298.909928	301.351706
AT3G22790	239.1136626	1.995223076	0.42271929	4.71997172	2.36E-06	4.33E-05	58.4911578	136.991657	92.1090147	197.598882	596.867914	352.623351
AT3G22840	3467.385351	-2.917024363	0.31531647	-9.2511005	2.22E-20	6.82E-18	8883.34459	4305.59704	5182.39731	546.512222	855.79626	1030.66469
AT3G22961	100.7293996	-3.679944769	0.5250384	-7.0089059	2.40E-12	1.69E-10	219.341842	117.71135	223.693321	24.0322964	2.85582734	16.7417614
AT3G23090	243.8699915	1.522850941	0.21863314	6.96532544	3.28E-12	2.23E-10	121.160255	138.00641	118.425876	298.178492	405.527482	381.921433
AT3G23170	225.8077428	1.119690933	0.37435524	2.99098511	0.00278079	0.01529957	215.163902	105.534313	106.279632	185.137691	392.200288	350.53063
AT3G23370	37.14486946	-1.490975976	0.46073268	-3.2360977	0.00121176	0.00800729	39.6904285	73.062217	51.6215357	14.2413608	28.5582734	15.6954014
AT3G23510	251.6909576	-1.080139499	0.30742869	-3.5134635	0.00044231	0.00355329	416.749499	407.930711	200.413021	149.534289	151.358849	184.159376
AT3G23560	460.8731049	-1.466858276	0.24172333	-6.0683356	1.29E-09	5.44E-08	570.288788	720.47464	739.908679	293.728067	176.109353	264.729103
AT3G23570	1787.221199	-1.079793901	0.23381568	-4.6181416	3.87E-06	6.65E-05	2227.88642	1936.14875	3115.51151	1330.67715	933.85554	1179.24782
AT3G23580	1152.456011	-1.612508286	0.17947716	-8.9844765	2.60E-19	6.18E-17	1691.02115	1602.29501	1918.09432	645.311663	578.781008	479.232921
AT3G23670	40.41529557	1.376627799	0.55167335	2.4953676	0.01258267	0.04890065	14.6227894	31.4573434	21.2559265	24.0322964	90.4345324	60.6888853
AT3G23710	393.1817074	-1.256780611	0.18826732	-6.6755111	2.46E-11	1.48E-09	547.310119	555.069898	560.751584	207.389817	275.111367	213.457458
AT3G23730	254.6384018	1.335159182	0.43354508	3.07963176	0.00207257	0.01222281	94.0036464	168.449	171.059599	146.864034	543.559137	403.894995
AT3G23830	367.6257977	-1.322945511	0.24342938	-5.4346172	5.49E-08	1.58E-06	505.530721	519.553543	550.629714	157.545054	278.919137	193.576617
AT3G23840	401.1425549	1.342064001	0.27481758	4.88347219	1.04E-06	2.11E-05	184.873838	286.16035	209.522704	404.098614	615.906763	706.293061
AT3G23890	121.2162502	1.19723922	0.38854267	3.08135836	0.00206058	0.01216723	59.5356427	88.2835122	72.8774622	84.5580799	228.466187	193.576617

Table S-5.1 Differentially Expressed Genes between lpa66 (LP) and wild type (WT) Arabidopsis plants.

ID	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	WT4	WT2	WT1	LP3	LP2	LP1
AT3G23940	2893.779629	-1.345433602	0.28956486	-4.646398	3.38E-06	5.89E-05	3176.27876	5216.84524	4065.95508	1036.94909	2138.06274	1728.58687
AT3G23990	1907.366879	-1.346878028	0.2227116	-6.0476331	1.47E-09	6.09E-08	2568.38852	2951.91652	2694.44173	894.535477	1429.81756	905.101478
AT3G24000	89.11165142	-1.614114272	0.35123321	-4.5955628	4.32E-06	7.31E-05	103.404011	120.755609	179.157095	58.7456134	38.0776979	34.529883
AT3G24450	24.26035844	1.664373567	0.63323023	2.62838617	0.00857911	0.03657459	18.8007293	7.1032711	9.10968277	62.3059536	19.9907914	28.2517224
AT3G24670	235.0136707	1.029081742	0.3248562	3.16780699	0.00153593	0.00965974	147.272379	184.685048	131.584307	180.687266	401.719713	364.133312
AT3G25130	53.145283	1.758308245	0.39306125	4.47336956	7.70E-06	0.00011904	25.067639	30.4425904	17.2071786	59.6356985	102.809784	83.7088072
AT3G25520	17953.58991	-1.154993524	0.2668499	-4.3282517	1.50E-05	0.00021016	25232.6677	26142.0671	22963.4859	7067.27531	15380.5341	10935.5093
AT3G25882	78.45763386	-1.596682211	0.35879165	-4.4501655	8.58E-06	0.00013022	145.183409	121.770362	87.0480798	52.5150181	27.606331	36.6226032
AT3G25900	84.59560117	1.211446964	0.41196669	2.94064301	0.00327532	0.01740647	31.3345488	56.8261688	64.7799664	69.4266341	162.782158	122.424131
AT3G25940	155.6883566	-1.069545265	0.26521857	-4.0326938	5.51E-05	0.0006434	214.119417	245.570229	173.083973	89.8985903	125.656403	85.8015274
AT3G26125	17.47824442	1.871108978	0.5766268	3.24492196	0.00117483	0.00780389	5.2224248	8.11802411	9.10968277	20.4719562	29.5102158	32.4371628
AT3G26410	249.0391423	-1.415568307	0.19076757	-7.4203824	1.17E-13	1.06E-11	355.124886	358.207814	373.496994	126.392077	152.310791	128.702291
AT3G26460	33.05149799	1.333556811	0.45076039	2.95846049	0.0030918	0.01663557	18.8007293	11.1622831	26.3168613	39.1637423	49.5010072	53.3643646
AT3G26540	95.41751564	-1.447443851	0.31588727	-4.5821532	4.60E-06	7.72E-05	120.11577	138.00641	160.937729	46.2844227	69.4917986	37.6689633
AT3G26710	5893.723172	-1.197741159	0.20713478	-5.7824241	7.36E-09	2.62E-07	8738.16118	7806.49493	8081.30081	2689.83703	4409.39741	3637.14767
AT3G26960	407.975009	1.158406722	0.22874439	5.06419729	4.10E-07	9.36E-06	326.923793	204.980109	225.717695	614.158686	554.982446	521.087325
AT3G27025	17.68090769	2.060907668	0.6882372	2.99447293	0.00274919	0.0151608	9.40036464	5.07376507	6.07312185	42.7240825	11.4233094	31.3908027
AT3G27180	801.0249514	-1.221903368	0.22921148	-5.3308996	9.77E-08	2.66E-06	1021.50629	1241.04294	1101.25943	371.165467	625.426188	445.749399
AT3G27250	65.21500291	3.411439415	0.51403893	6.63653898	3.21E-11	1.89E-09	4.17793984	18.2655542	11.1340567	176.23684	100.905899	80.569727
AT3G27280	747.5164241	-1.457781213	0.17004286	-8.5730224	1.01E-17	1.74E-15	1176.09007	1053.31363	1058.74758	367.605127	457.884317	371.457832
AT3G27500	17.5400407	4.01327468	0.77760579	5.16106585	2.46E-07	6.01E-06	1.04448496	4.05901205	1.01218697	29.3728067	35.2218705	34.529883
AT3G27550	131.2460842	-1.880605519	0.28138769	-6.6833255	2.34E-11	1.41E-09	169.206564	216.142392	233.815191	44.5042526	70.4437411	53.3643646
AT3G27620	13.69253193	-1.556137062	0.61822253	-2.5171148	0.01183203	0.04665879	20.8896992	17.2508012	23.2803004	9.79093557	5.71165468	5.23180045
AT3G27831	19.63365639	1.642240325	0.56531175	2.90501716	0.00367233	0.01908468	5.2224248	14.2065422	9.10968277	32.9331469	22.8466187	33.4835229
AT3G27940	66.80771159	1.060389943	0.37022775	2.86415576	0.00418122	0.02110925	44.9128533	40.5901205	44.5362269	128.172248	59.9723741	82.6624472
AT3G28270	1532.044628	-1.314777436	0.32178536	-4.0858833	4.39E-05	0.00052998	2912.02407	1530.24754	2114.45859	1147.31963	524.520288	963.697643
AT3G28345	111.4612818	1.34168061	0.36295867	3.6965107	0.00021858	0.00197806	54.3132179	86.2540062	48.5849748	110.370546	222.754533	146.490413
AT3G28420	38.24922016	1.32012224	0.44076165	2.99509326	0.00274361	0.01513439	28.2010939	26.3835784	11.1340567	60.5257835	56.1646044	47.0862041
AT3G28500	36.90398828	2.135935323	0.4961896	4.30467572	1.67E-05	0.00023096	14.6227894	9.13277712	17.2071786	39.1637423	52.3568346	88.9406077
AT3G28700	303.5538833	-1.021149349	0.21488848	-4.7519967	2.01E-06	3.77E-05	367.658706	435.329043	417.021034	168.226075	243.697266	189.391176
AT3G28860	3402.50502	1.216839204	0.16577914	7.34012253	2.13E-13	1.85E-11	2076.4361	2292.32706	1772.33939	5136.68084	4299.92403	4837.3227
AT3G29000	343.819202	-1.549175928	0.32392338	-4.7825381	1.73E-06	3.30E-05	642.35825	398.797934	496.983805	260.79492	144.695252	119.28505
AT3G29030	2207.69402	1.783299377	0.29240637	6.09870219	1.07E-09	4.64E-08	903.479491	1301.92812	776.34741	2162.01659	3909.62763	4192.76488
AT3G29140	41.51640552	1.198918143	0.40501604	2.96017449	0.00307465	0.01656393	22.9786691	19.2803073	33.4021702	66.7563789	63.7801439	42.9007637
AT3G29200	2069.853998	-1.233727031	0.16045978	-7.6886995	1.49E-14	1.65E-12	3235.81441	2719.53808	2758.20951	1101.03521	1338.43108	1266.09571
AT3G29370	31.78312285	3.213582774	0.68704149	4.67742167	2.91E-06	5.18E-05	13.5783045	2.02950603	3.03656092	80.9977397	31.4141007	59.6425252
AT3G29575	406.4565627	-1.551006864	0.43937139	-3.5300589	0.00041547	0.0033804	667.42589	486.066694	665.006843	353.363766	73.2995684	193.576617
AT3G30122	95.36586811	-1.393174771	0.41940547	-3.321785	0.00089444	0.00629047	116.982316	135.976904	160.937729	32.0430619	35.2218705	91.0333279
AT3G30180	376.7056972	1.758631574	0.28958835	6.07286724	1.26E-09	5.33E-08	169.206564	151.198199	195.352086	664.003449	721.572375	358.901511
AT3G30775	5331.777447	-1.354055409	0.39309122	-3.4446341	0.00057183	0.00436349	6281.53255	5134.65025	11579.419	4953.32331	1965.76115	2075.97842
AT3G42800	11.36268132	2.349658486	0.91951141	2.55533368	0.0106086	0.04297411	0	9.13277712	2.02437395	23.1422114	17.134964	16.7417614
AT3G43690	113.9761495	2.012232154	0.38387036	5.24195755	1.59E-07	4.08E-06	30.2900638	70.0179579	35.4265441	128.172248	228.466187	191.483897
AT3G43715	90.41690415	2.584294263	0.47116287	5.48492766	4.14E-08	1.22E-06	12.5338195	31.4573434	33.4021702	77.4373995	184.676835	202.993858
AT3G43960	91.50552015	1.210782418	0.37729788	3.20908883	0.00133156	0.00863407	83.5587968	43.6343796	38.463105	92.5688454	148.503022	142.304972
AT3G44120	24.1594139	-1.633014714	0.4717713	-3.4614541	0.00053727	0.00413788	41.7793984	35.5163555	32.3899832	14.2413608	9.51942447	11.509961
AT3G44730	106.6865133	1.542397216	0.39647448	3.89028118	0.00010013	0.00104413	43.8683683	81.1802411	38.463105	101.469696	216.090935	159.046734
AT3G44750	1147.352626	-2.052353507	0.28912097	-7.098598	1.26E-12	9.83E-11	1927.07475	1972.67986	1646.82821	274.146196	640.657267	422.729477
AT3G44970	166.7109719	-1.420937039	0.3149202	-4.5120543	6.42E-06	0.00010216	228.742206	177.581777	321.875458	70.3167191	118.040863	83.7088072
AT3G45030	3510.078376	-1.081274722	0.24022967	-4.501004	6.76E-06	0.00010673	5269.42662	4803.84077	4227.90499	1578.1208	2926.27108	2254.906
AT3G45160	386.2635163	1.794112193	0.31890398	5.62586958	1.85E-08	6.00E-07	195.318688	229.334181	94.1333887	566.984178	714.908778	516.901885
AT3G45300	1640.782814	-1.202526625	0.28404018	-4.2336497	2.30E-05	0.00030408	2296.82243	1717.97685	2848.29415	1360.94004	697.773813	922.8896
AT3G45390	33.32267414	1.244770922	0.42450626	2.93227933	0.00336484	0.01778785	16.7117594	19.2803073	23.2803004	35.6034021	59.0204317	46.039844
AT3G45430	78.50142259	1.078290107	0.28765228	3.74858881	0.00017783	0.00167458	44.9128533	48.7081447	57.6946576	94.3490155	122.800576	102.543289
AT3G45650	143.3963916	1.939143618	0.36099731	5.37162905	7.80E-08	2.16E-06	47.0018232	87.2687592	43.5240399	167.33599	206.571511	308.676227
AT3G45940	34.86335776	2.910294039	0.46737586	6.22688139	4.76E-10	2.30E-08	8.35587968	6.08851808	10.1218697	57.8555284	72.347626	54.4107247
AT3G46080	30.18604814	-2.821505258	0.60703113	-4.6480404	3.35E-06	5.85E-05	64.7580675	33.4868494	60.7312185	14.2413608	4.75971223	3.13908027
AT3G46090	215.3232582	-1.272596722	0.3734622	-3.407565	0.00065545	0.00488216	447.039563	181.640789	285.436727	177.126925	107.569496	93.1260481
AT3G46210	352.2794085	-1.421297015	0.19090449	-7.4450684	9.69E-14	8.95E-12	511.79763	503.317495	524.312853	192.258371	220.850648	161.139454
AT3G46490	112.2894107	1.796766693	0.57643227	3.11704736	0.00182672	0.0110644	50.1352781	82.1949941	18.2193655	66.7563789	293.198274	163.232174
AT3G46870	289.8374317	-1.004189187	0.2157037	-4.6554101	3.23E-06	5.66E-05	448.084048	372.414356	340.094824	177.126925	226.562302	174.742135
AT3G46950	113.0033838	-1.265744947	0.27566933	-4.5915334	4.40E-06	7.44E-05	162.939654	158.30147	157.901168	64.9762088	84.7228778	49.1789243
AT3G47030	18.46081873	-2.854407831	0.63823708	-4.4723315	7.74E-06	0.00011952	34.4680037	20.2950603	42.5118529	4.45042526	3.80776979	5.23180045
AT3G47090	148.7786498	1.408674673	0.35388515	3.98059847	6.87E-05	0.00076684	97.1371013	99.4457953	47.5727878	185.137691	170.397698	292.980825
AT3G47640	321.1773028	1.289233498	0.25240333	5.10783071	3.26E-07	7.68E-06	134.73856	182.655542	241.912687	401.428358	469.307626	497.021043
AT3G47950	27.39544713	2.442816864	0.49124967	4.97265854	6.60E-07	1.43E-05	5.2224248	11.1622831	9.10968277	48.9546779	42.8374101	47.0862041
AT3G47960	2028.750353	1.162800068	0.20091996	5.78737955	7.15E-09	2.56E-07	1062.2412	1248.14621	1447.42737	2290.18884	2899.61669	3224.8818
AT3G48250	182.7233865	-1.819113917	0.25963811	-7.006344	2.45E-12	1.72E-10	247.542936	277.027573	329.972954	80.1076547	99.9539569	61.7352453
AT3G48260	15.75412445	2.050018878	0.67556511	3.03452451	0.00240915	0.0137189	3.13345488	11.1622831	4.0487479	26.7025516	18.0869065	31.3908027
AT3G48290	63.44871644	1.181673056	0.38684093	3.05467431	0.00225305	0.01301694	35.5124886	45.6638856	35.4265441	129.062333	62.8282015	72.1988462
AT3G48350	160.2760268	-1.093733772	0.35960132	-3.0415176	0.00235389	0.01346463	182.784868	183.670295	288.473288	139.743353	57.1165468	109.86781
AT3G48360	1540.787572	-5.797736377	1.14709441	-5.05428	4.32E-07	9.79E-06	4206.14093	3107.17373	1768.29065	129.062333	4.75971223	29.2980825
AT3G48390	368.7185703	-1.290719853	0.39454876	-3.2713824	0.00107023	0.00724051	585.956063	441.417561	543.544406	378.286147	121.848633	141.258612
AT3G48500	1461.038855	-2.03105169	0.27421673	-7.4067387	1.29E-13	1.17E-11	2093.14786	2412.06791	2537.55275	378.286147	816.766619	528.411846
AT3G48830	104.4940616	-2.146746184	0.25999188	-8.2569739	1.49E-16	2.24E-14	168.162079	171.493259	172.071786	42.7240825	39.0296403	33.4835229
AT3G49170	118.7630914	-1.119353973	0.2945975	-3.7996045	0.00014493	0.00141297	152.494804	158.30147	177.132721	56.9654433	102.809784	64.8743256
AT3G49180	401.9860279	-1.410121336	0.23411934	-6.0230879	1.71E-09	6.90E-08	622.513036	537.819097	592.12938	175.346755	288.438561	195.669337
AT3G49220	2746.977447	1.137584447	0.23170531	4.90961761	9.13E-07	1.88E-05	1346.34111	2004.1372	1799.66844	2916.80872	4598.83396	3816.07525
AT3G49240	616.0110076	-1.783602317	0.2012143	-8.8641926	7.71E-19	1.73E-16	832.454513	1045.1956	986.882301	276.816451	325.564317	229.15286
AT3G49260	2469.877077	1.020470371	0.24193926	4.21787829	2.47E-05	0.00032212	1422.58852	1793.06858	1677.19382	2248.35484	4052.419	3625.63771
AT3G49320	267.4946196	-3.395427405	0.27037958	-12.558002	3.59E-36	5.70E-33	570.288788	363.281579	532.410349	54.2951882	42.8374101	41.8544036
AT3G49410	63.13406543	-2.489216019	0.36959108	-6.7350543	1.64E-11	1.03E-09	82.5143119	108.578572	130.57212	18.6917861	23.7985612	14.6490413

Table S-5.1 Differentially Expressed Genes between lpa66 (LP) and wild type (WT) Arabidopsis plants.

ID	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	WT4	WT2	WT1	LP3	LP2	LP1
AT3G49740	35.34606427	-1.444864074	0.45537504	-3.1729101	0.00150919	0.00953486	41.7793984	41.6048736	71.8652752	20.4719562	23.7985612	12.5563211
AT3G49790	2092.202257	-1.340506108	0.33113273	-4.0482441	5.16E-05	0.00060659	3752.83446	2711.42005	2535.52837	1741.89645	640.657267	1170.87694
AT3G49900	89.75157801	1.106889491	0.40937167	2.70387418	0.00685362	0.03082754	47.0018232	63.9294399	59.7190315	64.0861238	186.58072	117.19233
AT3G50010	25.44566097	1.604966218	0.49342911	3.25267845	0.00114323	0.00763932	8.35587968	11.1622831	18.2193655	34.713317	45.6932374	34.529883
AT3G50040	41.8198531	-1.304645817	0.38916026	-3.3524642	0.00080096	0.00575642	48.0463082	54.7966627	75.9140231	28.4827217	23.7985612	19.8808417
AT3G50050	140.470048	1.128913476	0.27591354	4.09154799	4.29E-05	0.00051942	62.6690976	112.637585	89.0724538	185.137691	212.283166	181.020296
AT3G50310	34.0278988	-2.142445462	0.5515464	-3.8844338	0.00010257	0.00106724	39.6904285	46.6786386	79.962771	14.2413608	4.75971223	18.8344816
AT3G50340	372.6457694	1.096866879	0.32067184	3.42052765	0.000625	0.00470504	333.190702	235.422699	143.73055	382.736572	609.243166	531.550926
AT3G50700	903.3590021	-1.038924467	0.34548913	-3.0071119	0.00263743	0.01468916	1137.44412	1088.82998	1420.09833	973.753047	436.941583	363.086951
AT3G50825	88.78358805	-1.252505186	0.33518842	-3.7367198	0.00018644	0.00173415	156.672744	97.4162893	121.462437	58.7456134	62.8282015	35.5762431
AT3G50890	71.58100316	2.084464836	0.36665581	5.6850725	1.31E-08	4.42E-07	26.112124	36.5311085	19.2315525	85.448165	131.368058	130.795011
AT3G51220	48.00480811	1.412874061	0.44657983	3.16376597	0.00155742	0.0097626	15.6672744	36.5311085	26.3168613	44.5042526	87.5787051	77.4306467
AT3G51290	19.76156706	2.17971681	0.58332289	3.73672426	0.00018643	0.00173415	5.2224248	7.1032711	9.10968277	29.3728067	44.741295	23.019922
AT3G51325	24.35900483	-2.651807842	0.54517266	-4.8641615	1.15E-06	2.30E-05	51.179763	28.4130844	46.5606008	8.01076547	5.71165468	6.27816054
AT3G51330	470.719313	-1.881976611	0.36657002	-5.1340167	2.84E-07	6.82E-06	981.815863	490.125706	750.030548	309.749598	119.944748	172.649415
AT3G51660	481.9673778	1.021056622	0.29673007	3.44102849	0.00057951	0.00440968	279.921969	293.263621	381.59449	943.490155	469.307626	524.226405
AT3G52170	355.8617823	-1.139150804	0.30757756	-3.7036213	0.00021254	0.00193075	465.840292	565.217429	437.264773	141.523523	326.516259	198.808417
AT3G52310	60.66569081	1.746986349	0.50676307	3.44734341	0.00056613	0.00433184	16.7117594	20.2950603	46.5606008	145.973949	58.0684893	76.3842866
AT3G52460	44.22868688	-1.212340709	0.3619203	-3.349745	0.00080886	0.0057979	71.0249773	61.8999338	52.6337227	32.0430619	24.7505036	23.019922
AT3G52748	42.93173303	1.572030428	0.48062059	3.27083452	0.00107231	0.00724683	32.3790338	19.2803073	13.1584307	57.8555284	42.8374101	92.079688
AT3G53190	336.4419672	1.826355129	0.38674418	4.72238556	2.33E-06	4.29E-05	133.694075	205.994862	104.255258	279.486706	792.968058	502.252843
AT3G53220	51.27839188	-1.706009419	0.44030724	-3.8745886	0.0001068	0.00110408	88.7812216	44.6491326	102.230884	32.0430619	19.0388489	20.9272018
AT3G53250	9.655651515	3.71780979	0.97302352	3.82088377	0.00013297	0.00131971	2.08896992	1.01475301	1.01218697	24.0322964	16.1830216	13.6026812
AT3G53460	11397.84918	-1.424181987	0.32678364	-4.3581802	1.31E-05	0.00018696	11180.167	21280.3854	17361.031	3579.92208	8338.06389	6647.52566
AT3G53630	972.3924203	-1.540224231	0.14862252	-10.36333	3.64E-25	2.10E-22	1548.9712	1382.0936	1410.98864	528.710521	496.913957	466.6766
AT3G53940	113.3182956	-1.290576729	0.27706509	-4.6580272	3.19E-06	5.60E-05	178.606928	172.508012	131.584307	58.7456134	80.915108	57.549805
AT3G53980	78.47767969	4.996199621	0.48838233	10.2300991	1.45E-24	7.48E-22	3.13345488	5.07376507	6.07312185	173.566585	163.734101	119.28505
AT3G54000	58.72880943	1.325142351	0.38440533	3.44725279	0.00056632	0.00433184	38.6459435	42.6196266	19.2315525	67.646464	94.2423022	89.9869678
AT3G54030	591.9238167	1.112100829	0.16824881	6.60985843	3.85E-11	2.22E-09	358.258341	392.709416	372.484807	906.996668	731.091799	790.001868
AT3G54090	1747.685933	-2.401183918	0.18184442	-13.204606	8.25E-40	1.57E-36	3039.45123	2601.82673	3175.23054	463.734312	628.282015	577.59077
AT3G54260	81.37468408	1.740239416	0.28451585	6.11649379	9.57E-10	4.22E-08	31.3345488	43.6343796	37.4509181	121.941652	130.416115	123.470491
AT3G54400	1952.780888	1.632749278	0.339514	4.80907789	1.52E-06	2.92E-05	754.118141	987.354682	1115.43005	1656.44828	4618.82475	2584.50942
AT3G54780	47.18872623	1.072843925	0.35797695	2.99696373	0.00272683	0.01506804	32.3790338	35.5163555	23.2803004	53.4051031	69.4917986	69.059766
AT3G54830	191.7377011	-1.383377245	0.37878696	-3.6521248	0.00026008	0.00228301	245.453966	376.473368	209.522704	119.271397	54.2607195	145.444053
AT3G55240	1465.915297	2.741103697	0.28231483	9.70938618	2.75E-22	1.07E-19	426.149864	286.16035	432.203838	3574.58157	1880.08633	2196.30983
AT3G55510	528.1724798	-1.492688396	0.21610973	-6.9070854	4.95E-12	3.33E-10	684.137649	853.407284	800.639897	238.542794	347.458993	244.848261
AT3G55605	193.5035665	-1.610739156	0.25776488	-6.2488697	4.13E-10	2.01E-08	311.256518	271.953808	291.509849	79.2175696	127.560288	79.5233669
AT3G55940	71.16946464	2.036734583	0.39434546	5.16484852	2.41E-07	5.91E-06	21.9341842	26.3835784	35.4265441	153.984714	117.088921	72.1988462
AT3G55990	121.9257802	1.052588417	0.37565782	2.80198727	0.00507889	0.02446376	52.224248	99.4457953	86.0358929	97.9093557	175.15741	220.781979
AT3G56030	106.0288294	-1.321267965	0.3984142	-3.3163175	0.00091212	0.00638183	196.363173	132.932645	125.511185	97.9093557	44.741295	38.7153234
AT3G56070	1524.148931	-1.963721472	0.19446021	-10.09832	5.62E-24	2.61E-21	2647.76937	2281.16477	2350.29816	588.346219	762.5059	514.809165
AT3G56290	4577.510052	-1.479063892	0.22419234	-6.5972988	4.19E-11	2.40E-09	8986.7486	5538.52195	5688.4908	2336.47326	2277.99828	2636.82743
AT3G56330	224.0770472	-1.639869517	0.23844672	-6.8772994	6.10E-12	4.07E-10	280.966454	345.016025	391.716359	92.5688454	128.51223	105.682369
AT3G56400	5430.657072	-1.661005517	0.27010215	-6.1495457	7.77E-10	3.51E-08	8418.54878	9955.74182	6381.83888	3535.41783	1843.91252	2448.48261
AT3G56430	631.9947218	-1.041652861	0.1977822	-5.2666662	1.39E-07	3.63E-06	953.614769	795.566363	802.664271	334.67198	471.211511	434.239438
AT3G56570	69.59228502	-1.600756422	0.30264432	-5.2892333	1.23E-07	3.26E-06	97.1371013	106.549066	110.32838	30.2628918	41.8854677	31.3908027
AT3G56710	936.0044695	-1.429153623	0.26953501	-5.3022931	1.14E-07	3.07E-06	1368.2753	1645.92939	1081.01569	600.80741	335.083741	584.915291
AT3G56810	192.9557649	1.221083193	0.32984246	3.70201941	0.00021389	0.00194205	90.8701915	163.375235	93.1212017	183.357521	324.612374	302.398066
AT3G56825	45.76565541	-1.16907015	0.40178333	-2.909703	0.00361772	0.01885596	86.6922517	49.7228977	53.6459097	31.1529768	20.9427338	32.4371628
AT3G56890	33.06007169	-2.407630972	0.46886605	-5.1350082	2.82E-07	6.79E-06	62.6690976	39.5753675	64.7799664	13.3512758	8.56748202	9.41724082
AT3G56990	442.4199496	-1.358289322	0.22103931	-6.1450124	8.00E-10	3.58E-08	547.310119	774.256549	588.080632	222.521263	293.198274	229.15286
AT3G57000	858.6107198	-1.111259623	0.15839895	-7.0155743	2.29E-12	1.63E-10	1198.02425	1161.8922	1161.99065	534.051031	610.195108	485.511082
AT3G57010	44.62964238	1.285690425	0.44053631	2.91846643	0.00351758	0.0184416	29.2455789	32.4720964	16.1949916	48.0645928	89.48259	52.3180045
AT3G57020	2803.441227	-1.092403626	0.26834375	-4.0709114	4.68E-05	0.00055805	4084.98068	3578.01913	3787.60366	2240.34408	1075.69496	2054.00486
AT3G57150	1873.553256	-1.297022651	0.29406256	-4.410703	1.03E-05	0.00015245	2368.89189	3224.88508	2395.84657	706.727531	1580.22446	964.744003
AT3G57180	884.3364848	-1.236535487	0.17675503	-6.9957582	2.64E-12	1.85E-10	1140.57758	1316.13466	1268.27028	463.734312	614.002878	503.299204
AT3G57190	871.3422307	-1.314585674	0.20219554	-6.5015562	7.95E-11	4.36E-09	1500.92489	1066.50542	1161.99065	559.863498	504.529497	434.239438
AT3G57240	38.04339229	2.332222165	0.49478359	4.71362066	2.43E-06	4.45E-05	9.40036464	22.3245663	6.07312185	66.7563789	60.9243166	62.7816054
AT3G57360	23.45777068	-1.215340356	0.47889576	-2.5377973	0.01115526	0.04462123	34.4680037	28.4130844	35.4265441	15.1314459	9.51942447	17.7881215
AT3G57460	87.83711848	1.464138329	0.42348104	3.45738819	0.00054544	0.00418896	40.7349134	56.8261688	42.5118529	125.501992	64.7320864	196.715697
AT3G57520	6993.37285	-2.180357077	0.39098552	-5.5765673	2.45E-08	7.73E-07	11231.3468	8223.55842	14921.6604	4241.25527	1230.86158	2111.55466
AT3G57680	79.68099693	1.599712434	0.29009946	5.51435861	3.50E-08	1.06E-06	36.5569736	45.6638856	36.4387311	136.183013	112.329209	110.91417
AT3G57765	36.8677121	-1.18851467	0.37942807	-3.1323847	0.00173393	0.01060698	54.3132179	50.7376507	48.5849748	17.801701	25.7024461	24.0662821
AT3G57770	47.34954309	-1.737481352	0.42821851	-4.0574644	4.96E-05	0.00058603	98.1815863	48.7081447	71.8652752	29.3728067	17.134964	18.8344816
AT3G57780	344.5817564	1.017065355	0.30539971	3.33027615	0.0008676	0.00613574	225.608751	253.688253	204.461769	334.67198	690.158274	358.901511
AT3G58120	489.4343318	2.787432448	0.25553243	10.9083313	1.05E-27	8.01E-25	119.071285	161.345729	91.0968277	732.539998	1019.53036	813.02179
AT3G58520	61.39457841	-1.105920824	0.33841952	-3.2678991	0.00108349	0.00730684	83.5587968	67.9884519	100.206511	48.9546779	35.2218705	32.4371628
AT3G58660	929.1866587	-1.293238644	0.24581817	-5.2609564	1.43E-07	3.73E-06	1172.95661	1554.60162	1231.83155	411.219294	715.86072	488.650162
AT3G58700	1808.208933	-1.12965744	0.23812652	-4.7439381	2.10E-06	3.90E-05	2677.01495	2605.88574	2163.04357	817.988163	1479.31856	1106.00262
AT3G58850	170.7181963	2.048734275	0.24042372	8.5213485	1.58E-17	2.66E-15	56.4021878	67.9884519	74.9018361	248.33373	315.09295	261.590023
AT3G58865	43.06109044	1.243250426	0.42072088	2.95504808	0.0031262	0.01676381	21.9341842	20.2950603	34.4143571	41.8339974	77.1073382	62.7816054
AT3G59010	453.1238818	1.874132662	0.23050588	8.13051986	4.27E-16	6.12E-14	195.318688	234.407946	152.840233	591.016475	731.091799	814.06815
AT3G59220	36.59718626	1.954860229	0.49760228	3.9285596	8.55E-05	0.00092004	14.6227894	10.1475301	20.2437395	72.0968892	32.3660432	70.1061261
AT3G59290	575.5792306	1.000710232	0.25345419	3.9482883	7.87E-05	0.00085915	250.67639	461.712621	438.27696	750.341699	836.757411	715.710302
AT3G59480	14.07111365	2.694806837	0.71783338	3.75408403	0.00017398	0.00164309	4.17793984	5.07376507	2.02437395	19.5818711	19.0388489	34.529883
AT3G59680	57.03919107	1.548054283	0.4276589	3.61983412	0.00029479	0.00253625	33.4235187	39.5753675	14.1706176	64.0861238	89.48259	101.496929
AT3G59820	278.4223691	-1.565835451	0.24484134	-6.3953066	1.60E-10	8.17E-09	310.212033	471.860151	466.618195	128.172248	161.830216	131.841371
AT3G59890	256.0745108	-1.20748777	0.26988034	-4.4741598	7.67E-06	0.00011869	363.480766	364.296332	344.143571	104.139951	206.571511	153.814933
AT3G59900	124.4727437	2.144659487	0.41106391	5.21733833	1.82E-07	4.60E-06	64.7580675	42.6196266	30.3656092	107.700291	251.312806	250.080062
AT3G60290	638.8820479	1.000463514	0.2366395	4.227796	2.36E-05	0.00031124	488.818961	379.517627	408.923538	616.828941	914.816691	1024.38653
AT3G60330	23.07804746	-1.98218048	0.49466521	-4.0071152	6.15E-05	0.0006996	31.3345488	37.5458615	41.499666	8.01076547	8.56748202	11.509961

Table S-5.1 Differentially Expressed Genes between lpa66 (LP) and wild type (WT) Arabidopsis plants.

ID	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	WT4	WT2	WT1	LP3	LP2	LP1
AT3G60360	450.7203469	-1.585194413	0.19665779	-8.0606744	7.59E-16	1.02E-13	731.139472	685.973037	611.360933	206.499732	268.44777	200.901137
AT3G60390	448.5628098	1.010979463	0.18191338	5.55747716	2.74E-08	8.47E-07	332.146217	310.514422	250.010183	609.708261	576.877123	612.120653
AT3G60540	72.48027551	1.696787078	0.34881513	4.86443088	1.15E-06	2.30E-05	38.6459435	37.5458615	26.3168613	118.381312	79.0112231	134.980452
AT3G60900	14.56008355	2.008215329	0.78669839	2.55271316	0.01068875	0.04322144	4.17793984	10.1475301	3.03656092	8.90085052	38.0776979	23.019922
AT3G60960	244.0708189	-1.273127759	0.25477457	-4.9970755	5.82E-07	1.28E-05	360.347311	356.178308	319.851084	158.435139	172.301583	97.3114884
AT3G60965	190.0467166	1.230031879	0.27029082	4.55077199	5.34E-06	8.75E-05	78.336372	119.740856	142.718363	298.178492	262.736115	238.570101
AT3G60980	755.2303983	-1.027851827	0.23304278	-4.4105715	1.03E-05	0.00015245	1012.10593	996.487459	1032.43071	665.783619	442.653238	381.921433
AT3G61100	417.7127212	-2.402529782	0.19508387	-12.315369	7.49E-35	1.02E-31	744.717777	640.309152	722.7015	121.051567	156.118561	121.377771
AT3G61380	229.4540784	1.038851385	0.24881185	4.17524887	2.98E-05	0.00038019	130.56062	180.626036	139.681803	342.682745	344.603166	238.570101
AT3G61460	1448.490554	1.029610677	0.19720401	5.22104322	1.78E-07	4.51E-06	1181.31249	903.130182	773.310849	2046.30553	1940.05871	1846.82556
AT3G61520	151.30379	-1.09344357	0.26288962	-4.1593258	3.19E-05	0.00040223	178.606928	188.744061	251.02237	99.6895258	112.329209	77.4306467
AT3G61680	16.28368073	1.653183972	0.56309459	2.93589036	0.00332592	0.01761145	8.35587968	8.11802411	7.08530882	20.4719562	28.5582734	25.1126422
AT3G61780	711.7116935	-1.265644346	0.25167672	-5.0288494	4.93E-07	1.11E-05	881.545306	1077.6677	1056.7232	331.111639	576.877123	346.34519
AT3G61810	27.73244518	1.617494653	0.49561461	3.26361372	0.00110001	0.00739205	13.5783045	14.2065422	13.1584307	38.2736572	59.9723741	27.2053624
AT3G61820	1542.891673	1.698152051	0.28119851	6.0389796	1.55E-09	6.35E-08	590.134002	939.661291	650.836225	1541.62731	2871.05842	2664.03279
AT3G61920	16.47057806	-2.252656653	0.69743278	-3.2299265	0.00123822	0.00814819	22.9786691	24.3540723	34.4143571	3.56034021	11.4233094	2.09272018
AT3G61950	52.20713977	1.527188373	0.52854634	2.88941244	0.00385962	0.01986814	18.8007293	35.5163555	26.3168613	35.6034021	134.223885	62.7816054
AT3G62270	59.04728237	-1.613732597	0.40232967	-4.0109709	6.05E-05	0.00068993	94.0036464	64.9441929	108.304006	41.8339974	19.0388489	26.1590023
AT3G62550	4238.15863	-1.647809977	0.662644	-2.4867198	0.01289269	0.04987999	6846.59891	4836.31286	7594.43887	3822.9153	849.132663	1479.55317
AT3G62570	22.97308217	1.991946736	0.54939362	3.62571873	0.00028816	0.00248604	12.5338195	4.05901205	11.1340567	32.9331469	44.741295	32.4371628
AT3G62870	13011.83099	-1.144869276	0.20672738	-5.5380631	3.06E-08	9.34E-07	18315.0438	18515.1835	16928.8272	6146.92737	10136.2832	8028.72097
AT3G62890	31.28694577	-1.386400444	0.45208027	-3.066713	0.00216427	0.01267327	41.7793984	44.6491326	49.5971618	25.8124665	13.3271943	12.5563211
AT3G62950	956.55707	-1.008140756	0.30864393	-3.2663554	0.00108941	0.00733639	1498.83592	1062.44641	1272.31903	868.723011	357.93036	679.087699
AT3G63090	157.3907275	-1.203661399	0.2561369	-4.6992894	2.61E-06	4.75E-05	203.674567	235.422699	219.644574	93.4589305	119.944748	72.1988462
AT3G63200	886.6111888	1.003635334	0.26510564	3.78579396	0.00015322	0.00148106	564.021878	641.323905	564.800332	809.977397	1644.00461	1095.53901
AT3G63440	158.4409816	1.922938016	0.26499984	7.25637428	3.98E-13	3.29E-11	53.268733	75.091723	69.8409013	199.379052	278.919137	274.146344
AT3G63450	113.657131	2.141778839	0.44260563	4.83902305	1.30E-06	2.57E-05	41.7793984	55.8114157	28.3412353	87.2283351	274.159425	194.622977
AT3G63470	26.20745408	1.701074878	0.54952257	3.09555053	0.00196448	0.01175291	17.7562443	13.1917892	6.07312185	28.4827217	56.1646044	35.5762431
AT3G66652	257.4004463	-1.328270163	0.21783528	-6.0975897	1.08E-09	4.65E-08	349.902462	395.753675	359.326376	154.874799	169.445756	115.09961
AT4G00026	598.4078177	-1.223464821	0.20001823	-6.1167665	9.55E-10	4.22E-08	830.365543	853.407284	829.993319	297.288407	444.557123	334.835229
AT4G00390	43.44997643	-2.246952929	0.39999701	-5.6174243	1.94E-08	6.26E-07	79.380857	56.8261688	78.950584	11.5711057	16.1830216	17.7881215
AT4G00480	51.62919851	1.501003233	0.50864155	2.95100395	0.00316743	0.01695621	25.067639	40.5901205	15.1828046	41.8339974	118.040863	69.059766
AT4G00620	985.2864202	-2.035612402	0.21056748	-9.6672687	4.15E-22	1.55E-19	1658.64212	1386.15262	1708.57161	453.943377	409.335252	295.073546
AT4G00820	84.81791764	1.731393709	0.31816473	5.44181536	5.27E-08	1.52E-06	38.6459435	45.6638856	33.4021702	97.9093557	155.166619	138.119532
AT4G00970	2363.286792	1.102258939	0.31051275	3.54980255	0.00038552	0.00317063	1786.06928	1594.17698	1125.55192	3150.90108	1941.01065	4582.01084
AT4G01037	1866.258539	-2.390296592	0.17681904	-13.518322	1.22E-41	3.31E-38	3388.30921	2749.98067	3266.32737	677.354725	599.723741	515.855525
AT4G01060	32.6676382	1.343772738	0.47991213	2.80003912	0.00510964	0.02455437	24.0231541	21.3098133	10.1218697	40.0538273	62.8282015	37.6689633
AT4G01200	40.84393759	1.333410195	0.37133782	3.5908279	0.00032963	0.00278066	24.0231541	23.3393193	22.2681134	51.624933	70.4437411	53.3643646
AT4G01380	23.97718111	3.427373728	0.80147444	4.27633566	1.90E-05	0.00025901	3.13345488	3.04425904	6.07312185	90.7886753	20.9427338	19.8808417
AT4G01390	209.1248715	3.476429111	0.85293712	4.07583283	4.58E-05	0.00054889	37.6014586	28.4130844	37.4509181	841.130374	196.100144	114.05325
AT4G01430	17.90710943	-5.209861382	1.06008144	-4.914586	8.90E-07	1.84E-05	48.0463082	17.2508012	39.475292	2.67025516	0	0
AT4G01525	9.998182983	3.137102356	1.15227044	2.72254	0.00647822	0.02957941	1.04448496	2.02950603	3.03656092	2.67025516	42.8374101	8.37088072
AT4G01540	50.61700098	1.319504747	0.41819128	3.15526607	0.00160352	0.00996601	30.2900638	26.3835784	30.3656092	107.700291	61.876259	47.0862041
AT4G01580	42.92175442	1.833041052	0.70974839	2.5826632	0.0098041	0.04057008	22.9786691	21.3098133	12.1462437	12.4611907	134.223885	54.4107247
AT4G01660	812.8608065	-1.241271005	0.18075097	-6.8672992	6.54E-12	4.34E-10	1140.57758	1024.90054	1262.19716	472.635163	553.078562	423.775837
AT4G01670	226.0023381	-1.61998219	0.26639355	-6.0811615	1.19E-09	5.08E-08	376.014586	279.057079	368.436059	144.193778	84.7228778	103.589649
AT4G01680	105.4477406	1.678761586	0.27248763	6.16087267	7.23E-10	3.33E-08	59.5356427	48.7081447	42.5118529	177.126925	165.637986	139.165892
AT4G01895	53.45652859	-1.075716775	0.38696047	-2.7799139	0.00543733	0.02584362	65.8025525	55.8114157	96.1577626	45.3943377	31.4141007	26.1590023
AT4G01985	17.59469353	2.449407293	0.70461482	3.47623586	0.0005085	0.00395223	5.2224248	3.04425904	8.0974958	48.9546779	16.1830216	24.0662821
AT4G01990	149.1946911	-1.218439019	0.27044264	-4.5053511	6.63E-06	0.00010491	245.453966	183.670295	197.37646	96.1291856	106.617554	65.9206857
AT4G02290	30.11059825	3.327572233	0.78237131	4.25318798	2.11E-05	0.00028265	4.17793984	11.1622831	1.01218697	21.3620413	99.0020145	43.9471238
AT4G02330	1119.187419	2.144011534	0.2738113	7.83025206	4.87E-15	5.83E-13	458.528898	361.252073	419.045408	1360.04996	1488.83799	2627.41019
AT4G02790	2803.864786	-1.155483234	0.15814788	-7.3063465	2.75E-13	2.33E-11	3976.35424	3674.42066	3959.67545	1491.78255	1929.58734	1791.36848
AT4G02930	1935.546793	-1.532747579	0.19433767	-7.887033	3.09E-15	3.80E-13	2645.6804	2977.28534	3007.2075	804.636887	1213.72662	964.744003
AT4G02990	1601.374199	-1.372064016	0.19179757	-7.153709	8.45E-13	6.70E-11	2247.73163	2229.41237	2453.54123	769.033485	1108.06101	800.465469
AT4G03070	110.3099993	1.004102634	0.27760913	3.61696548	0.00029808	0.00255412	75.2029171	80.1654881	64.7799664	117.491227	180.869065	143.351332
AT4G03190	426.6240917	1.852284654	0.29897711	6.19540623	5.81E-10	2.75E-08	229.786691	210.053874	115.389315	518.919585	835.805468	649.789616
AT4G03210	1165.879166	1.750272978	0.3237968	5.40546711	6.46E-08	1.82E-06	371.836646	450.550338	780.396158	1437.48736	2502.65669	1452.34781
AT4G03270	48.42275866	1.865654405	0.47445854	3.93217581	8.42E-05	0.00090767	22.9786691	28.4130844	11.1340567	45.3943377	99.9539569	82.6624472
AT4G03330	11.16401488	3.940674787	1.05130599	3.74836141	0.00017799	0.00167489	1.04448496	3.04425904	0	9.79093557	34.2699281	18.8344816
AT4G03400	699.6274189	1.6451665	0.3207427	5.12924061	2.91E-07	6.97E-06	188.007293	322.691458	506.093487	974.643132	1196.59166	1009.73749
AT4G03610	60.72173528	-1.733845056	0.43542143	-3.9819929	6.83E-05	0.00076325	92.9591615	53.7819097	133.608681	36.4934871	27.606331	19.8808417
AT4G04020	16742.27202	-1.341755677	0.27132299	-4.9452339	7.61E-07	1.61E-05	29595.4813	19926.7049	22512.0505	13298.7608	8168.61814	6952.01644
AT4G04180	125.8188573	-1.344989478	0.26455645	-5.0839413	3.70E-07	8.55E-06	163.984139	184.685048	193.327712	73.8770593	85.6748202	53.3643646
AT4G04220	290.9566916	1.016496623	0.21269173	4.77920142	1.76E-06	3.34E-05	194.274203	224.260416	158.913355	404.098614	344.603166	419.590396
AT4G04293	32.3084633	2.197543684	0.69136705	3.17854847	0.00148014	0.00938329	10.4448496	8.11802411	16.1949916	110.370546	25.7024461	23.019922
AT4G04408	43.03314819	2.597557209	0.64344175	4.03697336	5.41E-05	0.00063334	4.17793984	13.1917892	19.2315525	135.292928	37.1257554	49.1789243
AT4G04409	35.24040883	2.070369731	0.67019393	3.08920989	0.0020069	0.01194234	4.17793984	13.1917892	23.2803004	97.9093557	24.7505036	48.1325642
AT4G04410	451.3695593	1.174294126	0.3821434	3.07291484	0.00211979	0.01245499	113.848861	391.694663	325.924206	726.309403	533.08777	617.352453
AT4G04420	16.61716678	2.704551309	0.79164072	3.41638733	0.00063458	0.00476774	2.08896992	10.1475301	1.01218697	39.1637423	19.0388489	28.2517224
AT4G04423	13.10929101	2.051988541	0.73496241	2.79196394	0.00523892	0.02506332	1.04448496	9.13277712	5.06093487	18.6917861	23.7985612	20.9272018
AT4G04745	43.96665875	2.060880136	0.46816394	4.40204801	1.07E-05	0.00015739	10.4448496	12.1770362	28.3412353	66.7563789	88.5306475	57.549805
AT4G04750	552.987626	1.065212939	0.23194367	4.59255011	4.38E-06	7.41E-05	428.238834	361.252073	283.412353	606.14792	883.402591	755.471985
AT4G04790	184.5855721	-1.116922267	0.23895975	-4.6741022	2.95E-06	5.24E-05	254.85433	239.481711	264.1808	131.732588	130.416115	86.8478875
AT4G04940	294.9541578	-1.37228499	0.2677915	-5.1244532	2.98E-07	7.11E-06	351.991432	508.39126	416.008847	121.051567	213.235108	159.046734
AT4G05170	106.7981502	1.449900087	0.45573536	3.18145181	0.00146539	0.00931457	51.179763	54.7966627	65.7921534	254.564325	63.7801439	150.675853
AT4G05410	400.0899448	-1.193203971	0.25936501	-4.6004817	4.22E-06	7.16E-05	511.79763	609.866561	548.60534	202.939392	337.939569	189.391176
AT4G06534	180.0956068	-1.207031952	0.29101394	-4.1476775	3.36E-05	0.00041886	214.119417	261.806278	278.351418	148.644204	76.1553957	101.496929
AT4G06536	109.5431975	-1.397441423	0.31940253	-4.3751733	1.21E-05	0.00017467	145.183409	172.508012	158.913355	81.8878248	38.0776979	60.6888853
AT4G06701	89.33673438	1.107382482	0.27216774	4.06875001	4.73E-05	0.00056228	61.6246126	54.7966627	53.6459097	127.282162	136.12777	102.543289
AT4G06746	200.6619384	-1.225348949	0.2893143	-4.2353556	2.28E-05	0.00030242	313.345488	254.703006	275.314857	150.424374	75.2034533	134.980452

Table S-5.1 Differentially Expressed Genes between lpa66 (LP) and wild type (WT) Arabidopsis plants.

ID	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	WT4	WT2	WT1	LP3	LP2	LP1
AT4G08040	167.7114135	1.269551951	0.29787024	4.26209725	2.03E-05	0.00027295	106.537466	62.9146868	125.511185	198.488967	262.736115	250.080062
AT4G08160	60.83663853	1.793107102	0.44593934	4.02096636	5.80E-05	0.00066891	18.8007293	39.5753675	23.2803004	56.9654433	133.271943	93.1260481
AT4G08210	13.13545879	-2.170068845	0.6411414	-3.3846962	0.00071257	0.00521574	22.9786691	19.2803073	22.2681134	5.34051031	4.75971223	4.18544036
AT4G08555	56.9986863	-1.203300224	0.40268412	-2.9881988	0.00280627	0.01540857	100.270556	66.9736989	70.8530882	24.9223815	26.6543885	52.3180045
AT4G08590	95.88191377	1.123377877	0.26956764	4.16733212	3.08E-05	0.00039048	58.4911578	57.8409218	64.7799664	138.853268	147.551079	107.775089
AT4G08910	16.50109599	2.225292408	0.75081668	2.96382922	0.00303837	0.0164084	5.2224248	4.05901205	8.0974958	9.79093557	24.7505036	47.0862041
AT4G09080	11.72536917	-1.740746005	0.68355082	-2.5466227	0.0108771	0.04378216	15.6672744	24.3540723	14.1706176	7.12068042	3.80776979	5.23180045
AT4G09160	403.1978026	1.241315735	0.21109218	5.88044408	4.09E-09	1.55E-07	252.76536	257.747265	208.510517	463.734312	657.792231	578.63713
AT4G09420	104.6626611	1.007951055	0.25672084	3.92625339	8.63E-05	0.00092767	60.5801277	63.9294399	84.0115189	143.303693	138.031655	138.119532
AT4G09730	2964.783262	-1.433613449	0.16428888	-8.7261748	2.63E-18	5.01E-16	4187.34021	4148.31032	4646.9504	1465.97008	1865.8072	1474.32137
AT4G09760	3038.925692	-1.015490187	0.32107462	-3.1627856	0.00156267	0.00977943	3814.45907	4064.08582	4321.0262	3165.14245	1163.27367	1705.56695
AT4G09890	529.9629494	1.026687003	0.26348237	3.89660604	9.76E-05	0.00102511	480.463082	328.779976	237.863939	756.572294	694.917986	681.180419
AT4G09990	25.59193773	1.942377741	0.5559354	3.49389109	0.00047604	0.00375131	7.31139472	18.2655542	6.07312185	30.2628918	46.6451799	44.9934839
AT4G10290	13.80270183	6.215426586	1.33899986	4.64184258	3.45E-06	6.02E-05	0	0	1.01218697	32.0430619	15.2310791	34.529883
AT4G10310	18.16949362	1.634769176	0.54260121	3.01283731	0.00258818	0.01446566	8.35587968	9.13277712	9.10968277	32.9331469	28.5582734	20.9272018
AT4G10380	92.72883741	-1.065544387	0.36697331	-2.9036019	0.00368897	0.0191398	128.47165	114.667091	133.608681	89.8985903	34.2699281	55.4570848
AT4G10420	28.21514472	1.69872869	0.51792735	3.27985903	0.00103859	0.00707204	9.40036464	17.2508012	13.1584307	26.7025516	60.9243166	41.8544036
AT4G10450	1762.189234	-1.309447603	0.23067847	-5.6765056	1.37E-08	4.61E-07	2727.15023	2550.07432	2256.16477	761.02272	1331.76748	946.955882
AT4G10620	272.2818199	-1.022361334	0.24256313	-4.2148258	2.50E-05	0.00032584	348.857977	393.724169	352.241067	152.204544	237.033669	149.629493
AT4G10650	23.45193667	-1.684252804	0.51305948	-3.2827633	0.00102795	0.00701682	33.4235187	25.3688253	48.5849748	13.3512758	9.51942447	10.4636009
AT4G11060	304.7756332	-1.126165473	0.20947764	-5.3760653	7.61E-08	2.11E-06	473.151687	362.266826	419.045408	195.818711	215.138993	163.232174
AT4G11211	359.3646399	1.024142747	0.23138034	4.4262306	9.59E-06	0.00014313	257.987785	229.334181	223.693321	616.828941	394.104173	434.239438
AT4G11470	176.9388673	1.088764819	0.37665492	2.89061619	0.00384487	0.01980292	127.427165	131.917892	79.962771	170.006245	170.397698	381.921433
AT4G11630	1043.906755	-1.133659089	0.14403389	-7.8707801	3.52E-15	4.27E-13	1496.74695	1330.3412	1475.76861	674.684469	665.40777	620.491534
AT4G11690	21.93034771	-1.390378072	0.49417589	-2.8135287	0.0049001	0.02382857	35.5124886	27.3983314	32.3899832	10.6810206	16.1830216	9.41724082
AT4G12240	95.00881855	-1.274618289	0.25507404	-4.9970521	5.82E-07	1.28E-05	137.872015	121.770362	143.73055	54.2951882	59.0204317	53.3643646
AT4G12480	13.685558	-2.363402875	0.68241416	-3.463297	0.0005336	0.00411827	30.2900638	23.3393193	15.1828046	4.45042526	5.71165468	3.13908027
AT4G12600	2565.843684	-1.891473983	0.22182426	-8.526903	1.50E-17	2.55E-15	4305.36701	3948.40398	3872.62737	827.779098	1426.96173	1013.92293
AT4G12750	268.7219801	-1.590282613	0.30900124	-5.146525	2.65E-07	6.43E-06	259.03227	452.579844	499.008179	141.523523	161.830216	98.3578485
AT4G13170	2125.045387	-1.018042641	0.20999325	-4.847978	1.25E-06	2.46E-05	3267.14896	2706.34629	2561.84523	1108.15589	1718.25612	1388.51984
AT4G13370	53.90180515	1.024714652	0.40855225	2.5081606	0.01213615	0.04759181	36.5569736	41.6048736	28.3412353	43.6141676	99.0020145	74.2915664
AT4G13395	168.324212	1.403038962	0.46242809	3.03406949	0.00241279	0.0137355	49.0907931	62.9146868	164.986477	267.025516	144.695252	321.232548
AT4G13560	79.0856402	1.201207282	0.37725658	3.18405916	0.00145225	0.00924961	25.067639	58.8556748	59.7190315	93.4589305	106.617554	130.795011
AT4G13564	27.93724026	1.729414924	0.46276092	3.73716719	0.00018611	0.00173415	13.5783045	11.1622831	14.1706176	54.2951882	40.9335252	33.4835229
AT4G13570	309.251466	1.066934812	0.26695027	3.99675499	6.42E-05	0.000724	159.806199	225.275169	214.583639	557.193243	340.795396	357.855151
AT4G13750	253.5338138	-1.059661515	0.29624676	-3.5769556	0.00034762	0.002905	257.987785	430.255278	340.094824	176.23684	204.667626	111.96053
AT4G13850	2545.678907	-1.595650063	0.16497708	-9.6719499	3.97E-22	1.51E-19	3976.35424	3499.88314	4001.17511	1338.68792	1381.26849	1076.70453
AT4G14130	54.70866911	3.13480596	0.63040477	4.97268755	6.60E-07	1.43E-05	3.13345488	8.11802411	22.2681134	148.644204	99.0020145	47.0862041
AT4G14200	93.52789606	1.821825158	0.40400806	4.50937827	6.50E-06	0.00010311	34.4680037	55.8114157	33.4021702	90.7886753	217.99482	128.702291
AT4G14430	728.9823043	-1.586135233	0.2650798	-5.9836142	2.18E-09	8.65E-08	1365.14184	941.690797	974.736057	488.656694	275.111367	328.557068
AT4G14550	220.8733218	1.107074254	0.25494008	4.34248803	1.41E-05	0.00019889	152.494804	170.478506	97.1699496	285.717302	296.054101	323.325268
AT4G14690	5213.087151	-3.051274035	0.25437149	-11.995346	3.76E-33	3.97E-30	11313.8611	7934.35381	8662.29613	862.492415	975.741008	1529.77845
AT4G14750	122.962661	2.01935383	0.31284674	6.45477027	1.08E-10	5.81E-09	29.2455789	60.8851808	55.6702836	173.566585	201.811799	216.596539
AT4G14820	40.74001521	-1.712504666	0.42501339	-4.0292958	5.59E-05	0.00065078	66.8470374	47.6933916	72.8774622	25.8124665	12.3752518	18.8344816
AT4G14860	35.91592195	-1.066852546	0.42531367	-2.50839	0.01212827	0.04758243	60.5801277	51.7524037	33.4021702	20.4719562	19.9907914	29.2980825
AT4G15000	8250.704836	-1.010648036	0.27317009	-3.6997025	0.00021585	0.00195521	12570.3765	11298.2601	9214.95022	3417.03651	7200.49267	5803.11306
AT4G15248	131.9265417	2.044092699	0.30610957	6.67765043	2.43E-11	1.46E-09	44.9128533	39.5753675	69.8409013	175.346755	206.571511	255.311862
AT4G15500	147.6093411	1.440930684	0.36366462	3.96225148	7.42E-05	0.00081864	108.626436	85.2392531	44.5362269	150.424374	255.120576	241.709181
AT4G15640	553.8388752	-1.584696344	0.20950375	-7.5640478	3.91E-14	3.85E-12	902.435006	728.592664	861.371116	255.45441	340.795396	234.38466
AT4G15660	23.75733512	-2.313171185	0.82867007	-2.791426	0.00524764	0.0250924	4.17793984	45.6638856	68.8287143	9.79093557	5.71165468	8.37088072
AT4G15690	57.98687913	-1.970634799	0.46436951	-4.2436782	2.20E-05	0.00029202	44.9128533	114.667091	117.413689	16.0215309	26.6543885	28.2517224
AT4G15770	1199.878688	-1.843877762	0.20217076	-9.120398	7.48E-20	1.99E-17	2137.01623	1777.84728	1715.65692	428.13091	632.089785	508.531004
AT4G15850	115.0615046	-1.429267717	0.27334652	-5.228776	1.71E-07	4.34E-06	170.251049	167.434247	165.998664	59.6356985	79.9631655	47.0862041
AT4G15910	109.6182863	-1.21326263	0.29767539	-4.0757908	4.59E-05	0.00054889	154.583774	130.903139	174.09616	55.1852732	88.5306475	54.4107247
AT4G16000	509.234121	-1.485228991	0.44138965	-3.3648931	0.00076573	0.00554094	706.071833	694.091061	851.249246	427.240825	83.7709353	292.980825
AT4G16515	108.5140834	1.489723081	0.32419625	4.59512736	4.32E-06	7.32E-05	54.3132179	80.1654881	36.4387311	143.303693	169.445756	167.417614
AT4G16590	30.38666398	8.333684575	1.29438762	6.4383222	1.21E-10	6.37E-09	0	0	0	34.713317	94.2423022	53.3643646
AT4G16630	791.6648303	-1.345112088	0.28672189	-4.6913478	2.71E-06	4.91E-05	941.080949	1401.37391	1065.83288	318.650449	635.897554	387.153234
AT4G16690	1306.895337	-1.648524111	0.19153339	-8.6069802	7.50E-18	1.36E-15	2266.53236	1708.84407	1969.71585	689.815915	527.376116	679.087699
AT4G16700	88.03577764	-1.642412959	0.32738995	-5.0166871	5.26E-07	1.17E-05	120.11577	166.419494	113.364941	31.1529768	54.2607195	42.9007637
AT4G16720	10596.26374	-1.036868976	0.23978726	-4.3241204	1.53E-05	0.00021383	15638.0288	14765.6711	12340.5836	4866.98506	8978.72116	6987.59268
AT4G16740	33.13210709	3.135006012	0.82287362	3.80982685	0.00013906	0.00136913	1.04448496	3.04425904	16.1949916	103.249866	21.8946763	53.3643646
AT4G16780	576.8098091	1.312685205	0.35091708	3.74072765	0.00018349	0.00171427	451.217503	340.957013	201.425208	1210.51567	600.675684	656.067777
AT4G16835	43.84101797	-1.108181679	0.39113698	-2.8332317	0.004608	0.0227007	53.268733	51.7524037	74.9018361	36.4934871	25.7024461	20.9272018
AT4G16870	885.1632826	1.285514054	0.39478434	3.25624379	0.00112897	0.00755198	208.896992	748.887724	587.068445	1569.21995	932.903598	1264.00299
AT4G16910	24.26342249	1.414327576	0.5348094	2.64454507	0.00818008	0.03530048	5.2224248	17.2508012	17.2071786	37.3835722	37.1257554	31.3908027
AT4G17030	512.7413467	1.760149482	0.1968965	8.93946557	3.91E-19	9.19E-17	194.274203	280.071832	226.729882	752.121869	851.036547	772.213747
AT4G17460	797.5961092	1.735421686	0.2398681	7.23489989	4.66E-13	3.82E-11	503.441751	302.396398	299.607345	1233.65788	1138.52317	1307.95011
AT4G17483	36.5016504	-1.68667972	0.43800844	-3.8507927	0.00011774	0.00119692	62.6690976	47.6933916	56.6824706	20.4719562	9.51942447	21.9735619
AT4G17670	173.992716	1.707254362	0.33625748	5.07722352	3.83E-07	8.79E-06	122.20474	59.8704278	62.7555924	202.939392	318.90072	277.285424
AT4G17680	97.14374394	1.375188494	0.30381548	4.52639372	6.00E-06	9.64E-05	66.8470374	53.7819097	41.499666	127.282162	121.848633	171.603055
AT4G18100	8465.136985	-1.06016405	0.26910413	-3.9396053	8.16E-05	0.00088453	12305.0773	11780.2677	10242.32	3484.68298	7559.37497	5419.09891
AT4G18170	256.3524186	-1.68366888	0.37685527	-4.4676803	7.91E-06	0.00012175	476.285142	239.481711	457.508513	181.577351	72.347626	110.91417
AT4G18290	150.1447585	1.118055091	0.2588862	4.31871266	1.57E-05	0.00021817	72.0694622	109.593325	102.230884	178.01701	205.619568	233.3383
AT4G18340	291.1467631	-1.162368533	0.41096608	-2.8283807	0.00467841	0.02299455	495.085871	331.824235	380.582303	256.344495	68.5398562	214.503819
AT4G18590	711.9267064	-1.040990383	0.16940874	-6.1448445	8.00E-10	3.58E-08	1067.46363	869.643333	937.285139	423.680485	502.625612	470.862041
AT4G18670	1395.91538	1.401363318	0.17598831	7.96282025	1.68E-15	2.12E-13	688.315589	857.466297	754.079296	1801.53215	2313.22015	1960.87881
AT4G18730	6298.858859	-1.019269707	0.24433265	-4.1716475	3.02E-05	0.00038537	9199.82353	8509.71877	7597.47543	2804.658	5364.19569	4317.28173
AT4G18750	69.5292934	-1.408416218	0.32039622	-4.3958578	1.10E-05	0.00016103	103.404011	78.135982	121.462437	34.713317	42.8374101	36.6226032
AT4G18780	140.5211961	1.323879967	0.40287374	3.28609146	0.00101588	0.0069569	42.8238834	120.755609	76.9262101	129.952418	256.072518	216.596539
AT4G18840	53.24882851	-1.960117436	0.39181416	-5.0026713	5.65E-07	1.25E-05	72.0694622	79.1507351	103.243071	31.1529768	17.134964	16.7417614

Table S-5.1 Differentially Expressed Genes between lpa66 (LP) and wild type (WT) Arabidopsis plants.

ID	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	WT4	WT2	WT1	LP3	LP2	LP1
AT4G18905	1011.527174	-1.074651935	0.16681676	-6.4421101	1.18E-10	6.23E-09	1391.25397	1402.38866	1321.91619	622.169451	754.89036	576.54441
AT4G18970	2231.746882	2.023011502	0.38279565	5.28483403	1.26E-07	3.33E-06	746.806747	1339.47398	557.715023	1912.79278	5050.05468	3783.63809
AT4G19000	10.75108294	2.406359216	0.78523475	3.06450932	0.00218027	0.01274349	4.17793984	3.04425904	3.03656092	15.1314459	27.606331	11.509961
AT4G19191	44.80319102	-1.32978623	0.34458508	-3.8590941	0.00011381	0.00116445	62.6690976	59.8704278	69.8409013	25.8124665	27.606331	23.019922
AT4G19230	51.37451303	1.898277811	0.48002405	3.95454728	7.67E-05	0.00084061	12.5338195	17.2508012	35.4265441	115.711057	66.6359713	60.6888853
AT4G19380	177.571439	1.186996646	0.38103405	3.11519838	0.00183821	0.01112664	126.38268	118.726103	79.962771	125.501992	352.218705	262.636383
AT4G19390	373.7557881	-1.14206097	0.24837965	-4.5980457	4.26E-06	7.23E-05	453.306473	454.60935	635.65342	292.837982	188.484604	217.642899
AT4G19810	63.71272457	1.533000927	0.48886471	3.13583883	0.00171363	0.01050649	25.067639	47.6933916	25.3046744	41.8339974	130.416115	111.96053
AT4G20000	37.55933396	1.712856759	0.66160686	2.5889344	0.00962734	0.03998646	32.3790338	13.1917892	7.08530882	35.6034021	31.4141007	105.682369
AT4G20010	1228.349199	-1.085515903	0.17226616	-6.3013879	2.95E-10	1.46E-08	1703.55497	1669.26871	1636.70634	874.063521	647.320864	839.180793
AT4G20020	857.6472663	-1.371018188	0.18524943	-7.4009305	1.35E-13	1.21E-11	1155.20037	1308.01663	1248.02654	437.031761	575.92518	421.683116
AT4G20090	171.8767439	-1.200468986	0.24899602	-4.8212376	1.43E-06	2.77E-05	221.430812	232.37844	265.192987	113.930887	120.896691	77.4306467
AT4G20130	2082.378258	-1.11594976	0.21445591	-5.2036326	1.95E-07	4.91E-06	2730.28369	2760.1282	3058.82904	979.093557	1640.19684	1325.73823
AT4G20140	54.06894959	1.053041806	0.39919297	2.63792671	0.00834146	0.03581822	32.3790338	40.5901205	32.3899832	42.7240825	89.48259	86.8478875
AT4G20230	20.52756952	1.52476416	0.58326908	2.61416935	0.00894447	0.03772165	11.4893346	12.1770362	8.0974958	18.6917861	47.5971223	25.1126422
AT4G20940	268.4262286	1.071388312	0.40482021	2.64657812	0.00813107	0.03514477	176.517958	230.348934	112.352754	180.687266	555.934389	354.716071
AT4G21120	31.08832086	1.684211189	0.56773367	2.96655152	0.0030116	0.0163194	21.9341842	12.1770362	10.1218697	39.1637423	25.7024461	77.4306467
AT4G21140	294.3712008	-1.71762352	0.21672115	-7.9255001	2.27E-15	2.83E-13	490.907931	425.181513	438.27696	115.711057	168.493813	127.655931
AT4G21220	65.08736797	-1.297689845	0.32315356	-4.0157065	5.93E-05	0.00068014	103.404011	70.0179579	104.255258	37.3835722	40.9335252	34.529883
AT4G21400	196.7678492	1.275007474	0.28618857	4.45513062	8.38E-06	0.00012755	114.893346	144.094928	86.0358929	234.982454	242.745324	357.855151
AT4G21520	232.4642856	-1.692965958	0.2114259	-8.0073725	1.17E-15	1.52E-13	365.569736	331.824235	368.436059	122.831737	116.136979	89.9869678
AT4G21650	704.5009211	2.089830657	0.26753005	7.81157352	5.65E-15	6.59E-13	178.606928	342.986519	282.400166	1165.12133	1330.81554	927.07504
AT4G21760	203.3774042	1.030599703	0.26777552	3.84874507	0.00011872	0.00120568	170.251049	97.4162893	133.608681	305.299173	285.582734	228.1065
AT4G21870	500.116785	1.016998441	0.38833863	2.6188444	0.00882282	0.03732927	447.039563	266.880043	278.351418	294.618152	855.79626	858.015274
AT4G21960	33197.03517	1.335819783	0.13228025	10.098407	5.61E-24	2.61E-21	19743.8992	19298.5728	17476.4203	50178.5448	47651.3831	44833.3908
AT4G21990	1573.710734	1.602423611	0.31850245	5.03111856	4.88E-07	1.10E-05	612.068187	526.656814	1200.45375	2263.48629	2941.50216	1898.0972
AT4G22010	1481.690704	1.25980564	0.32693759	3.85335203	0.00011651	0.00118828	773.963355	1024.90054	819.87145	1107.2658	3045.26389	2118.87918
AT4G22270	59.33747251	1.149727362	0.38688099	2.9717856	0.00296073	0.01608499	34.4680037	44.6491326	31.3777962	50.734848	103.761727	91.0333279
AT4G22380	593.9394989	-1.145355101	0.21266246	-5.3857888	7.21E-08	2.01E-06	921.235735	668.722236	864.407677	346.243085	440.749353	322.278908
AT4G22390	21.54809653	-1.317701176	0.5265067	-2.5027244	0.01232415	0.04814618	28.2010939	38.5606145	25.3046744	8.01076547	11.4233094	17.7881215
AT4G22470	61.16050397	1.199036936	0.39196545	3.05903733	0.00222049	0.01290648	25.067639	31.4573434	54.6580966	75.6572294	72.347626	107.775089
AT4G22545	19.77563364	2.352060446	0.57614398	4.08241779	4.46E-05	0.00053616	6.26690976	7.1032711	6.07312185	41.8339974	22.8466187	34.529883
AT4G22620	152.2014698	-1.249247202	0.39426291	-3.1685638	0.00153194	0.00964776	182.784868	175.552271	284.42454	116.601142	41.8854677	111.96053
AT4G22780	463.3586683	1.005144397	0.23660788	4.24814415	2.16E-05	0.00028749	268.432635	349.075037	306.692653	578.555284	487.394533	790.001868
AT4G22840	238.9044723	1.342520298	0.24908453	5.389818	7.05E-08	1.97E-06	174.428988	130.903139	100.206511	362.264616	315.09295	350.53063
AT4G23130	189.3108354	1.634047267	0.32950738	4.95906124	7.08E-07	1.52E-05	108.626436	105.534313	62.7555924	384.516743	196.100144	278.331784
AT4G23140	130.6738213	3.357692616	0.43178987	7.77621908	7.47E-15	8.57E-13	25.067639	36.5311085	8.0974958	247.443644	177.061295	289.841745
AT4G23210	76.13928565	1.100356473	0.27039953	4.06937271	4.71E-05	0.0005614	45.9573382	51.7524037	47.5727878	103.249866	104.713669	103.589649
AT4G23215	99.15630292	1.512802195	0.45612719	3.31662355	0.00091112	0.00637719	42.8238834	57.8409218	53.6459097	176.23684	56.1646044	208.225658
AT4G23220	803.2917179	1.957545443	0.34873216	5.61332074	1.98E-08	6.39E-07	351.991432	451.565091	183.205842	1102.81538	936.711368	1793.4612
AT4G23230	71.1020959	1.674560134	0.43612237	3.83965662	0.00012321	0.0012439	49.0907931	39.5753675	13.1584307	111.260632	94.2423022	119.28505
AT4G23620	399.5954628	-1.174647887	0.2275857	-5.1613432	2.45E-07	6.01E-06	641.313766	492.155212	528.361601	232.312199	304.621583	198.808417
AT4G23800	173.4540962	1.118408383	0.40237359	2.77952732	0.00544381	0.02585927	89.8257066	131.917892	106.279632	104.139951	331.275971	277.285424
AT4G23820	2709.802628	1.234481623	0.23369507	5.28244605	1.27E-07	3.37E-06	1347.3856	1745.37518	1756.1444	2866.07387	4902.5036	3641.33312
AT4G24050	181.7912518	-1.155422408	0.29509659	-3.9154042	9.03E-05	0.00096332	309.167548	256.732512	187.25459	147.754119	90.4345324	99.4042086
AT4G24175	169.4466512	-1.430690524	0.24731827	-5.7848153	7.26E-09	2.59E-07	254.85433	205.994862	280.375792	74.7671444	97.0981296	103.589649
AT4G24180	32.71092723	-1.153573821	0.4433255	-2.6020922	0.00926569	0.03878914	59.5356427	44.6491326	31.3777962	24.9223815	19.0388489	16.7417614
AT4G24230	2784.757262	-1.261763421	0.27026354	-4.668641	3.03E-06	5.36E-05	5056.35169	3161.97039	3573.02002	2021.38315	1112.82072	1782.99759
AT4G24275	73.25211138	2.434168158	0.40514981	6.00806933	1.88E-09	7.51E-08	21.9341842	33.4868494	13.1584307	88.1184202	144.695252	138.119532
AT4G24415	46.18601737	1.056254571	0.34539797	3.05807982	0.0022276	0.0129091	25.067639	35.5163555	29.3534223	57.8555284	67.5879137	61.7352453
AT4G24780	4016.213771	1.08228361	0.29643167	3.65103905	0.00026118	0.00229163	3321.46217	2981.34435	1427.18363	4652.47457	5846.83051	5867.98739
AT4G25260	329.4665586	1.064634441	0.22137299	4.80923365	1.52E-06	2.92E-05	192.185233	223.245663	223.693321	345.353	502.625612	489.696522
AT4G25470	45.09442516	1.768522103	0.49336736	3.58459487	0.0003376	0.00283285	21.9341842	21.3098133	18.2193655	63.1960387	111.377266	34.529883
AT4G25480	34.41840565	1.800692737	0.45461574	3.96091156	7.47E-05	0.00082182	17.7562443	14.2065422	14.1706176	53.4051031	71.3956835	35.5762431
AT4G25490	30.60850069	2.374706558	0.54442608	4.36185304	1.29E-05	0.0001844	11.4893346	8.11802411	10.1218697	43.6141676	79.9631655	30.3444426
AT4G25630	785.7696009	-1.721824609	0.38297438	-4.4959263	6.93E-06	0.00010885	1121.77685	1524.15903	971.699496	170.89633	590.204317	335.881589
AT4G25730	1515.851672	-1.269128957	0.24167252	-5.2514409	1.51E-07	3.89E-06	1774.57995	2573.41364	2080.04423	729.869743	1167.08144	770.121027
AT4G25835	188.54324	-1.054361171	0.2914266	-3.6179304	0.00029697	0.00255036	327.968277	251.658747	184.218029	151.314459	99.9539569	116.14597
AT4G25850	11.45822484	-2.16194126	0.74007507	-2.9212459	0.00348635	0.01830812	12.5338195	23.3393193	20.2437395	4.45042526	1.90388489	6.27816054
AT4G25990	156.1157253	-2.086685934	0.31201267	-6.6878243	2.27E-11	1.38E-09	215.163902	265.86529	277.339231	49.8447629	86.6267627	41.8544036
AT4G26110	2758.95677	-1.102298693	0.15299274	-7.2049084	5.81E-13	4.68E-11	3881.30611	3665.28789	3747.11618	1650.21769	2005.74274	1604.07002
AT4G26150	420.2628701	-1.580688583	0.30857028	-5.1226209	3.01E-07	7.17E-06	734.272927	495.199471	660.958095	310.639683	176.109353	144.397692
AT4G26260	31.58264735	-4.793466014	0.78434739	-6.1114068	9.88E-10	4.33E-08	91.9146765	38.5606145	52.6337227	5.34051031	0	1.04636009
AT4G26590	58.9061159	1.336178382	0.36995564	3.61172596	0.00030417	0.00259694	30.2900638	47.6933916	22.2681134	89.8985903	73.2995684	89.9869678
AT4G26600	323.3190925	-1.317814193	0.25156265	-5.2385129	1.62E-07	4.15E-06	382.281495	551.010886	451.435391	173.566585	235.129784	146.490413
AT4G26760	263.3408985	1.844197524	0.37849118	4.87249804	1.10E-06	2.22E-05	119.071285	146.124434	78.950584	218.960923	602.579569	414.358596
AT4G26780	624.2046409	-1.869774687	0.21337929	-8.7626814	1.91E-18	3.86E-16	1083.1309	932.55802	925.138895	238.542794	339.843453	226.01378
AT4G26800	38.20465567	-1.276368607	0.45997854	-2.7748438	0.00552282	0.02609798	45.9573382	51.7524037	64.7799664	25.8124665	30.4621583	10.4636009
AT4G27010	319.6490137	-2.276709961	0.25777923	-8.8320146	1.03E-18	2.22E-16	368.703191	593.630513	627.555924	110.370546	116.136979	101.496929
AT4G27260	268.2507795	1.374559584	0.35868955	3.8321707	0.00012702	0.00127426	174.428988	154.242458	119.438063	574.994944	206.571511	379.828713
AT4G27280	1748.619285	-1.307790018	0.23389782	-5.5912878	2.25E-08	7.17E-07	2744.90648	1915.85369	2812.8676	1132.18819	1125.19597	760.703786
AT4G27340	730.0480385	-1.404108011	0.19343183	-7.2589294	3.90E-13	3.24E-11	897.212581	1026.93005	1255.11185	441.482186	370.305612	389.245954
AT4G27490	269.3342832	-1.256594821	0.20637091	-6.0890115	1.14E-09	4.86E-08	420.927439	370.38485	348.192319	156.654969	182.77295	137.073172
AT4G27654	21.59201004	2.901148046	0.62030789	4.67694848	2.91E-06	5.18E-05	2.08896992	5.07376507	8.0974958	48.0645928	28.5582734	37.6689633
AT4G27657	136.0776999	1.05424386	0.25855766	4.07740335	4.55E-05	0.00054612	101.315041	78.135982	86.0358929	168.226075	223.706475	159.046734
AT4G27730	245.7766208	1.408742665	0.2296852	6.13336273	8.60E-10	3.83E-08	100.270556	155.257211	147.779298	340.902575	378.873094	351.57699
AT4G27900	452.4617421	1.192814865	0.18022818	6.61835953	3.63E-11	2.12E-09	279.921969	247.599735	298.595158	571.434603	697.773813	619.445174
AT4G28070	71.0499703	1.08759437	0.30521922	3.563322	0.00036619	0.0030419	53.268733	47.6933916	35.4265441	84.5580799	102.809784	102.543289
AT4G28250	210.9136618	2.341270811	0.38316562	6.1103363	9.94E-10	4.35E-08	56.4021878	96.4015363	55.6702836	189.588116	495.962015	371.457832
AT4G28450	603.4182605	-1.536612836	0.22387493	-6.8637111	6.71E-12	4.43E-10	846.032818	927.484254	919.065773	266.135431	406.479425	255.311862
AT4G28510	1093.786796	-1.767689183	0.22036357	-8.0216941	1.04E-15	1.37E-13	1852.91632	1469.36236	1751.08347	625.729792	386.488633	477.140201

Table S-5.1 Differentially Expressed Genes between lpa66 (LP) and wild type (WT) Arabidopsis plants.

ID	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	WT4	WT2	WT1	LP3	LP2	LP1
AT4G28780	1477.307519	1.606516962	0.30272881	5.3067859	1.12E-07	3.00E-06	509.708661	862.540062	818.859263	1603.04318	3185.19943	1884.49452
AT4G28820	79.7939155	-1.112660776	0.27676206	-4.0202793	5.81E-05	0.00066965	104.448496	101.475301	121.462437	47.1745078	57.1165468	47.0862041
AT4G28950	15.54694926	2.113982188	0.68481793	3.08692589	0.00202238	0.01200496	8.35587968	5.07376507	4.0487479	14.2413608	22.8466187	38.7153234
AT4G29110	503.9864745	1.005975151	0.24235086	4.15090396	3.31E-05	0.00041436	373.925616	309.499669	321.875458	820.658418	475.971223	721.988462
AT4G29230	31.583909	1.647544017	0.50108052	3.28798258	0.00100908	0.0069178	7.31139472	21.3098133	17.2071786	47.1745078	60.9243166	35.5762431
AT4G29400	368.3729249	-1.120775973	0.25140136	-4.4581142	8.27E-06	0.00012609	486.729991	416.048736	611.360933	205.609647	297.957986	192.530257
AT4G29410	3819.939702	-1.107658067	0.19795643	-5.595464	2.20E-08	7.03E-07	5509.65816	5142.76827	5002.22803	1874.51912	2947.21382	2443.25081
AT4G29510	1000.747506	-1.110462834	0.16906615	-6.568215	5.09E-11	2.87E-09	1351.56354	1361.79854	1390.7449	606.14792	739.659281	554.570848
AT4G29880	12.10654952	2.444890323	0.74854209	3.26620285	0.00109	0.00733775	4.17793984	6.08851808	1.01218697	22.2521263	17.134964	21.9735619
AT4G29905	1857.388144	-1.868126073	0.22860461	-8.1718653	3.04E-16	4.45E-14	3382.0423	2939.73948	2426.21218	652.432343	1027.1459	716.756662
AT4G29920	93.59422116	1.19580256	0.36814043	3.24822398	0.00116128	0.00774091	40.7349134	84.2245001	45.5484139	94.3490155	152.310791	144.397692
AT4G30020	2140.055935	1.337129014	0.27206882	4.91467208	8.89E-07	1.84E-05	1058.06326	1547.49835	1035.46728	2234.11348	4171.4118	2793.78144
AT4G30130	18.73154902	1.414089527	0.53990548	2.61914275	0.00881511	0.03730493	7.31139472	14.2065422	9.10968277	23.1422114	31.4141007	27.2053624
AT4G30150	451.0776923	-1.437382562	0.24843972	-5.7856391	7.22E-09	2.58E-07	458.528898	774.256549	743.957427	244.773389	269.399712	215.550179
AT4G30180	16.09501578	3.44129358	0.87342207	3.94001216	8.15E-05	0.00088353	0	4.05901205	4.0487479	21.3620413	51.4048921	15.6954014
AT4G30190	5042.223338	1.387398398	0.29525261	4.69902168	2.61E-06	4.75E-05	2032.56773	3738.3501	2595.2474	4819.81056	9355.69037	7711.67387
AT4G30220	1436.977067	-1.108089316	0.17212881	-6.4375586	1.21E-10	6.38E-09	2265.48788	1765.67024	1858.37529	830.449354	995.731799	906.147838
AT4G30230	45.24211257	1.481184735	0.4101195	3.61159306	0.00030432	0.00259711	16.7117594	32.4720964	22.2681134	49.8447629	68.5398562	81.6160871
AT4G30250	32.21144946	1.217542111	0.45591948	2.67052003	0.00757339	0.03324777	13.5783045	24.3540723	20.2437395	54.2951882	50.4529497	30.3444426
AT4G30290	73.83731841	1.725866173	0.65274895	2.64399686	0.00819334	0.03534168	18.8007293	16.2360482	67.8165273	203.829477	39.0296403	97.3114884
AT4G30410	90.47989089	2.139831012	0.30620051	6.98833268	2.78E-12	1.94E-10	40.7349134	27.3983314	32.3899832	149.534289	170.397698	122.424131
AT4G30650	376.5676552	1.379677353	0.27064088	5.09781571	3.44E-07	8.05E-06	128.47165	253.688253	244.949248	551.852732	553.078562	527.365486
AT4G30660	669.4497457	1.189771855	0.24180252	4.92042785	8.64E-07	1.80E-05	300.811669	414.01923	509.130048	974.643132	764.409785	1053.68461
AT4G30800	224.3818026	-1.537764094	0.26334759	-5.8392943	5.24E-09	1.95E-07	338.413127	370.38485	292.522036	88.1184202	153.262734	103.589649
AT4G30930	465.8217054	-1.21071822	0.22799538	-5.3102752	1.09E-07	2.95E-06	670.559344	683.943531	597.190315	228.751858	366.497842	247.987341
AT4G30990	1078.007911	-1.275609336	0.24506151	-5.2052618	1.94E-07	4.88E-06	1077.90848	1841.77672	1657.96226	669.343959	707.293238	513.762804
AT4G31120	859.2129163	-1.109350299	0.19675526	-5.6382244	1.72E-08	5.66E-07	1129.08824	1251.19047	1142.75909	550.962647	650.176691	431.100357
AT4G31210	1317.529244	-1.914026435	0.21816947	-8.7731178	1.74E-18	3.59E-16	1685.79873	2287.25329	2274.38413	480.645928	686.350504	490.742882
AT4G31650	144.8108108	1.023620019	0.28729059	3.56301274	0.00036662	0.00304415	98.1815863	108.578572	79.962771	252.784155	181.821007	147.536773
AT4G31790	503.0248884	-1.238048803	0.22078723	-5.6074294	2.05E-08	6.59E-07	765.607476	649.441929	704.482135	243.883304	382.680864	272.053624
AT4G31810	511.8164035	-1.753172991	0.22211851	-7.8929621	2.95E-15	3.65E-13	741.584322	842.245001	784.444906	189.588116	302.717698	210.318378
AT4G31840	182.2234037	1.048048322	0.36962734	2.83541881	0.00457656	0.02261075	119.071285	120.755609	116.401502	115.711057	328.420144	292.980825
AT4G31870	1442.981332	-2.289545688	0.32471915	-7.0508489	1.78E-12	1.31E-10	3003.93875	1850.9095	2333.09098	682.695235	270.351655	516.901885
AT4G32000	146.3363096	1.082413705	0.24680548	4.38569559	1.16E-05	0.0001677	100.270556	102.490054	78.950584	184.247606	234.177842	177.881215
AT4G32270	244.2064011	1.125568135	0.18038188	6.23991806	4.38E-10	2.12E-08	148.316864	152.212952	159.925542	337.342235	328.420144	339.020669
AT4G32280	106.9435788	3.414874924	1.22619458	2.78493722	0.00535381	0.02550396	44.9128533	7.1032711	3.03656092	388.077083	139.93554	58.5961651
AT4G32290	263.2729092	1.090555416	0.18843725	5.78736654	7.15E-09	2.56E-07	178.606928	154.242458	172.071786	389.857253	342.699281	342.15975
AT4G32460	855.7601159	3.023388053	0.24263802	12.4604878	1.23E-35	1.80E-32	236.053601	184.685048	141.706176	1210.51567	1702.07309	1659.5271
AT4G32800	495.1619733	1.01834837	0.39225154	2.59616155	0.00942717	0.03933535	141.00547	303.411151	537.471284	756.572294	633.99367	598.517972
AT4G32880	457.6510061	1.221005463	0.22985556	5.31205541	1.08E-07	2.93E-06	209.941477	354.148802	260.132053	619.499196	691.110216	611.074293
AT4G33260	26.93315801	1.46368332	0.51550686	2.83930912	0.00452113	0.02239503	11.4893346	19.2803073	12.1462437	23.1422114	49.5010072	46.039844
AT4G33270	56.61007801	1.430618741	0.55379029	2.58332216	0.00978539	0.04051028	18.8007293	46.6786386	26.3168613	29.3728067	118.040863	100.450569
AT4G33495	267.6508513	-1.337734409	0.23283945	-5.7453083	9.18E-09	3.23E-07	377.059071	351.104543	423.094156	190.478201	142.791367	121.377771
AT4G33550	31.99423299	1.387244795	0.46887733	2.95865191	0.00308988	0.01662995	11.4893346	23.3393193	18.2193655	55.1852732	31.4141007	52.3180045
AT4G33790	32.87852726	5.562523527	0.9040649	6.15279225	7.61E-10	3.47E-08	0	1.01475301	3.03656092	31.1529768	96.1461871	65.9206857
AT4G33985	28.10641491	1.370321056	0.45445457	3.01530921	0.00256717	0.01436938	11.4893346	14.2065422	21.2559265	34.713317	40.9335252	46.039844
AT4G33990	65.64034966	-1.228931621	0.33162146	-3.7058266	0.0002107	0.00191677	83.5587968	77.121229	115.389315	44.5042526	31.4141007	41.8544036
AT4G34138	1721.117723	-1.206940614	0.22774371	-5.2995562	1.16E-07	3.11E-06	2472.2959	2504.41044	2228.83572	1271.04145	726.332087	1123.79074
AT4G34290	2501.895548	-1.043962711	0.25992363	-4.016421	5.91E-05	0.00067906	3542.89298	3395.36358	3170.16961	1058.31113	2212.31425	1632.32174
AT4G34360	96.05400228	-1.961036611	0.25871495	-7.5799123	3.46E-14	3.52E-12	154.583774	150.183446	153.85242	40.0538273	39.9815828	37.6689633
AT4G34560	286.6651132	1.229431768	0.21754016	5.65151638	1.59E-08	5.27E-07	186.962808	193.817826	133.608681	438.811931	381.728921	385.060513
AT4G34770	100.78072	2.79336838	0.45424533	6.1494708	7.77E-10	3.51E-08	44.9128533	22.3245663	9.10968277	148.644204	201.811799	177.881215
AT4G34790	126.1388608	2.013761637	0.38606213	5.21615953	1.83E-07	4.62E-06	79.380857	45.6638856	25.3046744	181.577351	241.793381	183.113016
AT4G34900	274.4155566	2.520865897	0.43527529	5.79142885	6.98E-09	2.51E-07	30.2900638	130.903139	82.9993319	348.91334	625.426188	427.961277
AT4G34970	40.66142716	1.496244778	0.52004507	2.87714446	0.00401292	0.02049097	37.6014586	15.2212952	11.1340567	77.4373995	41.8854677	60.6888853
AT4G35030	76.95217923	1.018366528	0.32633417	3.12062489	0.00180468	0.01095985	47.0018232	64.9441929	40.487479	83.6679949	99.0020145	126.609571
AT4G35060	87.15525251	1.004247521	0.31390895	3.19916821	0.00137825	0.00887028	50.1352781	51.7524037	71.8652752	99.6895258	100.905899	148.583133
AT4G35090	74068.21203	-1.221850601	0.21839399	-5.5947079	2.21E-08	7.04E-07	109574.828	92229.8867	109247.365	58182.1896	35559.8101	39615.193
AT4G35130	58.72764872	-1.704468462	0.40146481	-4.2456236	2.18E-05	0.0002901	77.2918871	70.0179579	122.474624	37.3835722	19.0388489	26.1590023
AT4G35160	9.812020203	3.112096738	1.13090384	2.7518668	0.00592566	0.02753877	0	1.01475301	5.06093487	24.9223815	3.80776979	24.0662821
AT4G35350	244.5144388	1.253297289	0.40932275	3.06188039	0.00219951	0.01281658	87.7367367	225.275169	120.45025	214.510498	518.808633	300.305346
AT4G35640	13.37216631	2.473643344	0.79022513	3.13030206	0.00174627	0.01066192	2.08896992	3.04425904	7.08530882	14.2413608	38.0776979	15.6954014
AT4G35850	758.231431	-1.05511721	0.19723034	-5.3496699	8.81E-08	2.42E-06	953.614769	969.089128	1148.83222	467.294652	593.060144	417.497676
AT4G35900	144.8737845	2.011894924	0.29499193	6.82016928	9.09E-12	5.99E-10	48.0463082	42.6196266	81.987145	247.443644	218.946763	230.19922
AT4G36130	3887.229236	-1.235452918	0.26017234	-4.7485944	2.05E-06	3.83E-05	6068.45762	5550.69898	4751.20566	1538.06697	3122.37123	2292.57496
AT4G36180	78.22362143	1.20381233	0.43166161	2.78878708	0.00529058	0.02524069	35.5124886	63.9294399	42.5118529	56.0753583	155.166619	116.14597
AT4G36230	87.68930618	1.388410746	0.34819193	3.98748682	6.68E-05	0.00074799	43.8683683	62.9146868	38.463105	97.9093557	111.377266	171.603055
AT4G36270	89.32307372	1.468029882	0.3513563	4.17818002	2.94E-05	0.00037557	43.8683683	67.9884519	30.3656092	106.810206	145.647194	141.258612
AT4G36280	170.0045802	1.103288002	0.24802974	4.44820847	8.66E-06	0.00013131	86.6922517	138.00641	99.1943235	222.521263	246.553094	227.06014
AT4G36380	172.6928779	-1.07772054	0.28424144	-3.7915673	0.0001497	0.00145651	276.788514	209.039121	217.6202	149.534289	83.7709353	99.4042086
AT4G36420	796.3606368	-1.200492226	0.18569669	-6.4648015	1.01E-10	5.47E-09	1203.24667	1009.67925	1116.44223	419.23006	570.213526	459.35208
AT4G36470	113.0093056	-1.702160226	0.3451858	-4.931142	8.18E-07	1.71E-05	242.320511	134.962151	141.706176	69.4266341	45.6932374	43.9471238
AT4G36570	35.31159829	4.152738063	0.6168662	6.73199156	1.67E-11	1.05E-09	5.2224248	5.07376507	1.01218697	51.624933	91.3864749	57.549805
AT4G36580	307.398597	-2.281191143	0.20892727	-10.918589	9.39E-28	7.45E-25	472.107202	521.583049	536.459097	108.590376	120.896691	84.7551673
AT4G36770	16.90126971	1.901086702	0.69087649	2.75170269	0.00592863	0.02753966	3.13345488	7.1032711	11.1340567	15.1314459	41.8854677	23.019922
AT4G36850	10683.55691	-2.261981985	0.3809899	-5.937118	2.90E-09	1.12E-07	20813.4518	14652.0188	17577.639	6059.69903	1634.48518	3364.04769
AT4G37170	44.54855384	-1.437580138	0.46174807	-3.113343	0.00184981	0.01117623	62.6690976	42.6196266	90.0846408	34.713317	15.2310791	21.9735619
AT4G37190	700.6964585	-1.446216034	0.21907025	-6.6016084	4.07E-11	2.34E-09	866.922517	929.51376	1279.40434	395.197763	415.046907	318.093468
AT4G37370	590.5180499	-2.093657213	0.33818126	-6.1909321	5.98E-10	2.82E-08	1411.09918	841.230248	618.446242	291.057812	154.214676	227.06014
AT4G37400	93.82295158	1.9092251	0.48669028	3.92287497	8.75E-05	0.00093866	25.067639	58.8556748	34.4143571	215.400583	62.8282015	166.371254
AT4G37450	761.6289095	1.464769403	0.24989109	5.86163118	4.58E-09	1.72E-07	306.034093	440.402808	468.642569	847.36097	1368.89324	1138.43978

Table S-5.1 Differentially Expressed Genes between lpa66 (LP) and wild type (WT) Arabidopsis plants.

ID	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	WT4	WT2	WT1	LP3	LP2	LP1
AT4G37540	588.7661161	-1.25363474	0.29294427	-4.2794308	1.87E-05	0.00025599	1211.60255	723.518899	553.666275	353.363766	307.47741	382.967793
AT4G37660	425.2335697	-1.063403642	0.20421075	-5.2073833	1.92E-07	4.83E-06	632.957886	536.804344	555.690649	225.191518	325.564317	275.192704
AT4G37770	19.03700949	2.583787143	0.67601865	3.82206487	0.00013234	0.00131654	5.2224248	7.1032711	4.0487479	53.4051031	26.6543885	17.7881215
AT4G37910	3952.348431	-1.017252852	0.18748284	-5.425845	5.77E-08	1.65E-06	4611.4011	6042.8542	5217.82386	2243.90442	3058.59108	2539.51594
AT4G38010	37.5424711	-1.983411209	0.4151055	-4.7780894	1.77E-06	3.35E-05	57.4466728	59.8704278	62.7555924	19.5818711	16.1830216	9.41724082
AT4G38020	360.7901719	-1.074652607	0.21707227	-4.9506674	7.40E-07	1.58E-05	545.221149	417.063489	505.0813	187.807946	242.745324	266.821823
AT4G38150	306.7748167	-1.523483592	0.20164703	-7.5551999	4.18E-14	4.08E-12	460.617867	485.051941	420.057595	145.083863	187.532662	142.304972
AT4G38160	2707.248947	-1.029659722	0.2408823	-4.2745346	1.92E-05	0.00026074	3714.18852	3523.22246	3665.12904	1188.26354	2271.33468	1881.35544
AT4G38380	104.2098483	-1.300346248	0.33869871	-3.8392418	0.00012341	0.00124468	106.537466	169.463753	169.035225	82.7779098	51.4048921	46.039844
AT4G38400	200.6457833	1.102657868	0.39881027	2.76486828	0.00569458	0.02669299	80.4253419	109.593325	192.315525	158.435139	382.680864	280.424504
AT4G38540	198.7795299	-1.487997538	0.54756858	-2.7174633	0.00657844	0.02989359	237.098086	247.599735	394.75292	198.488967	24.7505036	89.9869678
AT4G38560	61.39046189	1.315218438	0.39933797	3.29349711	0.00098949	0.00680067	35.5124886	47.6933916	22.2681134	69.4266341	75.2034533	118.23869
AT4G38620	542.8781785	1.144783915	0.20253907	5.65216339	1.58E-08	5.26E-07	329.012762	347.045531	338.07045	584.785879	855.79626	802.558189
AT4G38950	964.1247886	1.747612764	0.40437941	4.32171554	1.55E-05	0.00021585	346.769007	679.884519	300.619532	727.199488	2183.75597	1546.52021
AT4G39070	165.5014904	-1.247640903	0.40392141	-3.0888209	0.00200953	0.01194729	239.187056	190.773567	269.241735	170.006245	59.9723741	63.8279655
AT4G39110	19.84120783	1.659119261	0.52706023	3.14787411	0.00164463	0.01016527	7.31139472	8.11802411	13.1584307	26.7025516	32.3660432	31.3908027
AT4G39210	777.9747072	1.174443336	0.18303548	6.41647906	1.39E-10	7.21E-09	452.261988	423.152007	557.715023	1024.48789	1199.44748	1010.78385
AT4G39340	10.84477432	2.105542794	0.74722573	2.81781358	0.00483519	0.02359448	3.13345488	5.07376507	4.0487479	12.4611907	25.7024461	14.6490413
AT4G39400	3673.496516	1.019546849	0.13709507	7.43678714	1.03E-13	9.48E-12	2247.73163	2611.97426	2421.15124	5121.54939	4973.89928	4664.67328
AT4G39410	31.58010577	1.244441689	0.40723035	3.05586675	0.00224411	0.01297613	18.8007293	20.2950603	17.2071786	51.624933	42.8374101	38.7153234
AT4G39470	466.9993609	-1.401107039	0.15512775	-9.031956	1.69E-19	4.22E-17	662.203465	704.238591	666.019029	253.67424	263.688058	252.172782
AT4G39670	34.3876616	1.036369319	0.41663937	2.48744934	0.01286628	0.04979828	24.0231541	15.2212952	28.3412353	45.3943377	39.9815828	53.3643646
AT4G39675	20.0348807	-4.621233309	0.86009325	-5.3729445	7.75E-08	2.15E-06	41.7793984	35.5163555	38.463105	4.45042526	0	0
AT4G39830	114.2681504	1.730928017	0.36935101	4.68640385	2.78E-06	5.01E-05	48.0463082	62.9146868	47.5727878	119.271397	139.93554	267.868183
AT4G39880	1382.274833	-1.013657601	0.20053885	-5.0546696	4.31E-07	9.78E-06	2055.5464	1775.81777	1714.64474	707.617616	1027.1459	1012.87657
AT4G39955	147.69453	-1.253368944	0.34193197	-3.6655506	0.00024681	0.00217634	180.695898	157.286717	286.448914	114.820972	59.0204317	87.8942476
AT4G40000	102.0473999	-1.807163943	0.30587046	-5.9082657	3.46E-09	1.32E-07	131.605105	183.670295	160.937729	37.3835722	59.9723741	38.7153234
AT4G40010	27.32241503	1.405080226	0.46513101	3.02082682	0.00252085	0.01416427	12.5338195	12.1770362	20.2437395	40.9439124	46.6451799	31.3908027
AT4G40070	111.1435717	-1.099600042	0.29261388	-3.7578533	0.00017138	0.00162263	151.450319	140.035916	162.962103	73.8770593	48.5490648	89.9869678
AT5G01320	79.45307351	-1.150624082	0.43485338	-2.6460047	0.00814487	0.03518043	122.20474	93.3572773	113.364941	80.9977397	22.8466187	43.9471238
AT5G01380	17.00176968	2.742621011	0.72814444	3.76658922	0.00016549	0.00157632	3.13345488	2.02950603	8.0974958	44.5042526	18.0869065	26.1590023
AT5G01410	20612.91661	-1.106486759	0.20756697	-5.3307459	9.78E-08	2.66E-06	35199.1432	23850.7548	25404.8809	14199.5268	10987.3197	14035.8743
AT5G01540	66.45154077	1.281152592	0.40008849	3.20217311	0.00136395	0.00880208	56.4021878	35.5163555	24.2924874	82.7779098	75.2034533	124.516851
AT5G01740	128.7990734	1.225308793	0.33412794	3.66718444	0.00024524	0.00216771	88.7812216	58.8556748	84.0115189	246.553559	120.896691	173.695775
AT5G01820	1844.094136	1.533245827	0.16415021	9.34050491	9.59E-21	3.20E-18	823.054149	1026.93005	990.931048	2477.99679	2942.4541	2803.19868
AT5G01840	38.10142357	1.357115645	0.51516697	2.63432192	0.00843055	0.03609257	9.40036464	19.2803073	35.4265441	41.8339974	71.3956835	51.2716444
AT5G02050	886.3373639	-1.620233006	0.23187001	-6.9876782	2.79E-12	1.94E-10	1368.2753	1391.22638	1253.08747	326.661214	575.92518	402.848635
AT5G02170	75.45736541	1.184217076	0.29517076	4.01197288	6.02E-05	0.00068783	55.3577029	43.6343796	39.475292	117.491227	94.2423022	102.543289
AT5G02200	27.63911202	3.297535374	0.58438764	5.64271922	1.67E-08	5.54E-07	4.17793984	6.08851808	5.06093487	69.4266341	47.5971223	33.4835229
AT5G02430	171.8645529	1.421308954	0.25899312	5.48782513	4.07E-08	1.21E-06	82.5143119	104.51956	93.1212017	189.588116	289.390504	272.053624
AT5G02450	6073.06269	-1.091485348	0.24433006	-4.4672577	7.92E-06	0.00012189	9336.65106	7996.25375	7466.90331	2611.50954	4893.93612	4133.12236
AT5G02540	255.9056943	2.102614551	0.29771968	7.06239683	1.64E-12	1.22E-10	68.9360074	133.947398	87.0480798	392.527508	515.000864	337.974309
AT5G02550	28.0377783	2.621821515	0.66321468	3.95320186	7.71E-05	0.00084443	5.2224248	11.1622831	7.08530882	17.801701	80.915108	46.039844
AT5G02560	182.0358039	1.436388108	0.31791366	4.51817048	6.24E-06	9.98E-05	127.427165	111.622831	55.6702836	259.01475	236.081727	302.398066
AT5G02610	3129.535688	-1.349962438	0.24603242	-5.4869291	4.09E-08	1.21E-06	5131.55461	4385.76252	3968.78513	1206.06525	2257.05554	1827.99108
AT5G02750	22.69288275	1.779738261	0.49621344	3.58663853	0.00033497	0.00281696	10.4448496	10.1475301	10.1218697	30.2628918	43.7893526	31.3908027
AT5G02760	571.5464285	2.355177967	0.75286428	3.12829022	0.00175826	0.01072829	383.32598	109.593325	67.8165273	1097.47487	1101.39741	669.670458
AT5G02890	454.0281653	2.224188745	0.74323009	2.9925978	0.00276614	0.01523374	123.249225	268.909549	88.0602668	293.728067	1278.45871	671.763178
AT5G02960	12055.29264	-1.018281064	0.23256761	-4.3784304	1.20E-05	0.00017247	18045.5667	15922.4895	14456.0544	5645.80949	10130.5715	8131.26426
AT5G03120	1146.402693	1.36217807	0.33406897	4.07753548	4.55E-05	0.00054612	460.617867	431.270031	1034.45509	1975.98882	1601.1672	1374.91716
AT5G03150	145.9906898	1.998380044	0.34245684	5.83542155	5.37E-09	1.98E-07	68.9360074	76.106476	30.3656092	212.730327	272.25554	215.550179
AT5G03170	247.9908553	1.083730947	0.31285988	3.46394989	0.00053231	0.004113	115.937831	178.59653	182.193655	212.730327	410.287195	388.199594
AT5G03210	34.12995603	1.713078841	0.63226352	2.70943805	0.00673973	0.0304252	8.35587968	9.13277712	30.3656092	80.9977397	25.7024461	50.2252843
AT5G03240	8198.90975	-1.004970967	0.23581413	-4.261708	2.03E-05	0.00027324	10796.841	9037.39034	12999.5173	7109.9994	4337.04979	4912.66063
AT5G03350	3597.41757	-2.320224188	0.29647764	-7.8259669	5.04E-15	5.99E-13	5563.97138	8368.6681	4050.77227	1334.23749	850.084605	1416.77156
AT5G03470	565.7222287	-1.03614233	0.26533801	-3.9049902	9.42E-05	0.00099626	788.586145	713.371369	780.396158	529.600606	299.861871	282.517224
AT5G03545	482.8806426	-1.826092494	0.4516587	-4.0430806	5.28E-05	0.00061896	1035.0846	558.114157	667.031216	367.605127	79.0112231	190.437536
AT5G03995	73.9751089	1.018392168	0.31377829	3.24557884	0.00117212	0.00779135	58.4911578	40.5901205	47.5727878	78.3274846	114.233094	104.636009
AT5G04130	1222.145115	-1.407023617	0.14881261	-9.4550029	3.23E-21	1.10E-18	1601.19544	1829.59968	1893.80183	653.322428	654.936403	700.014901
AT5G04250	87.38130064	-1.446377532	0.37777442	-3.8286804	0.00012883	0.00128771	85.6477667	117.71135	180.169282	56.0753583	32.3660432	52.3180045
AT5G04770	124.9093872	-1.979318595	0.37641286	-5.2583713	1.45E-07	3.77E-06	244.409481	181.640789	172.071786	76.5473145	26.6543885	48.1325642
AT5G04840	44.37735396	1.117873403	0.41670947	2.68262057	0.00730478	0.03238232	24.0231541	34.5016025	25.3046744	38.2736572	65.6840288	78.4770068
AT5G04895	191.8523365	-1.324826417	0.28271164	-4.6861404	2.78E-06	5.01E-05	201.585597	346.030778	275.314857	114.820972	127.560288	85.8015274
AT5G05180	128.6321766	1.111251274	0.3187258	3.48654316	0.00048931	0.00382894	65.8025525	83.2097471	95.1455756	134.402843	244.649209	148.583133
AT5G05300	110.7459342	1.248836928	0.33199435	3.76162098	0.00016882	0.00160396	69.9804923	51.7524037	74.9018361	137.963183	113.281151	216.596539
AT5G05320	18.75654593	2.362938825	0.70236026	3.36428319	0.00076743	0.00555109	1.04448496	10.1475301	7.08530882	41.8339974	19.9907914	32.4371628
AT5G05840	25.79516971	1.566116209	0.58068757	2.69700315	0.00699666	0.03130076	20.8896992	12.1770362	6.07312185	30.2628918	57.1165468	28.2517224
AT5G05960	273.0774698	1.388440736	0.31586603	4.39566337	1.10E-05	0.00016105	94.0036464	207.009615	151.828046	494.887289	315.09295	375.643273
AT5G05990	346.0668113	-1.018685009	0.20779569	-4.9023396	9.47E-07	1.94E-05	520.15351	418.078242	452.447578	238.542794	259.880288	187.298456
AT5G06165	33.71853617	-1.19261068	0.43124754	-2.7654898	0.00568374	0.02665355	62.6690976	36.5311085	41.499666	21.3620413	16.1830216	24.0662821
AT5G06510	92.56620906	1.944092236	0.34969098	5.55945773	2.71E-08	8.39E-07	39.6904285	34.5016025	40.487479	161.105394	187.532662	92.079688
AT5G06550	244.7398105	-1.866235813	0.26033686	-7.1685423	7.58E-13	6.09E-11	379.148041	389.665157	383.618863	84.5580799	145.647194	85.8015274
AT5G06620	60.17470567	-1.313277685	0.3904599	-3.3634125	0.00076985	0.0055644	82.5143119	75.091723	100.206511	52.5150181	26.6543885	24.0662821
AT5G06790	268.3404022	-1.153513578	0.2524911	-4.5685317	4.91E-06	8.15E-05	481.507567	332.838988	296.570784	161.105394	189.436547	148.583133
AT5G06930	84.5804057	2.728966727	0.33530185	8.13883582	3.99E-16	5.75E-14	21.9341842	22.3245663	22.2681134	129.952418	187.532662	123.470491
AT5G06990	10.45729389	2.040617974	0.77267255	2.64098676	0.0082665	0.03556854	2.08896992	5.07376507	5.06093487	9.79093557	21.8946763	18.8344816
AT5G07000	190.3973543	1.707401464	0.33544035	5.09003013	3.58E-07	8.34E-06	109.670921	105.534313	52.6337227	218.960923	374.113382	281.470864
AT5G07030	530.5212115	1.448112197	0.40445212	3.58042928	0.00034303	0.0028708	207.852507	397.783181	247.985809	370.275382	1240.38101	718.849382
AT5G07440	10144.6385	-1.823089034	0.67181153	-2.7136912	0.00665382	0.03014971	12575.5989	11470.7681	23409.8604	7948.45952	2056.19568	3406.94845
AT5G07800	53.30374733	1.350872061	0.40597872	3.3274455	0.00087646	0.00618522	26.112124	35.5163555	28.3412353	46.2844227	100.905899	82.6624472
AT5G07860	895.270784	-1.041116466	0.18657519	-5.5801443	2.40E-08	7.60E-07	1441.38924	1007.64974	1166.0394	604.36775	568.309641	583.868931

Table S-5.1 Differentially Expressed Genes between lpa66 (LP) and wild type (WT) Arabidopsis plants.

ID	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	WT4	WT2	WT1	LP3	LP2	LP1
AT5G08130	1675.458221	1.337538408	0.26929907	4.96673974	6.81E-07	1.47E-05	587.000548	1106.08078	1156.92971	2784.18604	2259.91137	2158.64087
AT5G08180	1325.558308	-1.143336256	0.26075103	-4.3847813	1.16E-05	0.00016828	1902.00711	1861.05703	1711.60817	564.313923	1154.70619	759.657426
AT5G08185	211.2559137	1.644382793	0.22491953	7.31098285	2.65E-13	2.26E-11	113.848861	94.3720303	99.1943235	376.505977	297.957986	285.656305
AT5G08305	29.43777985	-1.782152721	0.45348062	-3.9299424	8.50E-05	0.00091562	42.8238834	42.6196266	51.6215357	16.911616	14.2791367	8.37088072
AT5G08310	66.17534706	-1.276186831	0.30734132	-4.1523439	3.29E-05	0.0004123	76.2474021	102.490054	102.230884	40.0538273	35.2218705	40.8080435
AT5G08350	330.4772348	-1.1231262	0.27515276	-4.0818278	4.47E-05	0.00053695	585.956063	322.691458	450.423204	240.322964	163.734101	219.735619
AT5G08400	229.3731718	-1.519376344	0.21444131	-7.0852783	1.39E-12	1.06E-10	369.747676	283.116091	367.423872	112.150717	126.608345	117.19233
AT5G08600	192.5812506	-1.032693422	0.33409756	-3.0909936	0.00199488	0.01188496	205.763537	301.381645	269.241735	121.941652	181.821007	75.3379265
AT5G08610	1807.981575	-2.022771016	0.21991487	-9.1979729	3.65E-20	1.05E-17	2198.64084	3162.98514	3344.26577	721.858977	820.574389	599.564332
AT5G08620	943.9385459	-1.629265282	0.18611497	-8.7540795	2.06E-18	4.01E-16	1307.69517	1535.32131	1437.3055	433.47142	551.174677	398.663195
AT5G09270	136.3929811	-1.455869345	0.30838111	-4.7210069	2.35E-06	4.32E-05	236.053601	127.85888	235.839565	68.536549	79.9631655	70.1061261
AT5G09300	53.74849911	1.651195745	0.48927486	3.37478149	0.00073874	0.0053763	25.067639	34.5016025	18.2193655	36.4934871	105.665612	102.543289
AT5G09585	30.08902761	-1.212877861	0.44781783	-2.708418	0.00676048	0.03049406	53.268733	28.4130844	44.5362269	19.5818711	19.0388489	15.6954014
AT5G09805	19.26633403	2.944643351	0.78975137	3.72857009	0.00019257	0.00178162	3.13345488	10.1475301	0	40.9439124	24.7505036	36.6226032
AT5G09840	111.3268	-1.215350474	0.38866098	-3.1270195	0.00176588	0.01077132	123.249225	172.508012	171.059599	39.1637423	107.569496	54.4107247
AT5G10140	156.7131769	-3.31086538	0.42917937	-7.7144095	1.22E-14	1.37E-12	354.080401	254.703006	245.961435	52.5150181	15.2310791	17.7881215
AT5G10572	14.08964615	-2.083804052	0.64670379	-3.2221924	0.00127214	0.00831389	19.8452142	29.4278374	19.2315525	6.23059536	6.66359713	3.13908027
AT5G10695	248.4844361	1.03454002	0.26026359	3.97497016	7.04E-05	0.00078245	184.873838	160.330976	143.73055	327.551299	247.505036	426.914917
AT5G11140	56.23626097	1.213160842	0.400418	3.02973606	0.00244768	0.01387186	47.0018232	37.5458615	17.2071786	81.8878248	74.2515108	79.5233669
AT5G11240	435.8166847	-1.269846673	0.24923749	-5.0949264	3.49E-07	8.16E-06	546.265634	700.179579	602.25125	244.773389	334.131799	187.298456
AT5G11310	140.6188657	-1.185803224	0.2443941	-4.8520124	1.22E-06	2.42E-05	195.318688	200.921097	190.291151	97.0192707	94.2423022	65.9206857
AT5G11410	133.5227125	-1.334943439	0.33026391	-4.0420506	5.30E-05	0.0006213	242.320511	113.652338	217.6202	68.536549	74.2515108	84.7551673
AT5G11540	22.02534161	1.661393739	0.52800086	3.14657395	0.00165195	0.0102006	9.40036464	14.2065422	8.0974958	24.0322964	41.8854677	34.529883
AT5G11550	222.2773062	1.620365771	0.37380649	4.33477161	1.46E-05	0.00020493	95.0481314	158.30147	73.8896492	205.609647	471.211511	329.603429
AT5G11630	307.6478101	-1.450511974	0.18623406	-7.7886502	6.77E-15	7.81E-13	474.196172	433.299537	444.350082	172.6765	178.013238	143.351332
AT5G11930	11.92945561	1.644186071	0.66010387	2.49079901	0.01274562	0.04944189	4.17793984	6.08851808	7.08530882	22.2521263	15.2310791	16.7417614
AT5G12020	11.40401321	-3.442274681	0.87972019	-3.91292	9.12E-05	0.00096935	27.156609	25.3688253	10.1218697	1.7801701	1.90388489	2.09272018
AT5G12050	425.3176332	1.801741076	0.44695076	4.03118471	5.55E-05	0.00064636	354.080401	132.932645	81.987145	716.518467	777.736979	488.650162
AT5G12220	302.4581282	-1.285194882	0.21550642	-5.9636037	2.47E-09	9.64E-08	373.925616	437.358549	475.727878	172.6765	207.523453	147.536773
AT5G12940	1255.716535	2.128721558	0.30340331	7.01614473	2.28E-12	1.63E-10	554.621514	539.848603	307.70484	2098.82055	1365.08547	2668.21823
AT5G13240	462.7488015	1.245744324	0.22972595	5.42274097	5.87E-08	1.67E-06	253.809845	351.104543	218.632387	617.719026	737.755396	597.471612
AT5G13320	129.5530207	1.219922191	0.38564894	3.16329711	0.00155993	0.0097679	75.2029171	110.608078	47.5727878	113.040802	234.177842	196.715697
AT5G13330	40.06637781	-2.643296313	0.51001514	-5.1827801	2.19E-07	5.45E-06	58.4911578	48.7081447	100.206511	16.911616	6.66359713	9.41724082
AT5G13370	1429.12705	-1.678388319	0.21626024	-7.7609659	8.43E-15	9.60E-13	2022.12288	1854.96851	2656.99081	817.098078	650.176691	573.40533
AT5G13460	449.4786919	1.023354744	0.18528023	5.52328074	3.33E-08	1.01E-06	280.966454	308.484916	299.607345	510.018735	672.071367	625.723334
AT5G13830	42.557503	-2.961945911	0.45237104	-6.5476028	5.85E-11	3.27E-09	69.9804923	79.1507351	76.9262101	4.45042526	13.3271943	11.509961
AT5G14050	1194.849071	-1.510927693	0.21423854	-7.0525485	1.76E-12	1.30E-10	1782.93583	1778.86203	1745.01034	484.206268	801.53554	576.54441
AT5G14105	437.338638	-1.050887905	0.21275684	-4.9393848	7.84E-07	1.65E-05	732.183957	476.933916	560.751584	284.827217	283.678849	285.656305
AT5G14180	14.74812992	-2.236060404	0.68195493	-3.2788976	0.00104213	0.00708192	31.3345488	28.4130844	13.1584307	4.45042526	3.80776979	7.32452063
AT5G14230	339.8180791	1.691606325	0.3287468	5.14562072	2.67E-07	6.46E-06	157.717229	129.888386	194.339899	328.441384	769.169497	459.35208
AT5G14470	43.46849123	-1.955679942	0.45353699	-4.3120627	1.62E-05	0.00022451	58.4911578	50.7376507	98.1821366	23.1422114	11.4233094	18.8344816
AT5G14520	1526.906157	-1.316822688	0.19918586	-6.6110251	3.82E-11	2.21E-09	2181.92908	2325.81391	2029.43488	723.639147	1092.82993	807.78999
AT5G14565	14.49192078	2.480290577	0.9960914	2.49002308	0.01277348	0.04950959	2.08896992	4.05901205	7.08530882	59.6356985	5.71165468	8.37088072
AT5G14580	177.5697645	-2.116804102	0.26065606	-8.1210623	4.62E-16	6.51E-14	263.21021	320.661952	282.400166	72.0968892	79.9631655	47.0862041
AT5G14770	149.8129005	-1.590125462	0.24761095	-6.4218705	1.35E-10	7.01E-09	208.896992	215.127639	251.02237	75.6572294	88.5306475	59.6425252
AT5G14920	915.2158162	2.094859339	0.24130893	8.68123404	3.91E-18	7.23E-16	338.413127	298.337386	404.87479	1239.88848	1956.24173	1253.53939
AT5G15070	86.89919434	1.059411837	0.33597115	3.15328215	0.00161446	0.01002111	59.5356427	71.032711	38.463105	92.5688454	144.695252	115.09961
AT5G15150	15.22672654	2.298256157	0.72275872	3.17983872	0.00147357	0.0093572	10.4448496	2.02950603	3.03656092	32.9331469	20.9427338	21.9735619
AT5G15160	75.63492185	1.814907225	0.38963246	4.657998	3.19E-06	5.60E-05	35.5124886	46.6786386	18.2193655	89.8985903	138.983597	124.516851
AT5G15230	726.0235284	1.17710393	0.34704885	3.39175282	0.00069447	0.00511869	294.544759	586.527242	454.471952	572.324688	1384.12432	1064.14821
AT5G15300	22.69121642	-1.42061173	0.49958085	-2.8436072	0.0044606	0.02219338	32.3790338	27.3983314	39.475292	16.911616	9.51942447	10.4636009
AT5G15410	2427.778383	1.12856311	0.29169316	3.86900786	0.00010928	0.00112659	903.479491	1486.61316	2181.26293	3133.98947	3667.83425	3193.491
AT5G15550	559.5704374	-1.159411472	0.20955535	-5.532722	3.15E-08	9.62E-07	697.715953	834.126977	787.481466	315.980193	431.229928	290.888105
AT5G15580	543.1553753	2.351486881	0.22810885	10.3086173	6.44E-25	3.50E-22	158.761714	228.319428	146.767111	792.175696	1020.4823	912.425999
AT5G15700	343.214185	-1.485575	0.25562804	-5.8114712	6.19E-09	2.25E-07	357.213856	594.645266	565.812519	197.598882	192.292374	151.722213
AT5G15750	609.5563686	-1.217376608	0.18462405	-6.5938138	4.29E-11	2.45E-09	852.299727	832.097471	873.517359	367.605127	428.374101	303.444426
AT5G15780	1782.913356	1.386498761	0.40628227	3.41264898	0.00064335	0.00481263	696.671468	1435.87551	826.956759	1116.16666	3803.96202	2817.84772
AT5G15800	33.02342043	-2.338294844	0.65905538	-3.5479489	0.00038824	0.00319027	109.670921	28.4130844	27.3290483	12.4611907	6.66359713	13.6026812
AT5G15860	493.0552944	-1.126569735	0.31686867	-3.5553207	0.00037752	0.00311965	877.367367	530.715826	621.482803	458.393802	237.033669	233.3383
AT5G16060	553.8419563	-1.403044049	0.19868668	-7.061591	1.65E-12	1.22E-10	935.858524	642.338658	833.02988	299.958663	297.957986	313.908027
AT5G16250	191.9693249	1.120221495	0.35399934	3.16447338	0.00155364	0.00974853	132.64959	138.00641	92.1090147	140.633438	330.324029	318.093468
AT5G16370	4321.917746	-1.096117274	0.35231183	-3.1112134	0.0018632	0.01125313	6776.61842	4727.73429	6163.20649	4294.66038	1366.98935	2602.29755
AT5G16420	87.46424073	-1.066428401	0.36580145	-2.9153203	0.00355324	0.01859781	98.1815863	103.504807	153.85242	81.8878248	47.5971223	39.7616834
AT5G16570	212.6372053	1.674172897	0.23604648	7.09255593	1.32E-12	1.02E-10	113.848861	86.2540062	104.255258	266.135431	368.401727	336.927949
AT5G16650	2362.658326	-1.169472426	0.1883336	-6.2095792	5.31E-10	2.53E-08	3696.43227	2878.8543	3237.98613	1629.74573	1193.73583	1539.19569
AT5G16750	653.3017105	-1.31087448	0.22972935	-5.7061689	1.16E-08	3.94E-07	846.032818	1019.82678	928.175456	351.583596	486.44259	287.749025
AT5G16930	274.7890827	-1.844154525	0.22389996	-8.236511	1.77E-16	2.64E-14	384.370465	468.815892	436.252586	99.6895258	146.599137	113.00689
AT5G16980	114.4945991	-1.956430601	0.34830121	-5.6170653	1.94E-08	6.27E-07	186.962808	142.065422	217.6202	69.4266341	34.2699281	36.6226032
AT5G17240	156.8603019	-1.422368652	0.22953781	-6.1966638	5.77E-10	2.73E-08	219.341842	210.053874	256.083305	80.1076547	97.0981296	78.4770068
AT5G17270	514.1238375	-1.249765735	0.19917335	-6.2747638	3.50E-10	1.72E-08	691.449044	719.459887	761.164605	315.980193	356.026475	240.662821
AT5G17420	128.5428677	1.536075568	0.42257693	3.63501998	0.00027796	0.00241435	32.3790338	92.3425242	72.8774622	113.930887	249.408921	210.318378
AT5G17760	214.9781464	-1.376703464	0.2400885	-5.73415	9.80E-09	3.42E-07	275.744029	334.868494	320.863271	146.864034	93.2903598	118.23869
AT5G18010	17.37193265	2.310622252	0.79685138	2.89969034	0.00373531	0.01934861	10.4448496	7.1032711	0	40.0538273	25.7024461	20.9272018
AT5G18060	100.312813	1.287120497	0.42684529	3.01542627	0.00256618	0.01436938	94.0036464	54.7966627	26.3168613	172.6765	138.983597	115.09961
AT5G18300	19.96223065	1.412372047	0.51217451	2.75759926	0.00582275	0.02717909	9.40036464	9.13277712	14.1706176	27.5926366	33.3179856	26.1590023
AT5G18360	190.4810656	1.239749425	0.20745685	5.97593869	2.29E-09	9.01E-08	118.0268	98.4310423	123.486811	261.685005	260.83223	280.424504
AT5G18362	34.74884889	1.028649934	0.39332624	2.61525885	0.00891599	0.03766484	26.112124	21.3098133	21.2559265	56.0753583	41.8854677	41.8544036
AT5G18430	162.0371836	2.12160824	0.54237692	3.91168606	9.17E-05	0.00097228	36.5569736	107.563819	37.4509181	91.6787604	390.296403	308.676227
AT5G18690	141.2178519	1.217259165	0.27873796	4.36703764	1.26E-05	0.00018035	75.2029171	103.504807	75.9140231	149.534289	216.090935	227.06014
AT5G18820	345.8827403	-2.351230919	0.21234449	-11.072719	1.70E-28	1.41E-25	503.441751	584.497736	647.799664	126.392077	118.992806	94.1724082
AT5G19030	358.1027792	-1.032833716	0.1853458	-5.5724688	2.51E-08	7.87E-07	539.998724	437.358549	465.606008	215.400583	237.033669	253.219142

Table S-5.1 Differentially Expressed Genes between lpa66 (LP) and wild type (WT) Arabidopsis plants.

ID	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	WT4	WT2	WT1	LP3	LP2	LP1
AT5G19300	276.4895698	-1.855102516	0.20117645	-9.2212707	2.94E-20	8.73E-18	414.660529	477.948669	406.899164	105.920121	134.223885	119.28505
AT5G19530	1050.801548	1.138827236	0.13547281	8.40631582	4.23E-17	6.77E-15	677.870739	663.648471	627.555924	1470.42051	1409.82676	1455.48689
AT5G19600	70.70771829	-3.090086761	1.22472517	-2.5230859	0.011633	0.04604567	91.9146765	163.375235	124.498998	38.2736572	0.95194245	5.23180045
AT5G20020	4338.592702	-1.075046811	0.1517009	-7.0866213	1.37E-12	1.05E-10	6533.25343	5389.35326	5729.99046	2602.60869	3033.84058	2742.5098
AT5G20160	2059.133238	-1.193826802	0.2081838	-5.7344846	9.78E-09	3.42E-07	3073.91924	2891.03134	2631.68613	991.554748	1582.12835	1184.47962
AT5G20250	11738.38996	-1.8874969	0.33489004	-5.6361691	1.74E-08	5.72E-07	19551.714	16664.274	19229.5281	8155.84933	2886.2895	3942.68482
AT5G20410	161.643738	1.347481903	0.26441023	5.09617922	3.47E-07	8.11E-06	110.715406	73.062217	90.0846408	274.146196	230.370072	191.483897
AT5G20635	55.8948021	-1.08181011	0.33786883	-3.2018642	0.00136541	0.00880854	83.5587968	70.0179579	73.8896492	27.5926366	34.2699281	46.039844
AT5G20710	10.53136981	2.731738542	0.91396554	2.9888857	0.00279997	0.01537841	6.26690976	1.01475301	1.01218697	9.79093557	19.9907914	25.1126422
AT5G20740	92.97810458	1.613155696	0.36291333	4.44501632	8.79E-06	0.00013274	51.179763	39.5753675	46.5606008	81.8878248	161.830216	176.834855
AT5G20820	43.9549153	1.531977101	0.54621685	2.80470497	0.00503627	0.02430768	26.112124	28.4130844	13.1584307	25.8124665	77.1073382	93.1260481
AT5G22100	328.3402548	-1.705030235	0.214955	-7.9320333	2.16E-15	2.70E-13	528.50939	526.656814	452.447578	131.732588	189.436547	141.258612
AT5G22300	716.7337886	-1.227499892	0.27890084	-4.4012055	1.08E-05	0.00015784	1251.29298	831.082718	931.212017	534.941116	278.919137	472.954761
AT5G22310	236.5408818	1.336940313	0.26140955	5.11435141	3.15E-07	7.44E-06	178.606928	129.888386	94.1333887	338.23232	334.131799	344.25247
AT5G22460	203.4797871	3.688807269	0.3477884	10.6064702	2.78E-26	1.89E-23	19.8452142	41.6048736	26.3168613	276.816451	502.625612	353.669711
AT5G22500	337.1843266	3.467623708	0.3751925	9.24225217	2.41E-20	7.29E-18	50.1352781	70.0179579	47.5727878	551.852732	962.413814	341.11339
AT5G22580	3685.9856	1.387380191	0.26212346	5.29285005	1.20E-07	3.21E-06	2849.35497	1830.61444	1436.29332	4858.08421	6182.86619	4958.70047
AT5G22740	546.9946734	1.086703709	0.27248308	3.98815118	6.66E-05	0.00074634	288.277849	431.270031	330.985141	574.104859	1013.81871	643.511456
AT5G22860	321.7784213	1.194142972	0.23194121	5.14847257	2.63E-07	6.39E-06	186.962808	215.127639	185.230216	561.643668	357.93036	423.775837
AT5G22920	8748.850092	-1.390460014	0.27312158	-5.0909929	3.56E-07	8.32E-06	14999.8485	10998.9079	12000.4888	6835.8532	3305.14418	4352.85798
AT5G22930	41.62622092	2.141659065	0.53155754	4.02902581	5.60E-05	0.00065113	17.7562443	19.2803073	9.10968277	36.4934871	108.521439	58.5961651
AT5G22940	85.47628827	2.292914381	0.43786748	5.23654875	1.64E-07	4.18E-06	22.9786691	37.5458615	26.3168613	72.0968892	208.475396	145.444053
AT5G23070	656.8373721	-1.406608508	0.21535645	-6.5315365	6.51E-11	3.62E-09	940.036464	994.457953	927.163269	299.958663	465.499856	313.908027
AT5G23300	385.7261616	-1.213917071	0.23105964	-5.2536959	1.49E-07	3.85E-06	496.130356	590.586254	530.385975	186.027776	299.861871	211.364738
AT5G23400	106.9494948	1.526703163	0.43488025	3.51062884	0.00044705	0.00357796	32.3790338	85.2392531	47.5727878	89.0085052	207.523453	179.973936
AT5G23535	558.8311711	-1.165915428	0.18486859	-6.3067255	2.85E-10	1.41E-08	864.833547	673.796001	780.396158	303.519003	368.401727	362.040591
AT5G23690	326.6419962	-1.670602969	0.2378405	-7.0240475	2.16E-12	1.55E-10	583.867093	443.447067	464.593821	197.598882	133.271943	137.073172
AT5G23800	36.42632387	1.862234663	0.46174561	4.03303166	5.51E-05	0.00064287	17.7562443	14.2065422	15.1828046	38.2736572	81.8670504	51.2716444
AT5G23870	350.0565822	1.377941419	0.22849141	6.03060478	1.63E-09	6.64E-08	199.496627	192.803073	191.303338	418.339974	646.368921	452.027559
AT5G23930	53.02448792	-1.738829308	0.36780786	-4.727548	2.27E-06	4.19E-05	94.0036464	74.07697	76.9262101	24.0322964	32.3660432	16.7417614
AT5G24105	213.3988742	1.376606953	0.25020265	5.50196788	3.76E-08	1.13E-06	143.09444	112.637585	100.206511	243.883304	333.179856	347.39155
AT5G24110	207.0107215	1.637666469	0.39979338	4.09628206	4.20E-05	0.00051021	133.694075	106.549066	61.7434055	183.357521	272.25554	484.464722
AT5G24160	931.8551476	-1.281719244	0.34862556	-3.6764925	0.00023646	0.00210976	861.700092	1022.87104	2077.00767	623.059536	370.305612	636.186935
AT5G24240	437.9107201	7.324339318	1.51575975	4.83212415	1.35E-06	2.64E-05	2.08896992	9.13277712	5.06093487	1466.86017	1132.81151	11.509961
AT5G24530	607.8526478	-1.180615995	0.45856113	-2.5746098	0.01003532	0.04126669	869.011487	1179.143	482.813187	651.542258	158.022446	306.583507
AT5G24660	169.9953529	2.662847709	0.39705974	6.70641571	1.99E-11	1.22E-09	43.8683683	26.3835784	68.8287143	217.180753	429.326043	234.38466
AT5G24850	733.8951103	-1.241525904	0.19233437	-6.4550393	1.08E-10	5.81E-09	982.860347	1023.88579	1087.08881	385.406828	388.392518	535.736366
AT5G25130	626.3609428	-1.440313254	0.16429437	-8.7666624	1.84E-18	3.77E-16	1003.75005	854.422037	887.687977	312.419853	338.891511	360.994231
AT5G25190	847.9288719	1.576873236	0.2643576	5.96492496	2.45E-09	9.58E-08	512.842115	476.933916	287.461101	1232.7678	1030.00173	1547.56657
AT5G25240	34.76091312	-1.208338612	0.41912299	-2.8830168	0.00393886	0.02018324	59.5356427	43.6343796	42.5118529	19.5818711	27.606331	15.6954014
AT5G25390	12.44303719	4.107478699	1.14007649	3.60280974	0.0003148	0.00267809	1.04448496	3.04425904	0	6.23059536	47.5971223	16.7417614
AT5G25450	14.33330705	1.768061195	0.62419722	2.83253614	0.00461803	0.02273889	9.40036464	6.08851808	4.0487479	18.6917861	24.7505036	23.019922
AT5G25460	9712.927362	1.327129132	0.22350592	5.93778064	2.89E-09	1.12E-07	5801.06947	6677.07483	4129.72286	11763.364	16201.1085	13705.2245
AT5G25800	335.0579762	-1.225375112	0.23372061	-5.2429056	1.58E-07	4.07E-06	444.950593	459.683115	504.069114	226.971688	231.322015	143.351332
AT5G25980	41781.32007	1.345066771	0.22160663	6.06961417	1.28E-09	5.42E-08	18605.4106	30103.6629	22098.066	49960.474	64457.927	65462.38
AT5G26180	383.232424	-1.228232196	0.23470269	-5.2331407	1.67E-07	4.26E-06	454.350958	623.05835	534.434723	228.751858	279.871079	178.927575
AT5G26200	148.6640687	-1.208074291	0.28519469	-4.2359635	2.28E-05	0.00030181	277.832999	182.655542	161.949916	87.2283351	81.8670504	100.450569
AT5G26220	127.239581	4.440368452	0.5236169	8.48018551	2.25E-17	3.72E-15	4.17793984	8.11802411	21.2559265	333.781895	268.44777	127.655931
AT5G26230	150.3043046	1.327889895	0.26941989	4.92870031	8.28E-07	1.73E-05	89.8257066	100.460548	66.8043403	259.904835	202.763741	182.066656
AT5G26280	111.5509567	-1.34356978	0.40509451	-3.3166823	0.00091093	0.00637719	162.939654	98.4310423	218.632387	38.2736572	91.3864749	59.6425252
AT5G26330	105.1818003	1.01871943	0.32904498	3.09598841	0.00196158	0.01175034	52.224248	93.3572773	62.7555924	125.501992	115.185036	182.066656
AT5G26670	281.5912534	1.205279055	0.38305959	3.14645317	0.00165264	0.0102006	138.9165	219.186651	152.840233	188.698031	579.73295	410.173155
AT5G26742	20365.2922	-1.076052251	0.215471	-4.9939539	5.92E-07	1.30E-05	25069.728	29136.6033	28673.2326	9995.65513	16798.9284	12517.6058
AT5G26800	647.6367102	-1.5849676	0.1622944	-9.7660032	1.58E-22	6.38E-20	1028.81769	874.717098	1011.17479	337.342235	330.324029	303.444426
AT5G26860	1246.771896	-2.001121526	0.16507634	-12.122401	8.04E-34	9.56E-31	1792.33619	2052.84535	2140.77545	558.973413	472.163454	463.53752
AT5G27030	518.8847489	1.054658515	0.19006171	5.54903215	2.87E-08	8.85E-07	287.233364	339.94226	384.63105	764.58306	710.149065	626.769694
AT5G27110	41.40068484	-1.191729939	0.39930629	-2.9845008	0.00284041	0.01556911	60.5801277	48.7081447	63.7677794	34.713317	22.8466187	17.7881215
AT5G27120	1618.826307	-1.445175425	0.24451836	-5.9102942	3.41E-09	1.31E-07	2353.22462	2622.12179	2128.62921	660.443109	1189.92806	758.611066
AT5G27220	21.34940282	2.15283267	0.67276708	3.19996733	0.00137443	0.00885171	9.40036464	3.04425904	11.1340567	58.7456134	23.7985612	21.9735619
AT5G27330	270.5447725	-1.184397597	0.40932094	-2.8935671	0.00380893	0.01963905	275.744029	449.535585	401.838229	76.5473145	274.159425	145.444053
AT5G27395	690.9893631	-1.635136719	0.19675312	-8.3106012	9.52E-17	1.45E-14	1047.61842	999.531718	1089.11319	289.277642	416.950792	303.444426
AT5G27440	54.8675506	-1.448063503	0.3385549	-4.2771897	1.89E-05	0.0002582	91.9146765	78.135982	70.8530882	24.9223815	36.173813	27.2053624
AT5G27850	10226.5562	-1.146664741	0.24443273	-4.691126	2.72E-06	4.91E-05	15602.5163	14141.598	12523.7894	4413.04169	8407.55569	6270.83602
AT5G28060	8091.60746	-1.165063275	0.18798445	-6.1976576	5.73E-10	2.72E-08	12361.4795	10857.8572	10356.6971	3992.03146	5812.56058	5169.01885
AT5G28145	85.57306187	-1.172892002	0.28391307	-4.1311659	3.61E-05	0.00044661	131.605105	101.475301	122.474624	53.4051031	43.7893526	60.6888853
AT5G28630	617.715447	1.03968296	0.31576507	3.29258383	0.00099271	0.00682033	569.244303	320.661952	322.887645	728.979658	608.291223	1156.2279
AT5G28640	35.7861904	-1.068783125	0.41436901	-2.5793027	0.0099	0.04083579	56.4021878	50.7376507	38.463105	25.8124665	27.606331	15.6954014
AT5G35180	2251.706792	1.015161712	0.15244645	6.6591364	2.75E-11	1.63E-09	1302.47275	1651.00315	1518.28046	3061.89258	2913.89583	3062.69599
AT5G35495	33.29918023	1.706818923	0.53275698	3.20374768	0.00135651	0.00876003	7.31139472	15.2212952	24.2924874	69.4266341	33.3179856	50.2252843
AT5G35510	14.86696087	3.116505481	0.76454178	4.07630503	4.58E-05	0.00054836	5.2224248	2.02950603	2.02437395	40.0538273	19.9907914	19.8808417
AT5G35670	106.6736199	1.507495666	0.3579129	4.21190645	2.53E-05	0.00032917	42.8238834	57.8409218	65.7921534	106.810206	226.562302	140.212252
AT5G35777	1039.617562	-1.794121682	0.32711613	-5.4846628	4.14E-08	1.22E-06	1895.7402	1410.50669	1535.48764	629.290132	235.129784	531.550926
AT5G35935	272.2427006	-5.927611426	0.41557997	-14.263468	3.70E-46	1.17E-42	475.240657	553.040392	577.958763	2.67025516	5.71165468	18.8344816
AT5G36910	904.8943135	-1.92434895	0.44926231	-4.2833527	1.84E-05	0.00025224	1844.56044	1314.10515	1138.71035	596.356985	117.088921	418.544036
AT5G36950	899.9463723	-1.149005526	0.15297225	-7.5112024	5.86E-14	5.57E-12	1135.35515	1247.13145	1339.12337	590.12639	530.231943	557.709928
AT5G37300	88.77580366	3.593395781	0.61502876	5.84264675	5.14E-09	1.91E-07	4.17793984	24.3540723	12.1462437	59.6356985	261.784173	170.556695
AT5G37540	209.7607437	1.261782933	0.20290105	6.21871083	5.01E-10	2.40E-08	113.848861	121.770362	134.620868	292.837982	273.207482	322.278908
AT5G37570	36.61759215	-1.264476872	0.48192072	-2.6238276	0.00869478	0.03691886	47.0018232	59.8704278	48.5849748	35.6034021	17.134964	11.509961
AT5G37950	10.79737087	6.842605142	1.3928087	4.91281045	8.98E-07	1.86E-05	0	0	0	16.911616	34.2699281	13.6026812
AT5G38096	12.98800705	2.137441699	0.8414767	2.54010799	0.01108182	0.04439962	7.31139472	6.08851808	1.01218697	8.90085052	19.0388489	35.5762431
AT5G38100	14.50478247	3.257980085	0.78577897	4.14617875	3.38E-05	0.00042134	5.2224248	2.02950603	1.01218697	16.911616	30.4621583	31.3908027

Table S-5.1 Differentially Expressed Genes between lpa66 (LP) and wild type (WT) Arabidopsis plants.

ID	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	WT4	WT2	WT1	LP3	LP2	LP1
AT5G38200	51.10067549	-1.938825908	0.5115921	-3.7897886	0.00015078	0.00146398	105.492981	78.135982	59.7190315	34.713317	7.61553957	20.9272018
AT5G38890	251.5664207	-1.682304201	0.21909246	-7.6785125	1.61E-14	1.76E-12	406.304649	381.547133	363.375124	120.161482	142.791367	95.2187682
AT5G38970	13.79194575	2.517017299	0.83536923	3.01305961	0.00258628	0.01446357	6.26690976	6.08851808	0	32.0430619	24.7505036	13.6026812
AT5G39050	994.8424001	-1.225186244	0.29027452	-4.2207847	2.43E-05	0.00031865	1079.99745	1461.24434	1639.7429	810.867482	380.776979	596.425252
AT5G39350	80.81506494	-1.172706613	0.36210389	-3.2385916	0.00120121	0.00794972	97.1371013	95.3867833	143.73055	70.3167191	43.7893526	34.529883
AT5G39680	23.47275722	-1.746398253	0.52599861	-3.3201575	0.00089967	0.00632025	40.7349134	23.3393193	44.5362269	14.2413608	8.56748202	9.41724082
AT5G39790	587.0473276	-1.142849003	0.28452947	-4.0166279	5.90E-05	0.00067887	532.68733	732.651676	1158.95409	379.176232	337.939569	380.875073
AT5G39840	215.6692896	-1.381803937	0.28655426	-4.8221372	1.42E-06	2.76E-05	264.254695	395.753675	275.314857	108.590376	158.022446	92.079688
AT5G39860	204.0513285	1.025975223	0.35547176	2.88623552	0.0038988	0.02003189	203.674567	127.85888	71.8652752	280.376791	310.333238	230.19922
AT5G39940	451.5036512	-1.322792315	0.17299777	-7.6462967	2.07E-14	2.24E-12	652.8031	587.541995	695.372452	280.376791	252.264748	240.662821
AT5G39980	368.172253	-1.195199172	0.22802655	-5.2414914	1.59E-07	4.09E-06	474.196172	472.874904	590.105006	171.786415	264.64	235.43102
AT5G40020	17.92998964	1.469173281	0.57171576	2.56976175	0.01017685	0.04169306	5.2224248	13.1917892	10.1218697	26.7025516	31.4141007	20.9272018
AT5G40330	88.04530038	1.01134742	0.35241349	2.86977497	0.00410764	0.02085712	57.4466728	69.0032049	48.5849748	72.9869743	149.454964	130.795011
AT5G40480	1023.52739	-1.007685658	0.26283884	-3.8338537	0.00012615	0.00126757	908.701915	1778.86203	1414.0252	749.451614	717.764605	572.35897
AT5G40770	2447.971498	-1.270213215	0.13610952	-9.332288	1.04E-20	3.40E-18	3642.11906	3265.4752	3475.85007	1459.73949	1502.16518	1342.48
AT5G40780	954.2624256	1.684878782	0.27929307	6.03265515	1.61E-09	6.58E-08	511.79763	488.0962	358.314189	1302.19443	1030.00173	2035.17038
AT5G41080	654.5382192	-1.856200986	0.24589991	-7.5486039	4.40E-14	4.27E-12	1222.0474	814.84667	1040.52821	339.122405	210.379281	300.305346
AT5G41140	1511.39544	1.273357517	0.21664387	5.87765309	4.16E-09	1.57E-07	818.876209	1065.49066	769.262101	1775.71968	2611.17813	2027.84586
AT5G41270	173.0768847	-1.080446907	0.23389167	-4.6194331	3.85E-06	6.62E-05	242.320511	210.053874	253.046744	117.491227	126.608345	88.9406077
AT5G41400	130.6546605	1.099053204	0.28195797	3.89793279	9.70E-05	0.00102064	109.670921	80.1654881	59.7190315	175.346755	167.541871	191.483897
AT5G41520	10177.52523	-1.074597505	0.17470858	-6.1507997	7.71E-10	3.50E-08	14840.0423	13762.0804	12803.153	5425.95848	7561.27885	6672.6383
AT5G41550	10.94047498	2.11835548	0.81364737	2.60353018	0.00922691	0.03867332	3.13345488	8.11802411	1.01218697	12.4611907	19.9907914	20.9272018
AT5G41650	37.62546362	-1.900146653	0.40615801	-4.6783435	2.89E-06	5.16E-05	61.6246126	53.7819097	62.7555924	20.4719562	11.4233094	15.6954014
AT5G41820	13.1669533	2.045420583	0.79579547	2.57028427	0.01016151	0.04165059	6.26690976	4.05901205	5.06093487	6.23059536	33.3179856	24.0662821
AT5G41830	18.86122695	-2.239157002	0.65613727	-3.412635	0.00064338	0.00481263	45.9573382	17.2508012	30.3656092	9.79093557	6.66359713	3.13908027
AT5G41900	458.3369727	1.710472889	0.23122638	7.39739498	1.39E-13	1.24E-11	171.295533	264.850537	207.49833	834.009694	633.041727	639.326015
AT5G42040	26.14475211	1.91956838	0.47649121	4.02854938	5.61E-05	0.00065205	12.5338195	8.11802411	12.1462437	34.713317	48.5490648	40.8080435
AT5G42150	597.826402	-1.270948154	0.14605718	-8.7017167	3.27E-18	6.10E-16	860.655607	823.979447	851.249246	343.57283	346.507051	360.994231
AT5G42280	47.86304515	1.062816323	0.41404911	2.56688472	0.01026167	0.04196173	24.0231541	41.6048736	27.3290483	52.5150181	90.4345324	51.2716444
AT5G42720	383.5151576	1.190044167	0.32403543	3.67257425	0.00024012	0.00213438	224.564266	289.204609	187.25459	300.848748	668.263598	630.955135
AT5G43020	103.4417371	1.321827832	0.42665853	3.0980931	0.0019477	0.01167824	65.8025525	55.8114157	55.6702836	67.646464	231.322015	144.397692
AT5G43240	15.14199459	2.303365349	0.80778081	2.85147322	0.00435172	0.021754	1.04448496	10.1475301	4.0487479	11.5711057	29.5102158	34.529883
AT5G43450	1491.480922	-1.055236242	0.3341507	-3.1579651	0.00158875	0.00989379	2511.98633	1715.94735	1813.83906	1376.96158	502.625612	1027.52561
AT5G43760	5526.229511	1.061956886	0.20216203	5.25299884	1.50E-07	3.86E-06	2935.00274	4436.50018	3366.53388	7150.94331	6805.43655	8462.96041
AT5G43990	114.458352	1.206874358	0.42093523	2.86712602	0.00414218	0.02097096	56.4021878	107.563819	43.5240399	96.1291856	219.898705	163.232174
AT5G44010	93.79335095	-1.090502682	0.31295831	-3.4844983	0.00049306	0.00385041	106.537466	108.578572	168.023038	66.7563789	64.7320864	48.1325642
AT5G44420	35.75014642	-1.785499479	0.52490087	-3.4015937	0.00066994	0.00497257	31.3345488	80.1654881	54.6580966	17.801701	8.56748202	21.9735619
AT5G44550	60.06737559	1.636065431	0.52751199	3.10147532	0.00192559	0.01156387	13.5783045	40.5901205	33.4021702	40.9439124	99.0020145	132.887732
AT5G44572	205.075707	-1.348056008	0.33026176	-4.0817804	4.47E-05	0.00053695	407.349134	210.053874	266.205174	148.644204	79.9631655	118.23869
AT5G44578	70.58349804	1.691273559	0.37784592	4.47609317	7.60E-06	0.00011793	21.9341842	34.5016025	43.5240399	75.6572294	117.088921	130.795011
AT5G44785	1717.852161	-1.094407514	0.17106386	-6.3976549	1.58E-10	8.07E-09	2353.22462	2362.34502	2303.73755	918.567774	1273.69899	1095.53901
AT5G45040	649.4077284	-1.222582227	0.22123197	-5.5262456	3.27E-08	9.93E-07	988.082772	813.831917	925.138895	286.607387	435.989641	446.795759
AT5G45080	60.81823645	2.075795598	0.45229958	4.58942631	4.44E-06	7.50E-05	36.5569736	16.2360482	17.2071786	60.5257835	126.608345	107.775089
AT5G45140	529.0225728	-1.408499639	0.20215879	-6.9672937	3.23E-12	2.22E-10	627.735461	805.713893	872.505172	323.100874	285.582734	259.497302
AT5G45340	1105.389777	1.474474219	0.19180021	7.68755279	1.50E-14	1.66E-12	669.514859	573.335453	512.166609	1398.32362	1594.5036	1884.49452
AT5G45775	3771.473619	-1.030568794	0.25124274	-4.1018849	4.10E-05	0.00049993	5377.00857	5073.76507	4741.08379	1692.05168	3382.25151	2362.68108
AT5G45840	878.8043237	-1.000989333	0.33744851	-2.9663469	0.0030136	0.01632244	1232.49225	995.472706	1288.51402	939.929815	345.555108	470.862041
AT5G46050	27.37234247	-1.618015737	0.4385631	-3.6893567	0.00022482	0.00202393	40.7349134	37.5458615	45.5484139	11.5711057	15.2310791	13.6026812
AT5G46090	60.57643828	-1.186955536	0.31455575	-3.7734346	0.00016102	0.00154238	77.2918871	84.2245001	91.0968277	34.713317	44.741295	31.3908027
AT5G46100	79.02780871	-1.499395468	0.31333383	-4.7852971	1.71E-06	3.26E-05	97.1371013	106.549066	146.767111	45.3943377	43.7893526	34.529883
AT5G46330	1485.550728	1.243666795	0.14206734	8.75406534	2.06E-18	4.01E-16	861.700092	865.584321	919.065773	2141.54464	1913.40432	2212.00523
AT5G46580	5375.52889	-1.431183313	0.20682258	-6.9198601	4.52E-12	3.06E-10	7344.81824	7770.97858	8412.28595	2299.97977	3698.29641	2726.8144
AT5G46690	201.9011804	2.007193392	0.27743165	7.2349113	4.66E-13	3.82E-11	71.0249773	95.3867833	74.9018361	283.937132	424.566331	261.590023
AT5G46830	13.51374715	7.167620792	1.37639728	5.20752323	1.91E-07	4.83E-06	0	0	0	27.5926366	40.9335252	12.5563211
AT5G46920	389.1408348	-1.280607552	0.21162321	-6.0513569	1.44E-09	5.98E-08	537.909754	521.583049	595.165941	260.79492	244.649209	174.742135
AT5G47455	289.9024985	-1.642558195	0.18197877	-9.0260979	1.78E-19	4.35E-17	406.304649	438.373302	472.691317	138.853268	140.887482	142.304972
AT5G47500	109.4255721	2.774979606	0.51502285	5.38807086	7.12E-08	1.99E-06	16.7117594	52.7671567	14.1706176	128.172248	295.102158	149.629493
AT5G47560	5998.709043	-1.09216784	0.3566827	-3.0620152	0.00219852	0.01281587	8747.56154	7795.33265	7957.814	6397.93135	1962.90533	3130.70939
AT5G47800	133.646785	1.281478033	0.33829508	3.78804813	0.00015184	0.00147202	85.6477667	104.51956	43.5240399	158.435139	204.667626	205.086578
AT5G48030	1705.383846	-1.594758926	0.18228494	-8.7487148	2.16E-18	4.15E-16	2664.48113	2429.31871	2594.23522	1031.60858	773.929209	738.730224
AT5G48240	426.0561443	-1.338153292	0.23908751	-5.5969185	2.18E-08	6.98E-07	590.134002	649.441929	592.12938	185.137691	320.804605	218.689259
AT5G48450	296.7702056	1.20605837	0.29533958	4.08363267	4.43E-05	0.00053404	104.448496	221.216157	212.559265	367.605127	432.181871	442.610318
AT5G48460	638.0773072	1.258344856	0.19269461	6.53025455	6.57E-11	3.64E-09	367.658706	369.370097	391.716359	876.733776	1073.79108	749.193825
AT5G48470	943.9628843	-2.021243218	0.19134719	-10.563224	4.41E-26	2.90E-23	1600.15096	1295.8396	1647.8404	364.044786	322.708489	433.193077
AT5G48530	351.8864213	1.310744126	0.30507352	4.29648607	1.74E-05	0.00023913	213.074932	235.422699	157.901168	448.602866	342.699281	713.617582
AT5G48540	1950.662954	1.396012219	0.31641316	4.41199167	1.02E-05	0.00015169	1200.11322	1223.79213	798.615523	2385.42794	1836.29698	4259.73193
AT5G48657	147.0026938	1.371501172	0.36208948	3.78774106	0.00015202	0.00147309	86.6922517	97.4162893	61.7434055	256.344495	116.136979	263.682743
AT5G48900	819.7242363	1.801292728	0.23584458	7.63762616	2.21E-14	2.34E-12	329.012762	460.697868	306.692653	1009.35645	1498.35741	1314.22827
AT5G48910	519.5686688	1.154005165	0.1817246	6.35029695	2.15E-10	1.08E-08	368.703191	272.968561	324.912019	678.24481	734.899569	737.683864
AT5G48920	47.59596695	1.095525723	0.43299608	2.53010541	0.01140283	0.04533261	24.0231541	44.6491326	22.2681134	43.6141676	80.915108	70.1061261
AT5G49120	22.02640822	1.420579976	0.53188749	2.67082793	0.00756644	0.03322496	18.8007293	8.11802411	9.10968277	38.2736572	28.5582734	29.2980825
AT5G49170	191.7554529	1.139341267	0.28059378	4.06046509	4.90E-05	0.00057999	151.450319	106.549066	101.218697	197.598882	322.708489	271.007263
AT5G49410	60.91001257	-1.317546291	0.38731757	-3.4017209	0.00066963	0.00497257	94.0036464	65.9589459	101.218697	49.8447629	31.4141007	23.019922
AT5G49500	93.10023843	1.042807868	0.29603396	3.52259543	0.00042734	0.0034534	71.0249773	69.0032049	42.5118529	113.040802	133.271943	129.748651
AT5G49520	137.6816948	1.168204703	0.29637861	3.9415958	8.09E-05	0.00087872	65.8025525	79.1507351	109.316193	207.389817	144.695252	219.735619
AT5G49800	87.5029034	1.301045209	0.29593555	4.39638026	1.10E-05	0.00016076	48.0463082	62.9146868	40.487479	107.700291	125.656403	140.212252
AT5G49910	16208.89145	-1.279756733	0.30273263	-4.2273498	2.36E-05	0.00031164	21132.0197	26305.4424	21445.2054	5489.15452	13865.0417	9016.4849
AT5G50150	471.2562705	1.180917135	0.17549275	6.72915048	1.71E-11	1.07E-09	264.254695	315.588187	285.436727	595.4669	714.908778	651.882336
AT5G50330	125.2294054	1.190243656	0.29345903	4.05591079	4.99E-05	0.00058921	58.4911578	86.2540062	84.0115189	130.842503	206.571511	185.205736
AT5G50335	156.0582109	3.348751846	0.31475653	10.6391813	1.96E-26	1.38E-23	16.7117594	34.5016025	32.3899832	304.409088	316.044892	232.29194
AT5G50740	740.0277427	1.401297506	0.24456052	5.72985982	1.01E-08	3.48E-07	372.881131	452.579844	393.740733	762.80289	1379.36461	1078.79725

Table S-5.1 Differentially Expressed Genes between lpa66 (LP) and wild type (WT) Arabidopsis plants.

ID	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	WT4	WT2	WT1	LP3	LP2	LP1
AT5G50810	650.6192711	-1.138226167	0.22945235	-4.960621	7.03E-07	1.51E-05	1027.7732	890.953146	765.213353	307.079343	493.106187	419.590396
AT5G50820	31.8582999	1.579387881	0.61309178	2.5761035	0.00999207	0.04111549	7.31139472	32.4720964	8.0974958	36.4934871	62.8282015	43.9471238
AT5G51030	37.7733936	-2.015378315	0.47435278	-4.2486909	2.15E-05	0.00028717	80.4253419	41.6048736	59.7190315	19.5818711	8.56748202	16.7417614
AT5G51190	493.3232118	-1.136574616	0.2334727	-4.8681265	1.13E-06	2.26E-05	750.984686	518.53879	765.213353	290.167727	370.305612	264.729103
AT5G51220	537.0123443	-1.353889097	0.17204171	-7.86954	3.56E-15	4.29E-13	776.052325	726.563158	813.798328	309.749598	332.227914	263.682743
AT5G51310	16.46646416	1.847543976	0.56940236	3.24470725	0.00117571	0.00780705	7.31139472	8.11802411	6.07312185	25.8124665	29.5102158	21.9735619
AT5G51330	10.36902819	2.176110746	0.80151152	2.71500871	0.0066274	0.03008016	4.17793984	5.07376507	2.02437395	10.6810206	26.6543885	13.6026812
AT5G51440	20.68619664	-3.30049752	0.61597639	-5.3581559	8.41E-08	2.32E-06	43.8683683	33.4868494	35.4265441	5.34051031	2.85582734	3.13908027
AT5G51540	187.463964	-1.481076814	0.29152772	-5.0803979	3.77E-07	8.68E-06	251.720875	313.558681	263.168613	95.2391006	135.175827	65.9206857
AT5G51670	97.93886109	1.196489302	0.2868313	4.17140423	3.03E-05	0.00038537	78.336372	50.7376507	49.5971618	145.083863	135.175827	128.702291
AT5G51720	6255.341322	-1.17583248	0.33852241	-3.4734258	0.00051386	0.00398503	12533.8195	5962.68871	7519.53704	2260.81603	4281.83713	4973.34951
AT5G51790	15.95460009	2.173628885	0.78781266	2.75906825	0.00579664	0.02709133	3.13345488	13.1917892	1.01218697	19.5818711	29.5102158	29.2980825
AT5G52470	5917.492714	-1.02309579	0.15803159	-6.4739953	9.54E-11	5.16E-09	8156.38305	8125.12738	7514.4761	3546.09885	4523.63051	3639.24039
AT5G52471	17.12034613	-1.642353978	0.54725807	-3.0010594	0.00269042	0.01491882	26.112124	28.4130844	23.2803004	7.12068042	10.4713669	7.32452063
AT5G52850	59.12580512	-1.431131025	0.33427335	-4.2813195	1.86E-05	0.00025419	89.8257066	79.1507351	90.0846408	41.8339974	26.6543885	27.2053624
AT5G53070	507.7184955	-1.17384007	0.18633846	-6.2995051	2.99E-10	1.47E-08	729.050502	736.710688	644.763103	266.135431	358.882302	310.768947
AT5G53090	94.00425258	1.419801572	0.37148825	3.8219286	0.00013241	0.00131658	42.8238834	66.9736989	43.5240399	82.7779098	175.15741	152.768573
AT5G53210	35.00276771	2.096098811	0.7595948	2.759496	0.00578906	0.02706254	7.31139472	19.2803073	13.1584307	8.01076547	94.2423022	68.0134059
AT5G53770	416.8065682	-1.15511314	0.2146072	-5.3824529	7.35E-08	2.04E-06	567.155333	543.907615	615.409681	287.497472	292.246331	194.622977
AT5G53920	171.1078347	-1.106355154	0.31595276	-3.5016474	0.00046239	0.00367537	239.187056	187.729308	274.30267	145.973949	68.5398562	110.91417
AT5G54095	13.89956621	-2.139742409	0.73565329	-2.9086289	0.00363018	0.01890691	35.5124886	14.2065422	18.2193655	6.23059536	1.90388489	7.32452063
AT5G54100	387.9618123	-1.149099726	0.20131568	-5.7079494	1.14E-08	3.91E-07	495.085871	620.014091	488.886309	206.499732	259.880288	257.404582
AT5G54190	1957.618094	2.463345685	0.38436205	6.40892011	1.47E-10	7.56E-09	572.377758	645.382917	585.044072	1290.62333	4906.31137	3745.96912
AT5G54580	1278.062103	-1.224125673	0.17573396	-6.9657889	3.27E-12	2.23E-10	2082.70301	1541.40983	1746.02253	826.889013	736.803454	734.544784
AT5G54620	10.62905884	-1.886129814	0.73522547	-2.5653761	0.0103064	0.04208135	14.6227894	18.2655542	17.2071786	4.45042526	1.90388489	7.32452063
AT5G54690	41.28132098	1.540248862	0.49656723	3.10179323	0.00192352	0.0115551	15.6672744	18.2655542	29.3534223	32.0430619	88.5306475	63.8279655
AT5G55010	18.22901869	1.790434631	0.66344205	2.69870538	0.00696098	0.03119246	9.40036464	9.13277712	6.07312185	49.8447629	17.134964	17.7881215
AT5G55140	750.5413692	-1.261201888	0.17814568	-7.0796098	1.45E-12	1.09E-10	1185.49043	950.823574	1041.5404	429.91108	497.8659	397.616834
AT5G55280	3826.401925	-1.099320858	0.12790307	-8.5949529	8.33E-18	1.48E-15	5103.35352	5015.92415	5533.62619	2528.73163	2372.24058	2404.53549
AT5G55400	399.8975657	1.107970806	0.25273523	4.38391916	1.17E-05	0.00016869	210.985962	297.322633	252.034557	451.273121	715.86072	471.908401
AT5G55570	836.4432331	-1.561111205	0.21895885	-7.1297013	1.01E-12	7.94E-11	1523.90356	1063.46116	1160.97846	462.844227	340.795396	466.6766
AT5G55580	1093.376705	-1.618153681	0.18317324	-8.8340072	1.01E-18	2.21E-16	1650.28624	1715.94735	1582.04824	463.734312	650.176691	498.067403
AT5G55730	793.770488	1.281334773	0.38560127	3.32295266	0.0008907	0.00626671	459.573382	567.246935	361.35075	500.227799	1752.52604	1121.69802
AT5G55930	421.362784	1.631677385	0.2397734	6.80508081	1.01E-11	6.56E-10	223.519781	163.375235	229.766443	498.447629	649.224749	763.842866
AT5G56090	489.4734338	-1.276900211	0.17082804	-7.4747694	7.73E-14	7.29E-12	706.071833	617.984585	755.091483	302.628918	279.871079	275.192704
AT5G56120	43.33720755	1.595606012	0.57154534	2.79174004	0.00524255	0.02507436	25.067639	24.3540723	15.1828046	21.3620413	101.857842	72.1988462
AT5G56220	96.23896923	2.397521161	0.34007718	7.04993248	1.79E-12	1.31E-10	29.2455789	33.4868494	29.3534223	121.051567	219.898705	144.397692
AT5G56490	19.68856391	2.01570723	0.77418809	2.6036402	0.00922395	0.03867332	1.04448496	15.2212952	7.08530882	15.1314459	40.9335252	38.7153234
AT5G56870	1589.174342	-1.887179691	0.41392596	-4.5592205	5.13E-06	8.44E-05	3424.86618	2087.34695	1994.00834	1101.92529	276.06331	650.835976
AT5G56890	1384.711578	1.208797418	0.27660825	4.37006996	1.24E-05	0.00017867	551.488059	1092.889	864.407677	1565.65961	2392.23137	1841.59376
AT5G56960	61.47833519	2.194277563	0.64252359	3.41509263	0.0006376	0.00478668	43.8683683	14.2065422	8.0974958	79.2175696	46.6451799	176.834855
AT5G57010	74.90439308	1.089588134	0.37382944	2.91466649	0.00356069	0.01862657	55.3577029	35.5163555	52.6337227	75.6572294	83.7709353	146.490413
AT5G57080	45.19443161	-1.345179708	0.34092007	-3.9457334	7.96E-05	0.00086641	69.9804923	60.8851808	63.7677794	25.8124665	26.6543885	24.0662821
AT5G57120	2224.479873	-1.388196296	0.17292097	-8.0279232	9.91E-16	1.31E-13	3475.00146	3032.082	3149.92587	1032.49866	1406.97094	1250.40031
AT5G57280	306.7344929	-1.03133593	0.26469024	-3.8963881	9.76E-05	0.00102547	419.882954	428.225772	387.667611	152.204544	280.823022	171.603055
AT5G57390	57.52976176	1.570299567	0.41742895	3.76183678	0.00016867	0.00160338	21.9341842	37.5458615	27.3290483	50.734848	100.905899	106.728729
AT5G57450	22.09998549	-1.502731663	0.55110226	-2.7267747	0.00639567	0.02927273	24.0231541	23.3393193	50.6093487	9.79093557	13.3271943	11.509961
AT5G57640	50.93719792	-1.269444588	0.50509249	-2.5132913	0.01196105	0.04707008	85.6477667	48.7081447	81.987145	53.4051031	18.0869065	17.7881215
AT5G57655	5843.47463	-1.169135196	0.31388674	-3.724704	0.00019554	0.00180388	8440.48296	6493.40453	9335.40047	5522.97775	2266.57497	3002.0071
AT5G57760	128.8150824	2.342498073	0.38449676	6.09237405	1.11E-09	4.77E-08	55.3577029	29.4278374	42.5118529	123.721822	287.486619	234.38466
AT5G57770	18.96319887	2.186855575	0.64825443	3.37345258	0.00074232	0.00539407	6.26690976	7.1032711	7.08530882	14.2413608	46.6451799	32.4371628
AT5G57780	205.4937451	1.391407907	0.30686728	4.53423346	5.78E-06	9.38E-05	168.162079	96.4015363	75.9140231	311.529768	303.669641	277.285424
AT5G57785	46.91105033	-1.77405243	0.66490602	-2.6681251	0.00762759	0.03341634	135.783045	37.5458615	44.5362269	33.823232	5.71165468	24.0662821
AT5G57870	2768.895057	2.654846269	0.16357193	16.2304512	3.07E-59	1.46E-55	681.004194	852.392531	742.94524	4390.78956	5279.47281	4666.766
AT5G57970	115.5587522	1.102838349	0.25617563	4.30500875	1.67E-05	0.00023078	79.380857	63.9294399	76.9262101	135.292928	180.869065	156.954014
AT5G58210	331.7603186	-1.36143383	0.22152493	-6.1457363	7.96E-10	3.58E-08	410.482589	509.406013	513.178796	220.741093	149.454964	187.298456
AT5G58370	658.0339722	-1.430377036	0.19376027	-7.3822	1.56E-13	1.37E-11	993.305197	940.676044	946.394822	380.066317	408.38331	279.378144
AT5G58540	286.346583	1.376920798	0.28191901	4.8841006	1.04E-06	2.11E-05	134.73856	205.994862	136.645242	298.178492	435.037698	507.484644
AT5G58550	280.3524546	1.303219789	0.25130928	5.18572101	2.15E-07	5.39E-06	116.982316	189.758814	178.144908	340.01249	461.692087	395.524114
AT5G58690	61.34529358	1.186041296	0.32445629	3.6554733	0.00025671	0.0022555	31.3345488	33.4868494	47.5727878	95.2391006	80.915108	79.5233669
AT5G58770	1090.021393	-1.021317434	0.32908399	-3.103516	0.00191236	0.01149166	2011.67803	1115.21356	1255.11185	1077.893	523.568346	556.663568
AT5G59070	112.0930402	1.296880258	0.39322636	3.29805019	0.00097359	0.0067156	103.404011	53.7819097	37.4509181	172.6765	118.992806	186.252096
AT5G59200	17.01567861	-1.579946779	0.56208793	-2.8108534	0.00494103	0.02397571	20.8896992	27.3983314	28.3412353	11.5711057	7.61553957	6.27816054
AT5G59340	54.6947586	-1.837689761	0.42711779	-4.3025362	1.69E-05	0.00023303	113.848861	73.062217	69.8409013	36.4934871	17.134964	17.7881215
AT5G59440	472.7176546	-1.141313758	0.22430679	-5.088182	3.62E-07	8.39E-06	728.006017	537.819097	686.262769	364.934871	260.83223	258.450942
AT5G59660	46.48312279	1.791842118	0.40173184	4.46029405	8.18E-06	0.00012501	25.067639	20.2950603	17.2071786	91.6787604	51.4048921	73.2452063
AT5G59720	34.13397129	1.472216012	0.4588081	3.20878385	0.00133298	0.00863734	14.6227894	24.3540723	15.1828046	32.9331469	58.0684893	59.6425252
AT5G59980	190.5872972	-1.332893143	0.26803593	-4.9728152	6.60E-07	1.43E-05	242.320511	277.027573	299.607345	112.150717	137.079712	75.3379265
AT5G60100	12.78182774	-2.004966822	0.64866097	-3.0909318	0.00199529	0.01188496	20.8896992	17.2508012	23.2803004	6.23059536	3.80776979	5.23180045
AT5G60490	76.70682087	1.739722694	0.52291766	3.32695343	0.00087801	0.00619326	16.7117594	63.9294399	25.3046744	63.1960387	156.118561	134.980452
AT5G60540	1128.683616	-1.310692469	0.20752974	-6.3156849	2.69E-10	1.34E-08	1682.66527	1380.0641	1764.2419	802.856717	552.126619	590.147091
AT5G60670	2352.486913	-1.161726744	0.33073972	-3.5125105	0.00044389	0.00356445	3614.96245	3443.05698	2696.4661	743.221018	2110.4564	1506.75853
AT5G60720	41.62220009	1.652323403	0.44696323	3.69677702	0.00021835	0.00197692	12.5338195	26.3835784	21.2559265	42.7240825	80.915108	65.9206857
AT5G60730	27.14236833	-2.040617781	0.6450686	-3.163412	0.00155931	0.0097679	41.7793984	44.6491326	44.5362269	2.67025516	21.8946763	7.32452063
AT5G60840	485.8008304	1.172463568	0.23117344	5.07179182	3.94E-07	9.03E-06	339.457612	318.632446	237.863939	805.526972	542.607195	670.716818
AT5G60870	100.07656	-1.210855757	0.29012688	-4.1735387	3.00E-05	0.0003828	129.516135	123.799868	165.998664	51.624933	76.1553957	53.3643646
AT5G60930	66.25304353	1.216867137	0.47464485	2.56374241	0.01035504	0.04222281	28.2010939	66.9736989	24.2924874	55.1852732	116.136979	106.728729
AT5G61030	777.7493717	-1.788136038	0.17080037	-10.469158	1.20E-25	7.35E-23	1239.80365	1202.48232	1177.17345	381.846487	372.209497	292.980825
AT5G61100	17.47169908	-1.998963629	0.64454634	-3.1013498	0.00192641	0.01156512	27.156609	29.4278374	27.3290483	4.45042526	13.3271943	3.13908027
AT5G61350	153.1030757	-2.169386173	0.31833724	-6.8147421	9.44E-12	6.18E-10	197.407657	312.543928	241.912687	76.5473145	39.9815828	50.2252843
AT5G61360	55.1018625	-1.123336643	0.4272618	-2.629153	0.00855978	0.03652495	98.1815863	45.6638856	82.9993319	48.9546779	27.606331	27.2053624

Table S-5.1 Differentially Expressed Genes between lpa66 (LP) and wild type (WT) Arabidopsis plants.

ID	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	WT4	WT2	WT1	LP3	LP2	LP1
AT5G61370	60.73777307	-1.337393562	0.42189994	-3.1699306	0.00152475	0.00961802	63.7135826	70.0179579	127.535559	48.0645928	24.7505036	30.3444426
AT5G61430	20.32493111	-1.945977609	0.59035487	-3.2962845	0.00097973	0.00674817	50.1352781	21.3098133	25.3046744	7.12068042	7.61553957	10.4636009
AT5G61600	1343.605597	-1.534013307	0.3107434	-4.9365917	7.95E-07	1.67E-05	1859.18323	1583.0147	2550.71118	809.977397	865.315684	393.431394
AT5G61800	25.24697851	-1.57777656	0.48123035	-3.2786306	0.00104312	0.00708481	37.6014586	34.5016025	41.499666	17.801701	8.56748202	11.509961
AT5G61820	3067.876952	-1.180117476	0.28357832	-4.1615222	3.16E-05	0.00039923	4142.42735	3691.67146	4937.44806	2683.60643	1209.91885	1742.18955
AT5G61880	175.1449631	-1.682650807	0.23733999	-7.0896221	1.34E-12	1.04E-10	286.188879	229.334181	285.436727	68.536549	91.3864749	89.9869678
AT5G61940	59.27329376	-1.04749644	0.42003522	-2.49383	0.0126373	0.04909176	57.4466728	58.8556748	123.486811	48.9546779	32.3660432	34.529883
AT5G62165	144.4963901	4.158701931	0.45840277	9.07215712	1.17E-19	2.96E-17	8.35587968	26.3835784	11.1340567	200.269137	207.523453	413.312236
AT5G62170	138.5783698	1.801298506	0.31842167	5.65695955	1.54E-08	5.13E-07	61.6246126	85.2392531	38.463105	181.577351	232.273957	232.29194
AT5G62190	4646.632283	-1.177185034	0.18345259	-6.416835	1.39E-10	7.21E-09	5798.9805	6796.81569	6736.10432	3098.38607	3164.25669	2285.25044
AT5G62220	891.8888453	1.12944199	0.28981649	3.89709361	9.74E-05	0.00102362	544.176664	705.253344	429.167277	806.417057	1610.68662	1255.63211
AT5G62230	32.52762772	1.918805761	0.6433572	2.98248896	0.00285915	0.01564476	7.31139472	25.3688253	8.0974958	25.8124665	85.6748202	42.9007637
AT5G62280	1101.03122	1.026763431	0.40242902	2.55141496	0.01072865	0.04334047	1270.09371	469.830645	435.240399	2055.20639	1165.17755	1210.63862
AT5G62290	490.4132305	-1.27842611	0.19733277	-6.4785293	9.26E-11	5.04E-09	737.406382	615.955079	730.798996	339.122405	272.25554	246.940981
AT5G62370	113.230498	-2.439055761	0.35994876	-6.7761194	1.23E-11	7.96E-10	176.517958	202.950603	194.339899	28.4827217	56.1646044	20.9272018
AT5G62440	780.145544	-1.550617888	0.23655299	-6.555055	5.56E-11	3.12E-09	1263.8268	1143.62665	1082.02788	295.508237	525.472231	370.411472
AT5G62550	120.2055302	1.065614774	0.3928875	2.71226438	0.00668253	0.03025099	65.8025525	94.3720303	72.8774622	82.7779098	237.985612	167.417614
AT5G62720	1526.004688	-1.313340438	0.26647128	-4.9286378	8.28E-07	1.73E-05	2034.6567	2576.4579	1917.08213	566.094093	934.807483	1126.92982
AT5G62730	86.03495921	1.624735441	0.57476099	2.82680187	0.00470154	0.02306652	24.0231541	45.6638856	56.6824706	57.8555284	260.83223	71.1524862
AT5G62920	1141.819129	-1.022088278	0.2215402	-4.6135567	3.96E-06	6.78E-05	1792.33619	1115.21356	1683.26694	783.274846	808.199137	668.624098
AT5G62990	155.3725895	-2.002708898	0.33218065	-6.0289752	1.65E-09	6.70E-08	266.343665	224.260416	256.083305	95.2391006	49.5010072	40.8080435
AT5G63160	1719.262851	-1.86439677	0.39287627	-4.7455062	2.08E-06	3.88E-05	3256.70411	2587.62018	2249.07946	1279.05222	344.603166	598.517972
AT5G63180	2333.36692	1.205120033	0.42402017	2.84212904	0.00448133	0.02225001	2036.74567	1643.89988	554.678462	1881.6398	4051.46705	3831.77065
AT5G63290	116.5811271	-1.692209053	0.3350125	-5.0511818	4.39E-07	9.92E-06	190.096263	151.198199	193.327712	81.8878248	39.0296403	43.9471238
AT5G63420	574.2244861	-1.13973607	0.28912425	-3.9420286	8.08E-05	0.00087763	514.931085	984.310423	870.480798	289.277642	458.836259	327.510708
AT5G63580	65.59903414	1.88625718	0.34553329	5.4589738	4.79E-08	1.39E-06	18.8007293	30.4425904	34.4143571	93.4589305	96.1461871	120.33141
AT5G63650	47.30674814	3.048468204	0.4628805	6.58586437	4.52E-11	2.57E-09	6.26690976	8.11802411	16.1949916	106.810206	74.2515108	72.1988462
AT5G64120	385.549339	1.11231787	0.23231206	4.78803323	1.68E-06	3.22E-05	261.12124	279.057079	191.303338	507.34848	444.557123	629.908775
AT5G64310	313.5360791	1.161384067	0.23383526	4.96667641	6.81E-07	1.47E-05	175.473473	231.363687	174.09616	346.243085	445.509065	508.531004
AT5G64330	966.3911661	1.392591915	0.19977798	6.97069782	3.15E-12	2.17E-10	509.708661	647.412423	442.325708	1480.21144	1485.03022	1233.65855
AT5G64420	1491.608917	-1.08414037	0.18806468	-5.7647208	8.18E-09	2.90E-07	1749.51231	2304.50409	2027.41051	906.996668	1114.72461	846.505313
AT5G64490	44.51800486	-1.636218434	0.4366454	-3.7472476	0.00017879	0.00167941	85.6477667	41.6048736	74.9018361	26.7025516	15.2310791	23.019922
AT5G64650	365.6419404	-1.108573815	0.17205916	-6.4429806	1.17E-10	6.21E-09	538.954239	469.830645	489.898496	217.180753	244.649209	233.3383
AT5G64670	1005.256396	-1.229777611	0.18904516	-6.5052053	7.76E-11	4.27E-09	1509.28077	1353.68052	1365.44023	501.117884	724.428202	577.59077
AT5G64680	419.4388	-1.532217806	0.18211538	-8.4134452	3.98E-17	6.48E-15	675.781769	578.409218	616.421868	235.872539	221.80259	188.344816
AT5G64710	52.53323691	-1.925716649	0.40712443	-4.7300445	2.24E-06	4.15E-05	69.9804923	84.2245001	95.1455756	12.4611907	31.4141007	21.9735619
AT5G64780	219.1457584	1.301637604	0.40131721	3.24341338	0.00118107	0.00783986	181.740383	140.035916	57.6946576	306.189258	217.99482	411.219516
AT5G64810	15.5076221	-2.203383996	0.84975352	-2.5929684	0.00951515	0.03962426	20.8896992	35.5163555	20.2437395	13.3512758	0.95194245	2.09272018
AT5G64816	782.2485704	-1.508937964	0.19967841	-7.5568407	4.13E-14	4.05E-12	1363.05287	985.325176	1124.53973	412.999464	350.31482	457.25936
AT5G64870	51.46294736	1.187201763	0.33670416	3.52594918	0.00042197	0.00342182	31.3345488	31.4573434	31.3777962	73.8770593	58.0684893	82.6624472
AT5G65010	2012.802073	-1.159344407	0.21891325	-5.2959079	1.18E-07	3.17E-06	2221.61951	3259.38668	2860.44039	979.093557	1369.84518	1386.42712
AT5G65070	184.2422556	-2.078363325	0.28474651	-7.2989948	2.90E-13	2.45E-11	290.366819	246.584982	356.289815	50.734848	70.4437411	91.0333279
AT5G65310	2748.125422	1.400421514	0.16705979	8.38275638	5.17E-17	8.07E-15	1463.32343	1486.61316	1580.02387	3371.64218	4560.75626	4026.39363
AT5G65380	3822.974903	-1.057288062	0.25303214	-4.1784733	2.93E-05	0.00037534	5687.22061	4541.01974	5265.39664	3488.24332	2007.64662	1948.32249
AT5G65390	114.9590742	2.762190859	0.5252103	5.25920919	1.45E-07	3.76E-06	13.5783045	24.3540723	50.6093487	123.721822	344.603166	132.887732
AT5G65850	51.695211	-1.465584413	0.39402049	-3.719564	0.00019957	0.00183743	101.315041	63.9294399	62.7555924	36.4934871	24.7505036	20.9272018
AT5G66052	520.3270206	-1.555796153	0.35734232	-4.3537977	1.34E-05	0.00019002	833.498998	632.191127	864.407677	437.031761	157.070504	197.762057
AT5G66310	359.0539278	1.719292484	0.33082861	5.19692798	2.03E-07	5.09E-06	133.694075	235.422699	132.596494	350.693511	714.908778	587.008011
AT5G66330	145.9248488	1.265231582	0.29051786	4.35509061	1.33E-05	0.00018919	90.8701915	101.475301	64.7799664	153.094629	235.129784	230.19922
AT5G66420	1259.823208	1.243080178	0.19420038	6.40101826	1.54E-10	7.92E-09	615.201642	840.215495	789.50584	1683.15083	2046.67626	1584.18918
AT5G66500	56.89521057	-1.204923242	0.37378451	-3.2235772	0.001266	0.00828802	74.1584322	80.1654881	84.0115189	49.8447629	22.8466187	30.3444426
AT5G66540	629.062923	-1.063591667	0.25691304	-4.1398898	3.47E-05	0.00043192	772.918871	975.177646	804.688645	293.728067	551.174677	376.689633
AT5G66630	100.0259882	1.017452048	0.25340625	4.01510237	5.94E-05	0.00068081	64.7580675	69.0032049	64.7799664	152.204544	122.800576	126.609571
AT5G66640	223.1350864	2.356579174	0.35409238	6.65526658	2.83E-11	1.67E-09	98.1815863	56.8261688	63.7677794	443.262356	213.235108	463.53752
AT5G66860	1093.417278	-1.144059121	0.15480303	-7.390418	1.46E-13	1.30E-11	1633.57448	1336.42972	1546.6217	650.652173	701.581583	691.64402
AT5G66960	64.50894342	-2.184060592	0.39217289	-5.5691268	2.56E-08	8.00E-07	82.5143119	118.726103	116.401502	31.1529768	25.7024461	12.5563211
AT5G67020	18.62263749	1.61138213	0.54732486	2.94410551	0.0032389	0.0172418	5.2224248	11.1622831	11.1340567	30.2628918	25.7024461	28.2517224
AT5G67180	377.3687414	1.171778509	0.20405498	5.7424647	9.33E-09	3.28E-07	203.674567	231.363687	261.14424	611.488431	483.586763	472.954761
AT5G67450	110.8581611	1.485224551	0.56896886	2.61037935	0.00904419	0.03805437	89.8257066	71.032711	14.1706176	123.721822	103.761727	262.636383
AT5G67480	823.6371085	-1.477375318	0.37933515	-3.8946439	9.83E-05	0.00103003	749.940201	1070.56443	1815.86343	673.794384	309.381295	322.278908
AT5G67520	87.69753933	1.715251924	0.29159668	5.88227517	4.05E-09	1.53E-07	42.8238834	40.5901205	39.475292	156.654969	108.521439	138.119532
AT5G67620	32.431628	-1.814912019	0.48916453	-3.7102282	0.00020707	0.00188826	53.268733	35.5163555	62.7555924	18.6917861	7.61553957	16.7417614
ATCG00010	205.0236041	-1.653985396	0.5543549	-2.9836218	0.00284859	0.0156094	579.689153	110.608078	242.924874	56.9654433	70.4437411	169.510335
ATCG00340	2947.977405	1.072652549	0.23133472	4.63679888	3.54E-06	6.15E-05	1306.65069	2403.94989	1988.94741	4018.73401	4014.3413	3955.24114
ATCG00350	2728.225134	1.141257718	0.25414884	4.49050921	7.11E-06	0.00011148	1084.17539	2206.07305	1815.86343	3686.73229	3852.51108	3723.99556
ATMG00040	31.72418536	-1.973805653	0.54408109	-3.6277784	0.00028587	0.00247174	66.8470374	31.4573434	53.6459097	21.3620413	7.61553957	9.41724082
ATMG00110	81.55348355	-1.869069494	0.44149998	-4.2334532	2.30E-05	0.00030414	181.740383	79.1507351	123.486811	52.5150181	19.9907914	32.4371628
ATMG00140	16.0187582	-2.095887151	0.57973584	-3.6152451	0.00030006	0.002566	29.2455789	24.3540723	24.2924874	6.23059536	5.71165468	6.27816054
ATMG00160	76.32440815	-1.555991984	0.36645381	-4.2460794	2.18E-05	0.00028972	148.316864	102.490054	91.0968277	51.624933	25.7024461	38.7153234
ATMG00670	87.53988521	-1.452222245	0.28729704	-5.0547762	4.31E-07	9.78E-06	150.405834	110.608078	123.486811	45.3943377	40.9335252	54.4107247
ATMG00690	125.7165641	-2.141666356	0.35087261	-6.1038289	1.04E-09	4.51E-08	277.832999	158.30147	179.157095	64.9762088	34.2699281	39.7616834
ATMG01090	34.71870449	-1.232083642	0.44593042	-2.7629504	0.00572815	0.02682391	49.0907931	50.7376507	46.5606008	32.0430619	15.2310791	14.6490413
ATMG01130	28.44564145	-1.617937576	0.4409313	-3.6693643	0.00024315	0.00215331	38.6459435	39.5753675	50.6093487	16.911616	12.3752518	12.5563211
ATMG01170	76.70719411	-2.119742851	0.38169356	-5.5535201	2.80E-08	8.65E-07	147.272379	82.1949941	144.742737	35.6034021	19.0388489	31.3908027
ATMG01200	17.1854142	-1.454728717	0.54210902	-2.6834616	0.00728643	0.03232203	21.9341842	27.3983314	26.3168613	11.5711057	8.56748202	7.32452063
ATMG01220	24.35992346	-1.948638646	0.6129098	-3.1793237	0.00147619	0.00936759	60.5801277	23.3393193	32.3899832	14.2413608	11.4233094	4.18544036
ATMG01370	161.073423	-1.250542114	0.33151024	-3.7722579	0.00016178	0.00154635	291.411304	173.522765	215.595826	120.161482	59.0204317	106.728729
ATMG01410	26.13819357	-1.905020811	0.50051856	-3.8060942	0.00014118	0.00138422	47.0018232	38.5606145	38.463105	16.911616	8.56748202	7.32452063

Table S-5.2. Subcellular targeting of signifcantly differentially expressed genes using SUBA4

Gene	Amino Acid Residues	Molecular Weight	Isoelectric Point	GRAVY	Location SUBAcon
AT1G01010.1	429	49428.400	4.894	-0.731	nucleus
AT1G01110.1	364	41208.700	10.589	-1.027	nucleus
AT1G01190.1	535	60318.300	8.222	0.004	endoplasmic reticulum
AT1G01200.1	237	26251.100	5.436	-0.251	cytosol
AT1G01210.1	106	12274.700	7.962	-0.567	nucleus
AT1G01225.1	260	28401.500	4.481	-0.097	cytosol
AT1G01600.1	554	62606.800	8.099	-0.101	endoplasmic reticulum
AT1G01760.1	420	46495.600	9.434	-0.369	nucleus
AT1G01900.1	774	83251.900	8.271	-0.006	extracellular
AT1G02205.1	461	52980.500	7.835	0.023	vacuole
AT1G02220.1	394	45155.000	5.672	-0.789	nucleus
AT1G02230.1	359	40898.600	6.515	-0.795	nucleus
AT1G02335.1	219	23442.500	8.838	0.118	extracellular
AT1G02340.1	292	33616.900	7.584	-0.708	nucleus
AT1G02350.1	140	15816.300	10.681	-0.127	extracellular
AT1G02370.1	537	60356.400	6.273	-0.323	mitochondrion
AT1G02390.1	530	59971.500	9.784	0.072	mitochondrion
AT1G02450.1	142	16818.500	4.725	-1.256	nucleus
AT1G02620.1	122	13826.700	4.693	0.037	endoplasmic reticulum
AT1G02660.1	713	78350.300	4.964	-0.305	plasma membrane
AT1G02700.1	247	27456.800	4.994	-0.926	mitochondrion
AT1G02710.1	96	8127.190	4.576	-0.401	extracellular
AT1G02730.1	1,181	132594.000	7.823	-0.276	golgi
AT1G02816.1	166	18497.200	4.849	0.174	extracellular
AT1G02850.1	470	52584.200	6.193	-0.210	extracellular
AT1G02870.1	193	22104.500	10.174	-0.842	mitochondrion
AT1G02930.1	208	23487.200	6.177	-0.219	cytosol
AT1G03010.1	634	71163.800	8.898	-0.215	cytosol
AT1G03090.1	714	78373.400	6.779	-0.284	mitochondrion
AT1G03340.1	385	44029.300	9.302	-0.298	cytosol,nucleus
AT1G03360.1	322	36576.000	7.364	-0.347	mitochondrion
AT1G03650.1	158	17844.400	9.305	-0.378	cytosol
AT1G03760.1	391	44058.100	4.708	-0.896	nucleus
AT1G03800.1	245	26393.900	4.837	-0.519	nucleus
AT1G03820.1	222	25206.400	4.225	-1.168	extracellular
AT1G03850.1	159	17576.100	9.834	-0.258	plastid
AT1G03860.1	286	31812.500	9.869	-0.155	mitochondrion
AT1G03990.1	758	83868.500	8.340	-0.213	mitochondrion
AT1G04010.1	633	71691.300	6.344	-0.258	extracellular
AT1G04090.1	572	64200.400	6.128	-0.273	cytosol
AT1G04110.1	775	83780.600	9.322	-0.073	extracellular
AT1G04160.1	1,500	169503.000	7.815	-0.326	cytosol
AT1G04220.1	528	59531.200	9.581	-0.112	plasma membrane,vacuole
AT1G04240.1	189	21521.600	7.023	-0.683	nucleus
AT1G04480.1	140	15027.700	11.189	-0.184	cytosol,nucleus
AT1G04540.1	601	66819.100	10.393	-0.678	plasma membrane
AT1G04680.1	431	47773.400	7.965	-0.368	extracellular
AT1G04760.1	220	24874.300	9.359	-0.194	plasma membrane
AT1G04770.1	303	34661.800	6.090	-0.442	cytosol
AT1G04800.1	200	18046.400	7.908	0.008	extracellular
AT1G04900.1	442	50607.100	8.569	-0.371	mitochondrion
AT1G04920.1	1,062	119483.000	6.216	-0.478	cytosol
AT1G04945.1	367	42208.100	5.921	-0.636	nucleus
AT1G05000.1	215	24538.600	7.788	-0.211	cytosol
AT1G05300.1	360	38169.700	6.746	0.533	plasma membrane
AT1G05370.1	417	47501.000	10.295	-0.283	cytosol
AT1G05560.1	469	52816.300	5.423	-0.210	plastid
AT1G05630.1	1,170	129491.000	6.376	-0.301	nucleus
AT1G05640.1	627	68702.100	10.310	-0.106	cytosol
AT1G05680.1	453	51053.500	5.666	-0.168	cytosol,mitochondrion
AT1G06080.1	305	36108.400	9.672	-0.201	endoplasmic reticulum
AT1G06180.1	246	27952.600	6.176	-0.719	nucleus
AT1G06360.1	299	35511.700	9.248	-0.144	endoplasmic reticulum
AT1G06380.1	254	28716.400	10.148	-0.256	plastid
AT1G06420.1	221	25853.000	10.545	-1.267	nucleus
AT1G06520.1	585	66518.100	9.471	-0.020	mitochondrion
AT1G06720.1	1,147	131192.000	7.976	-0.861	nucleus
AT1G06850.1	337	37056.300	5.232	-0.734	nucleus
AT1G06950.1	1,016	112127.000	5.733	-0.301	plastid
AT1G07090.1	196	21532.400	9.905	-0.726	nucleus
AT1G07210.1	261	29621.100	5.094	-0.966	mitochondrion
AT1G07380.1	779	86776.100	7.578	-0.320	vacuole
AT1G07410.1	214	23690.100	6.936	-0.282	cytosol
AT1G07450.1	260	27897.400	5.036	0.212	cytosol
AT1G07610.1	45	4495.080	4.544	-0.493	nucleus
AT1G07615.1	493	54303.200	5.025	-0.553	mitochondrion
AT1G08070.1	741	83516.400	7.076	-0.085	plastid
AT1G08610.1	559	62723.500	6.387	-0.045	cytosol
AT1G08630.1	358	38944.400	7.357	-0.131	cytosol

Table S-5.2. Subcellular targeting of signifcantly differentially expressed genes using SUBA4

Gene	Amino Acid Residues	Molecular Weight	Isoelectric Point	GRAVY	Location SUBAcon
AT1G08650.1	284	31831.000	5.636	-0.156	cytosol
AT1G09190.1	484	53965.200	7.517	-0.065	cytosol
AT1G09220.1	504	57137.000	8.630	0.027	mitochondrion
AT1G09240.1	320	35753.400	6.035	0.000	cytosol
AT1G09250.1	207	23154.100	11.376	-0.618	nucleus
AT1G09300.1	493	54985.200	7.350	-0.305	mitochondrion
AT1G09350.1	334	38679.400	6.400	-0.407	cytosol
AT1G09400.1	324	36415.400	6.787	-0.433	mitochondrion
AT1G09420.1	625	70206.400	6.431	-0.312	plastid
AT1G09500.1	325	35775.200	5.470	0.066	vacuole,endoplasmic reticulum
AT1G09680.1	607	68551.300	7.934	-0.121	mitochondrion
AT1G09750.1	449	47663.700	7.560	0.111	extracellular
AT1G09890.1	617	70724.800	4.905	-0.484	extracellular
AT1G09932.1	260	29669.600	6.346	-0.332	cytosol
AT1G10050.1	1,063	118378.000	4.875	-0.321	cytosol
AT1G10230.1	183	20659.900	3.843	-0.392	cytosol
AT1G10380.1	305	33952.000	5.238	-0.004	extracellular
AT1G10460.1	217	23196.100	7.559	0.144	extracellular
AT1G10490.1	1,028	115626.000	7.339	-0.229	nucleus
AT1G10522.1	179	20253.100	5.759	-0.275	plastid
AT1G10640.1	532	58351.000	8.691	-0.333	extracellular
AT1G10990.1	166	18153.600	7.340	-0.590	nucleus
AT1G11000.1	573	65469.300	8.226	-0.050	plasma membrane
AT1G11120.1	187	20606.600	8.258	-0.145	plasma membrane
AT1G11160.1	1,021	112533.000	6.972	-0.449	nucleus
AT1G11475.1	71	8315.170	4.931	-0.100	nucleus
AT1G11545.1	305	35566.500	5.030	-0.538	extracellular
AT1G11700.1	201	21780.000	5.646	-0.852	nucleus
AT1G11730.1	384	43624.300	9.068	-0.356	mitochondrion
AT1G11850.1	93	8371.290	6.486	0.613	extracellular
AT1G12010.1	320	36533.800	4.880	-0.430	peroxisome
AT1G12030.1	295	33659.700	5.854	-0.611	cytosol
AT1G12200.1	465	52985.300	5.236	-0.441	cytosol
AT1G12290.1	884	100508.000	6.414	-0.108	cytosol
AT1G12320.1	212	23087.500	9.531	-0.198	cytosol
AT1G12570.1	572	62004.000	8.818	-0.176	extracellular
AT1G12780.1	351	39159.900	6.523	-0.344	cytosol
AT1G12845.1	119	12822.600	4.880	0.547	extracellular
AT1G13270.1	369	40426.400	7.478	-0.194	plastid
AT1G13530.1	385	43987.400	7.035	-0.438	cytosol
AT1G13609.1	78	8444.380	6.980	0.197	extracellular
AT1G13630.1	806	91208.100	7.348	-0.014	cytosol
AT1G13670.1	225	25437.800	9.145	-0.970	nucleus
AT1G13800.1	883	100525.000	6.961	-0.014	mitochondrion
AT1G13810.1	303	35496.000	6.409	-0.602	mitochondrion
AT1G13920.1	345	39627.900	10.669	-1.245	nucleus
AT1G14040.1	813	93841.700	9.758	-0.156	golgi
AT1G14060.1	179	19428.000	3.984	-1.059	nucleus
AT1G14190.1	501	55141.500	6.520	-0.277	vacuole
AT1G14300.1	339	37687.800	4.657	-0.137	nucleus
AT1G14390.1	747	82283.300	8.701	-0.061	plasma membrane
AT1G14430.1	564	62768.500	8.924	-0.051	plasma membrane
AT1G14640.1	735	82819.700	4.598	-0.717	nucleus
AT1G14780.1	627	69921.200	9.497	-0.371	cytosol
AT1G14970.1	562	63411.500	9.931	-0.266	plastid,endoplasmic reticulum
AT1G14980.1	98	10813.200	7.690	-0.358	mitochondrion
AT1G15010.1	142	16460.200	9.326	0.098	mitochondrion
AT1G15250.1	95	10817.100	12.372	-1.009	cytosol
AT1G15380.1	174	19594.800	5.810	-0.148	cytosol
AT1G15420.1	278	30334.900	3.918	-0.563	nucleus
AT1G15440.1	900	100477.000	6.294	-0.222	nucleus
AT1G15510.1	866	97702.600	7.892	-0.062	plastid
AT1G15550.1	358	40164.000	6.838	-0.218	cytosol
AT1G15570.1	450	50644.500	8.872	-0.338	nucleus
AT1G15760.1	202	23595.100	9.952	-0.689	nucleus
AT1G15870.1	242	28152.300	5.080	-0.530	mitochondrion
AT1G15930.1	144	15377.800	5.248	0.134	cytosol
AT1G16000.1	86	9290.120	10.363	-0.574	mitochondrion
AT1G16350.1	502	54054.500	6.444	-0.129	peroxisome
AT1G16445.1	274	30157.000	8.566	0.103	plastid
AT1G16515.1	34	3840.520	3.918	0.247	cytosol
AT1G16640.1	134	15792.300	4.204	-0.749	nucleus
AT1G16830.1	608	69672.900	8.761	-0.021	mitochondrion
AT1G17090.1	93	10401.100	3.681	-0.065	extracellular
AT1G17170.1	218	25307.500	6.063	-0.335	cytosol
AT1G17480.1	371	41154.800	11.146	-0.629	nucleus
AT1G17700.1	180	20446.200	9.966	0.355	plasma membrane
AT1G18250.1	243	25908.100	8.531	-0.015	extracellular
AT1G18265.1	280	32810.900	4.589	-0.611	plasma membrane

Table S-5.2. Subcellular targeting of signifcantly differentially expressed genes using SUBA4

Gene	Amino Acid Residues	Molecular Weight	Isoelectric Point	GRAVY	Location SUBAcon
AT1G18320.1	142	15097.500	8.393	0.252	mitochondrion
AT1G18400.1	260	29365.300	6.919	-0.692	nucleus
AT1G18540.1	233	26154.200	10.811	-0.588	cytosol
AT1G18630.1	155	15961.000	10.282	-0.122	mitochondrion
AT1G18710.1	267	30594.000	5.462	-0.875	nucleus
AT1G18800.1	256	29483.400	3.911	-0.986	nucleus
AT1G18850.1	399	43951.300	4.943	0.018	nucleus
AT1G18870.1	562	62389.200	7.180	-0.258	plastid
AT1G18880.1	587	65178.100	9.197	0.276	plasma membrane
AT1G19300.1	351	39021.900	6.974	0.145	endoplasmic reticulum
AT1G19320.1	247	25431.700	6.419	0.060	extracellular
AT1G19380.1	147	16253.600	9.510	0.036	plasma membrane
AT1G19620.1	317	36325.900	6.963	-0.969	plasma membrane
AT1G19630.1	476	54529.800	8.618	-0.116	endoplasmic reticulum
AT1G19850.1	902	99655.800	5.930	-0.400	nucleus
AT1G19940.1	515	56710.600	5.610	-0.269	extracellular
AT1G19960.1	64	6017.790	10.764	-0.577	plasma membrane
AT1G20030.1	299	31559.700	4.885	-0.150	plasma membrane
AT1G20160.1	769	81484.400	5.823	-0.159	extracellular
AT1G20190.1	252	26762.700	8.717	0.032	extracellular
AT1G20620.1	492	56698.300	7.694	-0.482	peroxisome
AT1G21140.1	200	21031.000	8.457	0.520	vacuole
AT1G21550.1	155	17943.100	4.169	-0.324	cytosol
AT1G22030.1	333	37530.800	6.377	-0.365	cytosol
AT1G22160.1	147	16965.300	10.147	-0.768	nucleus
AT1G22250.1	200	22772.300	8.588	-0.661	nucleus
AT1G22330.1	291	31982.400	6.602	-0.891	nucleus
AT1G22500.1	381	42228.200	6.367	-0.320	vacuole
AT1G22960.1	718	82647.100	7.535	-0.214	mitochondrion
AT1G23010.1	581	66001.300	8.341	-0.300	endoplasmic reticulum
AT1G23060.1	367	41007.200	10.614	-0.887	nucleus
AT1G23080.1	619	67592.100	7.949	0.136	plasma membrane
AT1G23100.1	97	10547.000	9.113	-0.080	mitochondrion
AT1G23200.1	554	61273.200	9.405	-0.314	extracellular
AT1G23280.1	303	35761.500	5.552	-0.942	nucleus
AT1G23340.1	409	45863.100	8.615	-0.417	extracellular
AT1G23410.1	156	17672.600	10.418	-0.709	cytosol
AT1G23450.1	666	74271.100	5.663	0.140	mitochondrion
AT1G23800.1	534	58155.800	7.357	-0.074	mitochondrion
AT1G23870.1	867	98501.100	6.300	-0.229	cytosol,vacuole
AT1G23965.1	117	13683.100	11.686	-0.469	mitochondrion
AT1G24020.1	155	17055.400	4.851	-0.163	golgi
AT1G24070.1	552	64158.200	8.640	0.205	plasma membrane
AT1G24090.1	353	38547.200	7.811	-0.163	mitochondrion
AT1G24580.1	113	13005.400	4.187	-0.204	plasma membrane
AT1G25260.1	235	27243.900	8.445	-0.548	cytosol
AT1G25450.1	492	55656.000	8.964	-0.018	vacuole
AT1G25530.1	440	48818.800	8.967	0.484	plasma membrane
AT1G26200.1	312	37168.600	8.871	0.168	plasma membrane
AT1G26210.1	148	16249.800	4.374	-1.479	nucleus
AT1G26420.1	529	59220.500	9.617	-0.150	extracellular
AT1G26500.1	505	58908.100	9.736	-0.278	mitochondrion
AT1G26730.1	750	87337.400	9.630	-0.084	plasma membrane
AT1G26740.1	134	14800.400	10.771	-0.154	mitochondrion
AT1G26930.1	421	47197.200	7.335	-0.351	peroxisome
AT1G26945.1	94	10718.500	9.251	-0.766	nucleus
AT1G27020.1	308	35081.000	5.456	-0.223	cytosol
AT1G27045.1	227	26625.200	4.965	-0.870	nucleus
AT1G27470.1	810	89787.200	7.149	-0.304	nucleus
AT1G28130.1	609	68867.700	4.897	-0.315	cytosol
AT1G28210.1	408	45680.700	8.137	-0.565	mitochondrion
AT1G28290.1	359	38490.700	10.848	-0.472	extracellular
AT1G28330.1	122	13406.900	10.710	-0.603	cytosol
AT1G28390.1	470	53078.900	10.161	-0.397	cytosol
AT1G28395.1	95	10370.500	11.890	-0.148	mitochondrion
AT1G28400.1	335	39656.800	4.518	-1.633	extracellular
AT1G28530.1	614	68460.800	8.044	-0.252	plastid
AT1G28660.1	383	42035.700	4.636	-0.068	extracellular
AT1G28680.1	451	49682.100	5.639	-0.165	plastid
AT1G29030.1	556	62283.500	9.177	-0.516	cytosol
AT1G29250.1	130	14574.500	5.011	-0.453	cytosol
AT1G29290.1	107	11762.600	11.515	-0.065	extracellular
AT1G29300.1	459	51429.600	9.190	-0.189	mitochondrion
AT1G29320.1	468	52273.600	7.729	-0.666	nucleus
AT1G29395.1	225	24355.300	11.071	0.559	plastid
AT1G29560.1	572	68855.800	6.995	-1.541	nucleus
AT1G29600.1	389	45581.500	9.657	-1.302	nucleus
AT1G30160.1	311	36079.000	6.703	-0.512	cytosol
AT1G30240.1	825	89738.400	5.961	-0.088	nucleus

Table S-5.2. Subcellular targeting of signifcantly differentially expressed genes using SUBA4

Gene	Amino Acid Residues	Molecular Weight	Isoelectric Point	GRAVY	Location SUBAcon
AT1G30250.1	82	9134.040	4.939	0.016	cytosol
AT1G30420.1	1,495	168113.000	7.753	0.134	vacuole
AT1G30680.1	709	80407.000	8.487	-0.508	mitochondrion
AT1G30760.1	534	60195.400	6.368	-0.194	extracellular
AT1G30820.1	600	65732.400	7.233	-0.115	endoplasmic reticulum
AT1G30960.1	437	49673.500	7.681	-0.564	mitochondrion
AT1G31010.1	360	40629.500	8.422	-0.760	plastid
AT1G31290.1	1,194	129192.000	9.776	-0.502	nucleus
AT1G31660.1	444	51475.700	6.374	-0.615	nucleus
AT1G31710.1	681	76714.800	6.831	-0.243	extracellular
AT1G31790.1	409	46256.900	7.878	-0.206	plastid
AT1G31840.1	840	94171.900	7.718	0.185	plastid
AT1G31970.1	537	59606.800	8.889	-0.468	nucleus
AT1G32580.1	229	26025.900	9.457	-0.669	mitochondrion
AT1G32860.1	426	45423.600	8.354	0.006	plasma membrane
AT1G33055.1	66	7464.330	9.779	0.367	extracellular
AT1G33120.1	194	22018.900	10.137	-0.351	cytosol
AT1G33340.1	374	42112.700	7.248	-0.156	cytosol
AT1G33350.1	538	60477.100	8.100	0.045	mitochondrion
AT1G33760.1	184	21087.500	4.911	-0.753	nucleus
AT1G33770.1	614	68472.200	9.782	-0.508	nucleus
AT1G33800.1	297	33672.000	6.990	-0.463	golgi
AT1G33811.1	370	41699.700	9.510	-0.291	extracellular
AT1G33930.1	336	37824.600	5.383	-0.378	cytosol
AT1G34030.1	152	17546.500	11.230	-0.680	cytosol
AT1G34060.1	463	52432.600	7.964	-0.220	extracellular
AT1G34180.1	564	63410.200	5.033	-0.577	nucleus
AT1G34245.1	120	13317.200	8.704	-0.153	extracellular
AT1G35230.1	133	12597.900	9.692	0.247	extracellular
AT1G36622.1	74	8083.810	10.546	-0.095	extracellular
AT1G36675.1	268	28641.300	10.292	-0.826	nucleus
AT1G36940.1	182	20255.400	11.003	-0.643	cytosol
AT1G37130.1	917	102850.000	6.512	-0.346	cytosol
AT1G42980.1	299	34170.500	4.743	-0.160	cytosol
AT1G43980.1	621	70036.800	5.489	0.106	plastid
AT1G44800.1	370	39949.800	9.890	0.622	plasma membrane
AT1G44830.1	211	23040.500	5.244	-0.439	plastid
AT1G44890.1	281	31883.900	10.403	0.163	mitochondrion
AT1G45110.1	343	38054.600	6.277	-0.270	mitochondrion
AT1G45332.1	754	83183.300	6.230	-0.270	mitochondrion
AT1G45545.1	752	84458.200	4.831	-0.765	nucleus
AT1G46480.1	251	28676.800	9.833	-0.879	nucleus
AT1G47510.1	334	37582.100	9.760	-0.461	cytosol,plastid
AT1G47560.1	887	99927.200	5.620	-0.296	cytosol
AT1G48120.1	1,340	149462.000	4.797	-0.452	nucleus
AT1G48330.1	75	8516.000	9.265	-0.772	mitochondrion
AT1G48460.1	340	38072.800	10.092	0.314	plastid
AT1G48570.1	455	51820.200	8.555	-0.662	plastid
AT1G48630.1	326	35802.400	7.125	-0.176	cytosol
AT1G48650.1	1,197	134261.000	9.278	-0.343	mitochondrion,nucleus
AT1G48920.1	557	58776.200	4.842	-1.173	nucleus
AT1G49000.1	156	17612.300	10.710	-0.796	nucleus
AT1G49210.1	225	25185.800	8.313	0.004	nucleus
AT1G49230.1	219	24287.300	7.321	-0.002	plasma membrane
AT1G49450.1	471	52498.900	6.719	-0.579	nucleus
AT1G49620.1	195	21965.900	4.381	-1.001	nucleus
AT1G49650.1	374	41695.300	6.987	-0.299	mitochondrion
AT1G49790.1	283	33339.000	8.626	-0.368	cytosol
AT1G50040.1	460	49651.500	9.618	-0.237	plastid
AT1G50110.1	356	38863.600	6.624	-0.188	cytosol
AT1G50750.1	816	92034.100	5.818	-0.663	nucleus
AT1G51170.1	404	45667.400	8.822	-0.466	plastid
AT1G51310.1	497	55824.500	6.636	-0.238	plastid
AT1G51380.1	392	44359.700	8.194	-0.339	cytosol
AT1G51790.1	882	97785.300	5.607	-0.174	plasma membrane
AT1G51800.1	894	99644.300	6.067	-0.181	plasma membrane
AT1G51820.1	885	98103.800	6.916	-0.140	plasma membrane
AT1G51850.1	865	96125.900	6.115	-0.222	plasma membrane
AT1G51890.1	876	98568.300	6.472	-0.252	extracellular
AT1G52000.1	730	73943.000	4.788	-0.736	mitochondrion,nucleus
AT1G52030.1	642	68853.000	6.771	-0.329	cytosol
AT1G52040.1	462	50169.500	5.326	-0.415	cytosol
AT1G52160.1	890	98645.200	6.714	-0.196	mitochondrion
AT1G52190.1	607	66907.600	9.095	0.241	plasma membrane
AT1G52342.1	87	9428.080	8.656	-0.583	plasma membrane
AT1G52400.1	528	60462.400	7.229	-0.510	peroxisome
AT1G52720.1	117	12737.900	8.497	-0.481	plastid
AT1G52750.1	633	70298.100	9.416	0.134	mitochondrion
AT1G52800.1	314	35736.600	5.594	-0.336	cytosol

Table S-5.2. Subcellular targeting of signifcantly differentially expressed genes using SUBA4

Gene	Amino Acid Residues	Molecular Weight	Isoelectric Point	GRAVY	Location SUBAcon
AT1G52830.1	189	21032.300	6.590	-0.339	nucleus
AT1G52910.1	175	19305.800	8.384	0.577	extracellular
AT1G52930.1	320	36698.600	10.365	-0.683	nucleus
AT1G53070.1	272	30379.900	8.844	-0.259	extracellular
AT1G53460.1	314	36512.500	9.262	-0.520	mitochondrion
AT1G53480.1	193	21416.600	5.355	-0.366	cytosol
AT1G53490.1	304	34766.500	8.929	-0.791	nucleus
AT1G53510.1	615	69355.700	9.590	-0.507	nucleus
AT1G53830.1	587	64176.200	9.329	-0.272	extracellular
AT1G54010.1	386	43145.600	8.187	-0.175	vacuole
AT1G54160.1	308	33775.600	9.361	-0.628	nucleus
AT1G54200.1	366	41772.100	9.798	-1.047	nucleus
AT1G54570.1	704	78208.000	8.061	-0.161	plastid
AT1G54740.1	299	34828.300	6.853	-1.055	nucleus
AT1G55040.1	849	94868.400	7.022	-0.995	plastid
AT1G55205.1	97	10307.600	11.060	0.156	plastid
AT1G55265.1	175	19137.800	4.824	0.154	extracellular
AT1G55380.1	661	75504.900	6.443	-0.412	nucleus
AT1G55500.1	549	60655.500	6.794	-0.822	nucleus
AT1G56110.1	522	58676.500	9.176	-0.570	nucleus
AT1G56150.1	110	12782.600	10.103	-0.371	cytosol
AT1G56690.1	704	79709.800	7.452	-0.159	mitochondrion
AT1G57660.1	164	18709.900	11.179	-0.675	cytosol
AT1G57770.1	574	61727.300	6.975	0.006	plastid
AT1G58170.1	185	20564.000	9.863	0.018	extracellular
AT1G58225.1	143	16293.600	10.181	-0.017	extracellular
AT1G58390.1	907	104602.000	6.949	-0.206	cytosol
AT1G58400.1	900	104541.000	7.117	-0.280	cytosol
AT1G59865.1	175	20023.200	10.019	0.078	plasma membrane
AT1G59930.1	132	14869.400	4.393	-0.709	nucleus
AT1G59990.1	581	64750.900	5.942	-0.308	plastid
AT1G60060.1	386	43521.400	6.354	-0.653	nucleus
AT1G60080.1	302	32700.600	4.699	0.051	cytosol
AT1G60390.1	624	67765.800	6.908	-0.493	extracellular
AT1G60850.1	375	41782.000	5.473	-0.256	nucleus
AT1G60960.1	425	45091.600	6.687	0.428	plasma membrane
AT1G61400.1	819	91967.100	7.791	-0.218	plasma membrane
AT1G61500.1	804	90335.800	6.465	-0.206	extracellular
AT1G61570.1	87	9412.210	5.036	-0.244	mitochondrion
AT1G61740.1	458	50074.600	5.040	0.560	plasma membrane
AT1G61870.1	408	45760.400	8.773	-0.255	mitochondrion
AT1G62010.1	415	46441.400	10.147	-0.139	mitochondrion
AT1G62150.1	463	52068.600	8.679	-0.061	mitochondrion
AT1G62290.1	513	55751.400	6.265	-0.067	vacuole
AT1G62350.1	196	23288.200	4.758	-0.451	mitochondrion
AT1G62720.1	485	55174.600	8.052	0.011	mitochondrion
AT1G62730.1	304	34034.100	9.005	-0.155	mitochondrion
AT1G62770.1	204	22685.500	9.892	-0.029	extracellular
AT1G63090.1	289	32556.700	7.949	-0.291	cytosol
AT1G63100.1	658	73485.500	6.951	-0.525	nucleus
AT1G63250.1	798	89595.800	9.887	-0.544	mitochondrion
AT1G63300.1	1,029	118457.000	4.769	-0.933	mitochondrion
AT1G63660.1	534	59318.500	6.513	-0.157	cytosol
AT1G63780.1	294	34108.000	9.858	-0.635	nucleus
AT1G63810.1	1,053	120157.000	6.841	-0.256	cytosol
AT1G63860.1	1,004	115440.000	5.136	-0.443	nucleus
AT1G63930.1	415	45640.000	7.009	-0.287	cytosol
AT1G64185.1	118	13068.800	6.956	0.041	cytosol
AT1G64220.1	77	8362.210	10.982	-0.216	mitochondrion
AT1G64390.1	620	68595.300	9.870	-0.286	extracellular
AT1G64450.1	342	35892.800	9.537	-0.144	golgi,extracellular
AT1G64600.1	537	61793.900	8.583	-0.741	mitochondrion
AT1G64625.1	527	59579.800	4.673	-0.372	nucleus
AT1G64640.1	191	20252.300	7.334	0.217	extracellular
AT1G65010.1	1,345	152710.000	4.609	-0.897	nucleus
AT1G65030.1	345	37457.400	6.906	-0.240	nucleus
AT1G65080.1	525	58289.800	6.349	0.084	mitochondrion
AT1G65310.1	282	31993.800	8.741	-0.451	extracellular
AT1G65390.1	411	47965.500	5.563	-0.299	plastid
AT1G65450.1	450	50508.100	5.000	-0.254	cytosol
AT1G65486.1	88	9373.530	11.204	0.197	extracellular
AT1G65690.1	252	28575.800	10.205	-0.256	plasma membrane
AT1G65920.1	1,006	111119.000	8.522	-0.433	cytosol
AT1G65970.1	162	17415.000	5.230	0.097	cytosol
AT1G66350.1	511	56757.500	5.467	-0.204	nucleus
AT1G66460.1	467	52494.900	9.745	-0.292	nucleus
AT1G66520.1	355	38504.700	9.801	-0.043	mitochondrion
AT1G66700.1	353	39782.500	5.154	-0.251	cytosol
AT1G66760.1	466	51064.000	7.950	0.628	plasma membrane

Table S-5.2. Subcellular targeting of signifcantly differentially expressed genes using SUBA4

Gene	Amino Acid Residues	Molecular Weight	Isoelectric Point	GRAVY	Location SUBAcon
AT1G66920.1	609	68420.400	7.005	-0.111	plasma membrane
AT1G66930.1	674	75125.100	6.298	-0.198	plasma membrane
AT1G66940.1	332	36660.000	7.873	-0.055	plasma membrane
AT1G67120.1	5,393	611190.000	4.917	-0.315	nucleus
AT1G67260.1	359	40756.600	5.087	-0.799	nucleus
AT1G67400.1	281	32377.800	8.196	-0.335	mitochondrion
AT1G67750.1	408	44888.400	8.655	-0.236	extracellular
AT1G68110.1	379	43843.000	7.825	-0.259	mitochondrion
AT1G68238.1	65	6361.520	4.629	0.589	extracellular
AT1G68330.1	268	29216.200	9.511	-0.531	nucleus
AT1G68500.1	93	10355.800	3.943	-0.214	plasma membrane
AT1G68600.1	537	60225.500	6.431	-0.026	endoplasmic reticulum
AT1G68810.1	368	40827.500	5.413	-0.646	nucleus
AT1G68990.1	976	110936.000	8.226	-0.468	mitochondrion
AT1G69070.1	901	103647.000	5.204	-0.871	nucleus
AT1G69200.1	616	69262.100	4.884	-0.550	plastid
AT1G69210.1	305	34222.200	4.662	-0.545	mitochondrion
AT1G69690.1	325	34754.700	7.756	-0.770	nucleus
AT1G69790.1	387	42698.400	10.239	-0.339	cytosol
AT1G70270.1	86	9888.460	11.003	-0.652	cytosol
AT1G70300.1	782	87207.000	8.200	0.298	plasma membrane
AT1G70350.1	105	10672.700	12.394	0.225	mitochondrion
AT1G70360.1	174	19420.900	4.543	0.313	plasma membrane
AT1G70710.1	492	54613.300	9.601	-0.192	vacuole
AT1G70810.1	165	18658.600	4.911	-0.286	cytosol
AT1G70940.1	640	69470.100	8.425	0.136	plasma membrane
AT1G71100.1	267	28333.300	4.745	0.144	cytosol
AT1G71140.1	485	52428.500	6.361	0.595	vacuole
AT1G71210.1	879	100437.000	8.171	-0.147	cytosol
AT1G71260.1	238	26296.400	10.295	-0.354	mitochondrion
AT1G71420.1	745	84026.300	6.961	-0.081	cytosol
AT1G71830.1	625	69026.000	5.190	-0.111	plasma membrane
AT1G71850.1	470	53883.400	9.665	-0.651	mitochondrion
AT1G71890.1	512	54837.200	8.757	0.455	plasma membrane
AT1G72040.1	580	64608.700	7.052	-0.424	plastid
AT1G72210.1	320	35973.800	5.139	-0.752	nucleus
AT1G72230.1	181	18371.800	6.070	0.247	extracellular
AT1G72240.1	120	13357.600	9.748	-0.857	nucleus
AT1G72360.1	211	23662.300	4.554	-0.729	nucleus
AT1G72416.1	187	21258.500	4.381	-0.776	nucleus
AT1G72440.1	1,043	117030.000	4.843	-0.782	nucleus
AT1G72680.1	355	38673.600	7.129	-0.043	cytosol
AT1G72870.1	512	58752.700	6.444	-0.390	cytosol
AT1G72900.1	363	41211.600	8.194	-0.240	cytosol
AT1G72970.1	594	65347.800	10.252	-0.190	extracellular
AT1G73330.1	209	23113.900	8.314	-0.025	extracellular
AT1G73370.1	942	106881.000	8.094	-0.391	cytosol
AT1G73550.1	152	16510.400	8.406	0.384	extracellular
AT1G73590.1	622	67023.000	9.336	0.102	plasma membrane
AT1G73620.1	264	28215.000	8.742	-0.027	extracellular
AT1G73700.1	476	51057.200	8.070	0.731	plasma membrane
AT1G73805.1	451	50707.500	7.658	-0.396	nucleus
AT1G74290.1	371	42336.500	8.851	-0.346	mitochondrion
AT1G74310.1	911	101301.000	5.998	-0.388	cytosol
AT1G74400.1	462	52666.800	8.218	-0.223	mitochondrion
AT1G74430.1	271	30651.200	5.703	-0.577	nucleus
AT1G74560.1	256	29417.300	3.959	-0.986	cytosol,nucleus
AT1G74670.1	101	11342.000	8.721	-0.251	extracellular
AT1G75030.1	246	25443.800	4.774	0.137	extracellular
AT1G75040.1	239	25253.600	4.545	-0.133	extracellular
AT1G75200.1	647	72083.900	6.749	-0.334	mitochondrion
AT1G75240.1	309	33894.800	8.577	-0.890	nucleus
AT1G75300.1	322	35620.900	6.531	-0.088	cytosol
AT1G75310.1	1,448	161856.000	4.614	-1.041	nucleus
AT1G75500.1	389	42573.400	9.251	0.566	vacuole
AT1G75590.1	154	17677.400	10.180	-0.254	mitochondrion
AT1G75670.1	196	22287.100	9.424	-0.208	nucleus
AT1G75750.1	98	10745.300	9.283	-0.155	extracellular
AT1G75780.1	447	50220.100	4.419	-0.380	cytosol
AT1G76040.1	323	37163.700	5.107	-0.362	plasma membrane
AT1G76240.1	308	34884.100	9.895	-0.339	mitochondrion
AT1G76300.1	128	13812.900	10.896	-0.315	nucleus
AT1G76590.1	245	27781.300	8.751	-0.476	nucleus
AT1G76610.1	226	25040.800	8.370	-0.269	cytosol
AT1G76780.1	1,871	216912.000	4.512	-1.509	nucleus
AT1G77030.1	845	93509.000	10.593	-0.643	nucleus
AT1G77110.1	570	62047.400	9.479	0.359	plasma membrane
AT1G77270.1	682	77492.100	9.826	-0.840	nucleus
AT1G77380.1	476	52040.000	9.065	0.506	plasma membrane

Table S-5.2. Subcellular targeting of signifcantly differentially expressed genes using SUBA4

Gene	Amino Acid Residues	Molecular Weight	Isoelectric Point	GRAVY	Location SUBAcon
AT1G77405.1	458	52997.700	9.719	-0.340	mitochondrion
AT1G77460.1	2,136	231446.000	5.278	0.152	plasma membrane
AT1G77570.1	147	17225.000	10.293	-0.301	nucleus
AT1G77580.1	629	71589.100	4.378	-0.743	cytosol
AT1G77750.1	154	17273.100	11.658	-0.712	mitochondrion
AT1G77760.1	917	103046.000	6.795	-0.367	cytosol
AT1G77765.1	174	21085.400	10.950	-0.919	cytosol
AT1G77855.1	317	36245.800	7.442	-0.298	nucleus
AT1G78000.1	653	71711.400	9.350	0.390	plasma membrane
AT1G78060.1	767	83896.400	8.119	-0.186	extracellular
AT1G78090.1	374	42450.800	8.353	-0.384	plastid
AT1G78120.1	530	59622.700	9.978	-0.673	nucleus
AT1G78130.1	490	52612.000	6.424	0.429	plasma membrane
AT1G78210.1	314	35662.900	9.984	-0.111	peroxisome
AT1G78260.1	287	31469.200	7.284	-0.746	nucleus
AT1G78320.1	220	25682.000	4.929	-0.312	cytosol
AT1G78580.1	942	105982.000	7.161	-0.445	plasma membrane
AT1G78930.1	591	67567.600	8.310	-0.136	plastid
AT1G78940.1	680	75936.700	6.053	-0.510	nucleus
AT1G78970.1	757	87356.800	6.435	-0.315	cytosol
AT1G78990.1	455	50917.200	6.789	-0.123	plasma membrane
AT1G79150.1	830	94895.200	8.966	-0.654	nucleus
AT1G79330.1	410	44848.700	6.590	-0.468	cytosol
AT1G79420.1	417	45968.800	6.617	-0.281	mitochondrion
AT1G79460.1	785	89626.900	5.719	-0.348	plastid
AT1G79470.1	503	54197.000	6.785	-0.103	cytosol
AT1G79490.1	836	94177.300	9.441	-0.034	mitochondrion
AT1G79560.1	1,008	115111.000	6.917	-0.341	plastid
AT1G79760.1	299	33672.600	9.001	-0.203	plastid
AT1G80080.1	496	54508.400	7.810	-0.099	plasma membrane
AT1G80120.1	210	23454.900	5.423	-0.311	cytosol
AT1G80150.1	397	45509.000	9.770	-0.121	mitochondrion
AT1G80160.1	167	19030.000	5.050	-0.225	cytosol
AT1G80190.1	201	23321.100	6.962	-0.519	cytosol
AT1G80245.1	127	14688.900	9.386	-0.457	nucleus
AT1G80270.1	596	67285.900	7.793	-0.486	mitochondrion,plastid
AT1G80280.1	647	71110.000	9.059	0.130	endoplasmic reticulum
AT1G80720.1	190	21902.900	4.759	-0.570	mitochondrion
AT1G80750.1	247	28345.800	10.431	-0.628	cytosol
AT1G80820.1	332	36620.000	6.859	-0.166	golgi,plasma membrane
AT1G80830.1	532	57565.500	8.705	0.663	plasma membrane
AT2G01150.1	147	16241.600	8.163	0.070	plasma membrane
AT2G01610.1	222	23955.200	5.804	-0.122	extracellular
AT2G01740.1	559	62494.200	6.420	0.067	mitochondrion
AT2G01830.1	1,057	117961.000	6.191	-0.235	endoplasmic reticulum
AT2G01850.1	333	38417.200	7.062	-0.520	extracellular
AT2G01918.1	187	21534.800	9.816	-0.470	plastid
AT2G01950.1	1,143	125683.000	6.971	-0.125	golgi
AT2G02150.1	761	86089.800	5.602	0.024	mitochondrion
AT2G02710.1	399	44892.700	7.058	-0.257	nucleus
AT2G02740.1	268	29729.400	10.101	-0.245	plastid
AT2G02750.1	613	67939.700	6.508	0.073	mitochondrion
AT2G02880.1	314	35965.900	4.975	-0.865	nucleus
AT2G02955.1	666	75479.200	4.729	-0.468	cytosol
AT2G03380.1	689	76688.900	7.255	0.002	mitochondrion
AT2G03500.1	432	47964.400	7.126	-0.975	nucleus
AT2G03590.1	390	42736.400	9.643	0.492	plasma membrane
AT2G03820.1	516	59296.700	5.460	-0.458	golgi
AT2G04030.1	780	88667.600	4.648	-0.552	plastid
AT2G04040.1	476	51847.800	7.741	0.703	plasma membrane
AT2G04050.1	476	51471.300	7.894	0.726	plasma membrane
AT2G04100.1	483	51936.000	7.599	0.730	plasma membrane
AT2G04530.1	354	39953.300	9.329	-0.231	plastid
AT2G04570.1	350	38480.100	7.749	-0.081	extracellular
AT2G04790.1	152	16868.600	9.174	-0.020	plastid
AT2G05185.1	88	9804.710	9.427	-0.224	plastid
AT2G05440.1	127	11637.300	7.019	-0.475	extracellular
AT2G05540.1	135	14093.400	8.553	-0.619	extracellular
AT2G07674.1	251	26674.300	4.013	-0.390	extracellular
AT2G07698.1	777	85938.200	5.235	-0.066	mitochondrion,plastid
AT2G07739.1	199	23238.300	9.736	0.677	extracellular
AT2G07774.1	116	13163.200	11.190	-0.504	cytosol
AT2G07779.1	91	10563.700	11.281	-0.501	cytosol,mitochondrion
AT2G07787.1	105	12108.600	7.346	-0.435	cytosol
AT2G12400.1	541	60283.000	7.510	0.240	plasma membrane
AT2G12462.1	249	28198.100	10.818	-0.527	cytosol
AT2G13610.1	649	73318.600	9.078	0.067	plasma membrane
AT2G13820.1	169	16817.300	6.979	0.620	plasma membrane
AT2G14060.1	359	41372.500	6.881	-0.281	cytosol

Table S-5.2. Subcellular targeting of signifcantly differentially expressed genes using SUBA4

Gene	Amino Acid Residues	Molecular Weight	Isoelectric Point	GRAVY	Location SUBAcon
AT2G14880.1	141	15903.400	10.580	-0.340	plastid
AT2G14890.1	191	18416.900	4.156	-0.088	extracellular
AT2G15000.1	93	9983.880	12.501	-0.153	mitochondrion
AT2G15220.1	225	25165.600	8.827	-0.314	extracellular
AT2G15390.1	503	58059.500	7.392	-0.383	golgi
AT2G15620.1	586	65508.700	6.171	-0.396	plastid
AT2G15690.1	579	65617.700	7.508	-0.703	mitochondrion
AT2G15830.1	66	7312.130	8.492	0.488	plasma membrane
AT2G15890.1	203	23155.500	5.645	-0.619	plastid
AT2G16060.1	160	18035.100	8.693	-0.148	cytosol
AT2G16630.1	359	38811.900	6.110	0.012	extracellular
AT2G16650.1	528	59231.100	6.333	-0.383	nucleus
AT2G16660.1	546	58980.700	8.222	0.613	plasma membrane
AT2G16720.1	269	31011.000	8.774	-0.752	nucleus
AT2G16850.1	278	29502.100	9.069	0.521	plasma membrane
AT2G16890.1	312	35188.000	6.438	-0.249	plasma membrane,endoplasmic reticulum
AT2G17280.1	271	29891.300	5.350	-0.337	cytosol
AT2G17670.1	463	51410.900	8.320	-0.316	plastid
AT2G18010.1	112	12942.600	8.854	-0.393	mitochondrion
AT2G18120.1	222	24880.700	7.954	-0.981	nucleus
AT2G18193.1	495	56472.500	7.155	-0.498	endoplasmic reticulum
AT2G18220.1	764	86966.000	7.011	-0.557	nucleus
AT2G18328.1	77	8983.460	9.602	-1.147	nucleus
AT2G18330.1	636	71198.400	9.475	-0.677	mitochondrion
AT2G18480.1	508	54822.200	9.868	0.581	plasma membrane
AT2G18700.1	862	98280.500	7.366	-0.370	cytosol
AT2G18900.1	804	88017.000	7.023	-0.130	nucleus
AT2G18969.1	175	19997.000	9.014	-0.712	mitochondrion
AT2G19190.1	876	98717.200	7.170	-0.227	plasma membrane
AT2G19385.1	275	30658.300	9.518	-0.989	nucleus
AT2G19480.1	379	43544.600	4.058	-1.130	nucleus
AT2G19540.1	469	51406.600	4.680	-0.494	nucleus
AT2G19670.1	366	41173.800	4.958	-0.283	cytosol
AT2G19730.1	143	15896.400	11.305	-0.622	cytosol
AT2G19870.1	589	65563.400	8.636	-0.752	plastid
AT2G19930.1	977	110895.000	7.102	-0.349	cytosol
AT2G20020.1	701	79059.200	8.751	-0.737	plastid
AT2G20060.1	300	33265.500	10.970	-0.348	mitochondrion
AT2G20390.1	183	19821.700	7.058	-0.147	mitochondrion
AT2G20450.1	134	15507.400	10.853	-0.231	cytosol
AT2G20490.1	64	7391.920	9.951	-0.798	nucleus
AT2G20530.1	286	31638.500	10.192	-0.140	mitochondrion
AT2G20570.1	420	45990.100	6.541	-0.519	nucleus
AT2G20585.1	100	10451.400	10.434	0.040	mitochondrion
AT2G20880.1	336	38399.700	6.413	-0.927	nucleus
AT2G20940.1	129	14143.500	10.629	-0.022	mitochondrion
AT2G21050.1	483	54705.900	8.751	0.436	plasma membrane
AT2G21140.1	321	35509.600	10.373	-0.126	extracellular
AT2G21350.1	222	24716.600	8.261	-0.420	plastid
AT2G21430.1	361	39821.300	7.411	-0.252	extracellular
AT2G22240.1	510	56340.600	5.146	-0.168	cytosol
AT2G22360.1	442	47763.900	9.491	-0.442	plastid
AT2G22410.1	681	76718.400	7.189	-0.100	mitochondrion
AT2G22620.1	677	77622.500	9.010	-0.447	extracellular
AT2G22760.1	295	33789.000	6.082	-0.344	nucleus
AT2G22810.1	474	53798.300	8.328	-0.351	vacuole
AT2G22830.1	585	64796.300	10.265	-0.001	mitochondrion
AT2G22860.1	87	9627.750	5.035	-0.123	extracellular
AT2G22870.1	300	33693.900	10.203	-0.215	mitochondrion
AT2G23170.1	595	67540.400	6.223	-0.277	cytosol
AT2G23300.1	773	84153.700	7.324	-0.225	plasma membrane
AT2G23470.1	520	58623.200	9.556	0.017	plastid
AT2G23550.1	265	29745.100	5.385	-0.058	cytosol
AT2G23950.1	634	69697.900	8.122	-0.091	plasma membrane
AT2G24120.1	993	112630.000	9.697	-0.421	plastid
AT2G24170.1	637	73355.800	7.887	0.302	golgi
AT2G24210.1	591	69282.600	5.992	-0.397	plastid
AT2G24300.1	552	62688.100	7.277	-0.627	cytosol
AT2G24440.1	183	20713.000	9.441	-1.043	nucleus
AT2G24610.1	726	83459.000	9.459	-0.106	plasma membrane
AT2G24692.1	69	7516.790	4.400	-0.293	nucleus
AT2G24762.1	156	16852.100	5.292	-0.271	plasma membrane
AT2G25060.1	182	19483.200	7.381	0.165	plasma membrane
AT2G25090.1	469	53554.300	5.810	-0.434	cytosol
AT2G25355.1	241	26481.100	8.308	-0.124	cytosol
AT2G25460.1	423	46876.600	8.703	-0.400	cytosol
AT2G26360.1	387	41934.200	9.900	0.160	plastid
AT2G26750.1	320	36259.700	5.664	-0.068	cytosol
AT2G26790.1	799	90365.600	6.188	-0.004	mitochondrion

Table S-5.2. Subcellular targeting of signifcantly differentially expressed genes using SUBA4

Gene	Amino Acid Residues	Molecular Weight	Isoelectric Point	GRAVY	Location SUBAcon
AT2G26980.1	382	43849.500	5.770	-0.527	cytosol
AT2G27530.1	216	24426.400	10.615	-0.409	cytosol
AT2G27610.1	868	97190.600	8.682	-0.148	cytosol
AT2G27660.1	718	76568.500	4.862	-0.815	plastid
AT2G27710.1	115	11444.400	4.327	-0.157	cytosol
AT2G27775.1	100	10876.000	12.359	-0.234	mitochondrion
AT2G28000.1	586	62075.600	4.815	0.002	plastid
AT2G28120.1	577	63978.000	8.687	0.452	plasma membrane
AT2G28410.1	115	12161.400	4.640	0.260	extracellular
AT2G28460.1	720	82909.800	7.335	-0.294	nucleus
AT2G28500.1	232	25536.200	4.642	-0.428	nucleus
AT2G28790.1	249	27019.100	7.682	-0.056	extracellular
AT2G28950.1	257	27819.300	10.027	-0.038	extracellular
AT2G29110.1	947	107194.000	6.912	-0.094	plasma membrane
AT2G29130.1	573	63835.200	9.921	-0.076	extracellular
AT2G29200.1	968	106570.000	6.045	-0.534	cytosol,nucleus
AT2G29260.1	322	35240.200	7.764	-0.016	plastid
AT2G29300.1	263	28257.800	6.889	0.093	plasma membrane
AT2G29490.1	224	25915.900	5.859	-0.209	cytosol
AT2G29540.1	122	14079.400	4.852	-0.811	nucleus
AT2G29680.1	539	59844.200	9.447	-0.139	plastid
AT2G29750.1	481	53878.100	4.550	0.025	plasma membrane
AT2G29760.1	738	82790.600	6.825	-0.164	plastid
AT2G29890.1	909	102955.000	5.348	-0.488	cytosol
AT2G30540.1	102	11080.700	7.342	0.275	cytosol,plasma membrane
AT2G30600.1	809	92179.800	5.996	-0.190	plasma membrane
AT2G30770.1	503	56792.200	8.806	-0.178	endoplasmic reticulum
AT2G30900.1	368	41249.800	9.912	-0.261	extracellular
AT2G31010.1	775	87368.300	6.851	-0.460	nucleus
AT2G31060.1	527	57355.400	5.967	-0.183	mitochondrion
AT2G31141.1	165	19455.800	10.672	-0.072	mitochondrion
AT2G31160.1	219	24124.400	10.415	-0.703	nucleus
AT2G31170.1	563	63917.300	7.207	-0.399	plastid
AT2G31240.1	617	68748.300	5.978	-0.348	mitochondrion
AT2G31340.1	559	64385.200	8.200	-0.251	mitochondrion
AT2G31830.1	1,144	125715.000	7.105	-0.394	cytosol
AT2G31840.1	350	40541.500	4.515	-0.725	plastid
AT2G31890.1	671	75683.500	6.525	-0.430	plastid
AT2G31945.1	95	10062.100	10.691	0.025	extracellular
AT2G32180.1	139	16329.700	8.874	-0.439	plastid
AT2G32220.1	135	15471.300	10.896	-0.477	cytosol
AT2G32530.1	755	84893.300	7.257	0.020	plasma membrane
AT2G32650.1	139	16271.700	8.871	-0.417	plastid
AT2G32680.1	890	98487.900	6.724	-0.062	extracellular
AT2G32880.1	318	36730.300	9.190	-0.275	cytosol
AT2G32930.1	453	49750.000	6.437	-0.763	nucleus
AT2G32990.1	525	59090.400	5.989	-0.377	extracellular
AT2G33210.1	585	61982.200	6.588	-0.038	mitochondrion
AT2G33385.1	365	42203.400	10.105	-0.398	cytosol
AT2G33430.1	219	24716.200	8.349	-0.700	plastid
AT2G33750.1	358	39463.400	8.737	0.804	plasma membrane
AT2G33760.1	583	64861.200	7.554	-0.039	plastid
AT2G33847.1	93	10034.100	10.606	0.032	mitochondrion
AT2G34080.1	345	38269.100	7.307	-0.350	extracellular
AT2G34150.1	700	78393.600	4.481	-0.837	nucleus
AT2G34170.1	523	58389.600	7.877	-0.865	nucleus
AT2G34180.1	502	56733.800	8.294	-0.300	plastid
AT2G34260.1	353	38427.800	4.668	-0.331	nucleus
AT2G34360.1	480	52189.700	8.539	0.643	plasma membrane
AT2G34400.1	621	70535.700	6.858	-0.162	cytosol
AT2G34640.1	527	60898.400	4.689	-1.137	plastid
AT2G34650.1	438	49274.200	9.812	-0.283	plasma membrane
AT2G34680.1	1,708	186872.000	6.133	-0.293	plasma membrane
AT2G34850.1	236	26110.300	8.558	-0.406	cytosol
AT2G35035.1	294	32615.100	7.775	-0.115	cytosol
AT2G35150.1	323	36027.700	6.618	-0.121	extracellular
AT2G35190.1	265	29874.000	6.313	-0.465	plasma membrane
AT2G35240.1	232	26369.400	9.142	-0.601	mitochondrion
AT2G35290.1	121	14180.200	6.525	-0.146	mitochondrion
AT2G35340.1	1,044	119134.000	6.053	-0.586	nucleus
AT2G35790.1	238	26416.500	10.072	-0.244	mitochondrion
AT2G35880.1	432	46699.000	10.463	-1.044	cytosol
AT2G36026.1	183	20361.900	9.633	-0.553	nucleus
AT2G36080.1	244	28436.700	6.798	-0.950	nucleus
AT2G36170.1	128	14734.300	10.606	-0.638	cytosol,nucleus
AT2G36490.1	1,393	156556.000	7.379	-0.659	nucleus
AT2G36570.1	672	73543.300	6.678	-0.181	plasma membrane
AT2G36750.1	491	55226.800	5.113	-0.202	plasma membrane
AT2G36800.1	495	55801.400	5.211	-0.211	plasma membrane

Table S-5.2. Subcellular targeting of signifcantly differentially expressed genes using SUBA4

Gene	Amino Acid Residues	Molecular Weight	Isoelectric Point	GRAVY	Location SUBAcon
AT2G36885.1	256	27493.600	6.886	0.355	plastid
AT2G37020.1	308	35055.800	7.003	-0.322	plastid
AT2G37030.1	124	14187.400	8.488	-0.105	cytosol,plasma membrane
AT2G37060.1	173	18999.400	6.934	-0.821	nucleus
AT2G37190.1	166	17942.800	9.575	-0.330	cytosol
AT2G37230.1	757	85709.900	9.163	-0.382	plastid
AT2G37310.1	657	73346.900	5.847	-0.057	cytosol
AT2G37380.1	321	34975.400	7.476	-0.531	nucleus
AT2G37400.1	333	38157.900	7.184	-0.463	plastid
AT2G37510.1	142	15712.700	10.466	-0.285	mitochondrion
AT2G37600.1	113	12737.200	12.277	-0.703	cytosol,nucleus
AT2G37690.1	642	69756.300	6.998	-0.080	plastid
AT2G37760.1	311	34686.800	7.004	-0.238	cytosol
AT2G37770.1	283	31682.000	8.202	-0.283	plastid
AT2G38010.1	757	83269.000	8.704	-0.210	extracellular
AT2G38080.1	558	61530.000	9.605	-0.074	extracellular
AT2G38110.1	501	56142.100	10.015	0.033	endoplasmic reticulum
AT2G38230.1	309	32863.900	5.797	0.086	cytosol
AT2G38530.1	118	11938.800	9.093	0.354	extracellular
AT2G39120.1	387	45210.900	9.323	-0.429	mitochondrion
AT2G39180.1	776	85307.100	5.692	-0.167	plasma membrane
AT2G39230.1	867	97674.800	6.430	-0.101	mitochondrion
AT2G39250.1	325	36442.400	9.246	-0.586	nucleus
AT2G39430.1	322	33763.500	4.408	0.030	extracellular
AT2G39460.1	154	17441.600	10.913	-0.763	cytosol
AT2G39620.1	836	92677.600	6.789	0.125	cytosol
AT2G39670.1	428	47353.400	9.165	-0.186	plastid
AT2G39690.1	498	56742.100	7.280	-0.295	nucleus
AT2G39700.1	257	27849.200	9.981	-0.080	extracellular
AT2G39795.1	250	28062.800	4.456	-0.452	mitochondrion
AT2G40180.1	390	42597.700	6.529	-0.403	cytosol
AT2G40240.1	351	39882.800	6.534	-0.295	mitochondrion
AT2G40260.1	410	46234.200	6.765	-1.069	nucleus
AT2G40320.1	425	49321.200	8.513	-0.419	plasma membrane
AT2G40330.1	215	23844.000	6.646	-0.336	cytosol
AT2G40360.1	753	85387.600	4.933	-0.749	nucleus
AT2G40475.1	193	21270.900	10.310	-0.633	nucleus
AT2G40530.1	105	11373.500	5.649	-0.349	extracellular
AT2G40610.1	253	27261.800	6.976	-0.283	extracellular
AT2G40700.1	609	68217.700	9.970	-0.395	nucleus
AT2G40750.1	346	38647.300	5.120	-0.816	nucleus
AT2G40820.1	492	54437.000	8.461	-0.423	cytosol
AT2G40850.1	561	61369.100	5.606	-0.207	plasma membrane
AT2G41070.1	262	29619.500	9.365	-0.787	nucleus
AT2G41170.1	371	43486.500	8.586	-0.697	plasma membrane,endoplasmic reticulum
AT2G41540.1	462	51494.300	7.290	-0.106	cytosol
AT2G41640.1	500	57366.400	8.042	-0.379	plasma membrane
AT2G41670.1	386	42986.500	9.737	-0.161	mitochondrion
AT2G41820.1	890	97251.300	6.252	0.068	plasma membrane
AT2G41905.1	61	5859.270	6.349	1.089	extracellular
AT2G41990.1	297	33114.700	9.209	-0.096	cytosol
AT2G42200.1	375	40849.000	8.228	-0.926	nucleus
AT2G42270.1	2,172	247403.000	5.775	-0.340	nucleus
AT2G42360.1	236	26444.500	8.601	-0.332	nucleus
AT2G42380.1	310	34663.800	5.824	-0.844	nucleus
AT2G42540.1	127	13452.600	7.518	-0.725	plastid
AT2G42650.1	372	41691.200	9.902	-0.651	cytosol,nucleus
AT2G42710.1	415	45782.900	10.190	-0.568	mitochondrion
AT2G42870.1	118	13151.500	4.619	-0.581	nucleus
AT2G43290.1	215	24115.600	4.532	-0.469	endoplasmic reticulum
AT2G43620.1	283	30379.300	8.608	-0.084	extracellular
AT2G43650.1	654	73976.700	4.753	-1.140	nucleus
AT2G43780.1	67	7138.580	8.973	0.028	mitochondrion
AT2G43820.1	449	50774.500	5.002	-0.194	plasma membrane,extracellular
AT2G43920.1	227	25127.800	4.472	-0.300	cytosol
AT2G44040.1	347	37552.300	6.426	-0.034	plastid
AT2G44120.1	242	27941.500	10.581	-0.459	cytosol
AT2G44300.1	204	21707.200	6.875	0.088	extracellular
AT2G44510.1	326	37948.300	4.754	-0.585	nucleus
AT2G44640.1	451	49833.500	9.166	-0.237	plastid
AT2G44740.1	202	23044.700	7.563	0.012	plasma membrane
AT2G44860.1	159	18943.100	10.805	-1.126	cytosol,nucleus
AT2G44940.1	295	31986.600	4.623	-0.540	plastid
AT2G45030.1	754	83116.300	6.292	-0.259	mitochondrion
AT2G45040.1	342	38507.600	6.754	-0.332	plasma membrane
AT2G45050.1	264	28865.500	8.290	-0.767	nucleus
AT2G45080.1	222	25820.100	8.201	-0.237	cytosol
AT2G45400.1	364	40263.100	5.356	-0.161	cytosol
AT2G45540.1	2,946	321953.000	5.643	-0.206	golgi

Table S-5.2. Subcellular targeting of signifcantly differentially expressed genes using SUBA4

Gene	Amino Acid Residues	Molecular Weight	Isoelectric Point	GRAVY	Location SUBAcon
AT2G46140.1	166	17847.400	4.328	0.123	cytosol
AT2G46150.1	221	24097.700	10.375	0.017	plasma membrane
AT2G46240.1	1,043	116765.000	4.941	-0.933	nucleus
AT2G46310.1	294	33157.500	4.845	-0.683	nucleus
AT2G46530.1	601	67230.800	7.090	-0.448	nucleus
AT2G46535.1	175	19628.100	10.965	-0.553	cytosol
AT2G46590.1	357	39116.100	9.346	-0.842	nucleus
AT2G46630.1	394	43248.800	11.173	-1.410	mitochondrion
AT2G46710.1	455	50785.200	6.110	-0.495	nucleus
AT2G46970.1	416	46582.300	9.440	-0.788	nucleus
AT2G47010.1	493	55053.100	6.504	-0.476	extracellular
AT2G47050.1	216	23777.000	9.354	-0.037	extracellular
AT2G47060.1	365	39933.500	7.435	-0.338	plasma membrane
AT2G47140.1	257	26848.200	6.791	0.168	cytosol
AT2G47240.1	660	74602.100	6.297	-0.214	cytosol
AT2G47260.1	337	37686.600	6.954	-0.809	nucleus
AT2G47270.1	102	11880.000	11.720	-0.373	mitochondrion
AT2G47420.1	353	39689.000	9.603	-0.459	nucleus
AT2G47440.1	526	58654.700	9.224	-0.289	nucleus
AT2G47630.1	351	39711.000	8.390	-0.256	cytosol
AT2G47860.1	635	71002.100	8.844	-0.310	plasma membrane
AT2G47990.1	530	58906.300	10.155	-0.241	nucleus
AT3G01080.1	423	47132.600	8.240	-0.952	nucleus
AT3G01490.1	411	46052.100	8.017	-0.491	cytosol
AT3G01600.1	370	40829.400	5.498	-0.462	nucleus
AT3G01790.1	205	23381.500	11.054	-0.766	mitochondrion
AT3G01800.1	267	29173.700	10.366	-0.299	mitochondrion
AT3G01860.1	223	24944.700	5.055	-0.940	nucleus
AT3G01970.1	147	17226.200	9.206	-1.065	nucleus
AT3G02060.1	823	93934.600	9.143	-0.258	plastid
AT3G02080.1	143	15829.100	10.669	-0.508	cytosol
AT3G02170.1	905	101633.000	9.990	-0.841	nucleus
AT3G02330.1	903	101720.000	6.365	-0.063	mitochondrion
AT3G02560.1	191	22197.100	10.370	-0.520	cytosol
AT3G02640.1	185	20383.000	8.198	0.543	plasma membrane
AT3G02650.1	576	63841.400	4.801	-0.195	mitochondrion
AT3G03030.1	474	54397.600	4.801	-0.177	cytosol
AT3G03060.1	628	69570.700	9.638	-0.594	mitochondrion
AT3G03480.1	454	50292.800	6.847	0.030	cytosol
AT3G03630.1	404	43163.300	9.462	-0.025	plastid
AT3G03680.1	1,017	114272.000	9.032	-0.424	cytosol
AT3G03820.1	96	10449.800	10.064	-0.040	mitochondrion
AT3G03840.1	95	10415.700	9.132	0.033	mitochondrion
AT3G03910.1	411	44530.400	6.021	-0.200	mitochondrion
AT3G03920.1	202	20984.000	11.937	-0.665	nucleus
AT3G04000.1	272	28436.300	7.343	0.215	plastid
AT3G04030.1	388	43852.900	6.960	-0.819	nucleus
AT3G04060.1	338	37782.700	6.795	-0.537	nucleus
AT3G04070.1	359	40851.700	7.026	-0.780	nucleus
AT3G04290.1	366	40151.300	5.689	0.113	extracellular
AT3G04440.1	482	53123.900	9.018	0.352	plastid
AT3G04620.1	164	17667.200	5.840	-0.243	cytosol
AT3G04690.1	850	94053.500	6.906	-0.356	plasma membrane
AT3G04950.1	231	25611.700	10.273	-0.621	mitochondrion
AT3G05030.1	546	60526.300	8.161	0.465	vacuole
AT3G05400.1	462	50605.200	8.598	0.694	plasma membrane
AT3G05470.1	884	98540.300	9.087	-0.480	extracellular
AT3G05560.1	124	14018.900	10.158	-0.648	cytosol
AT3G05600.1	331	37201.300	5.414	-0.254	cytosol
AT3G05660.1	875	97619.400	8.100	-0.082	extracellular
AT3G05690.1	295	32141.000	10.047	-0.585	nucleus
AT3G05936.1	113	13393.400	12.209	-0.928	mitochondrion
AT3G05937.1	53	6667.560	12.447	-0.434	mitochondrion
AT3G06320.1	58	6958.730	11.332	-0.647	mitochondrion
AT3G06370.1	503	55609.600	7.429	0.594	vacuole
AT3G06530.1	2,197	246336.000	7.025	0.040	plasma membrane
AT3G06690.1	187	21038.200	5.317	-0.205	peroxisome
AT3G06790.1	244	27641.800	9.406	-0.639	mitochondrion
AT3G06880.1	1,261	141418.000	7.067	-0.194	cytosol,plasma membrane
AT3G06890.1	128	13265.200	4.022	0.906	vacuole
AT3G06920.1	871	98344.100	6.878	-0.188	cytosol
AT3G07010.1	416	46176.800	8.417	-0.259	extracellular
AT3G07050.1	582	65789.100	8.958	-0.754	nucleus
AT3G07110.1	206	23467.300	11.087	-0.387	cytosol
AT3G07290.1	880	98064.500	7.386	0.103	mitochondrion
AT3G07430.1	232	24923.500	11.212	0.363	plastid
AT3G07540.1	841	93016.400	8.718	-0.402	plasma membrane
AT3G07650.1	372	40756.100	6.235	-0.678	nucleus
AT3G07750.1	286	29963.600	4.436	-0.001	cytosol

Table S-5.2. Subcellular targeting of signifcantly differentially expressed genes using SUBA4

Gene	Amino Acid Residues	Molecular Weight	Isoelectric Point	GRAVY	Location SUBAcon
AT3G07860.1	165	18673.800	10.451	-0.450	nucleus
AT3G07960.1	715	81426.600	8.639	-0.727	plasma membrane
AT3G08030.1	365	39068.000	7.639	0.035	extracellular
AT3G08660.1	582	65736.900	5.589	-0.272	plastid
AT3G08670.1	567	60142.500	11.680	-0.806	nucleus
AT3G08770.1	113	11878.500	7.543	0.345	extracellular
AT3G08980.1	154	17327.000	9.838	-0.208	mitochondrion
AT3G09070.1	685	75444.600	8.108	-0.887	nucleus
AT3G09162.1	66	7364.020	8.221	0.311	cytosol,mitochondrion
AT3G09200.1	320	34135.000	4.699	0.024	cytosol
AT3G09260.1	524	59723.600	6.912	-0.442	endoplasmic reticulum
AT3G09430.1	301	33480.400	9.775	-0.630	nucleus
AT3G09450.1	775	85688.700	8.413	0.217	vacuole
AT3G09500.1	123	14286.000	11.604	-0.762	cytosol
AT3G09520.1	628	70996.200	6.611	-0.219	cytosol
AT3G09720.1	541	60919.400	10.020	-0.494	nucleus
AT3G09730.1	397	43643.500	5.286	-0.596	nucleus
AT3G10050.1	592	64638.300	7.606	-0.063	plastid
AT3G10110.1	173	18183.800	7.307	0.069	mitochondrion
AT3G10530.1	536	60264.600	10.137	-0.617	nucleus
AT3G10690.1	950	104544.000	6.886	-0.177	plastid
AT3G10870.1	276	30869.200	4.836	-0.195	mitochondrion
AT3G11050.1	253	28379.600	5.614	-0.351	plastid
AT3G11460.1	623	69130.900	6.911	0.041	mitochondrion
AT3G11510.1	150	16273.800	11.300	-0.501	cytosol
AT3G12080.1	663	73129.900	6.446	-0.311	plastid
AT3G12220.1	435	49239.600	6.402	-0.311	extracellular
AT3G12270.1	601	67347.500	4.315	-0.388	nucleus
AT3G12340.1	499	55180.800	7.465	-0.870	nucleus
AT3G12520.1	677	74666.400	8.783	0.396	vacuole
AT3G12580.1	650	71105.400	4.879	-0.434	cytosol
AT3G12610.1	372	39558.500	4.690	0.101	extracellular
AT3G12700.1	461	50570.800	9.529	-0.105	plasma membrane
AT3G12710.1	312	34918.100	10.234	-0.423	nucleus
AT3G12770.1	694	77939.900	7.812	-0.090	mitochondrion
AT3G12820.1	239	27318.000	7.473	-0.766	nucleus
AT3G12920.1	335	37710.900	6.658	-0.490	nucleus
AT3G12930.1	238	26379.300	5.138	-0.164	plastid
AT3G13000.1	553	62631.600	6.679	-0.416	nucleus
AT3G13150.1	551	60632.900	8.078	-0.523	cytosol
AT3G13160.1	394	44930.300	8.179	-0.318	mitochondrion
AT3G13175.1	106	11702.400	4.629	0.858	endoplasmic reticulum
AT3G13230.1	215	24010.400	10.348	-0.284	cytosol
AT3G13310.1	157	17450.600	10.370	-0.524	plastid
AT3G13380.1	1,164	126668.000	6.715	-0.062	plasma membrane
AT3G13600.1	605	68949.200	5.619	-0.695	nucleus
AT3G13880.1	748	83198.400	6.071	0.008	mitochondrion
AT3G13940.1	442	50628.200	9.518	-0.793	nucleus
AT3G13980.1	357	40078.500	9.859	-0.897	nucleus
AT3G14060.1	125	14416.900	11.732	-0.191	plastid
AT3G14200.1	230	25642.200	5.716	-0.947	nucleus
AT3G14390.1	484	53560.400	6.979	-0.160	plastid
AT3G14440.1	599	65860.200	6.298	-0.283	plastid
AT3G14460.1	1,424	158916.000	5.539	-0.168	cytosol
AT3G14470.1	1,054	121425.000	8.088	-0.335	plasma membrane
AT3G14560.1	154	17739.600	3.634	-0.455	nucleus
AT3G14580.1	405	46714.000	9.288	-0.306	mitochondrion
AT3G14770.1	236	26469.000	8.340	0.739	vacuole
AT3G14850.1	253	28375.200	8.581	-0.185	plasma membrane,endoplasmic reticulum
AT3G14900.1	611	71224.700	4.613	-0.812	plastid
AT3G15080.1	275	31127.600	10.646	-0.859	nucleus
AT3G15140.1	337	38672.400	7.832	-0.308	mitochondrion
AT3G15270.1	181	20992.800	10.363	-1.243	nucleus
AT3G15352.1	74	8051.650	7.781	-0.566	mitochondrion
AT3G15357.1	143	16079.300	4.180	-0.942	plastid
AT3G15450.1	253	27701.800	7.072	-0.233	peroxisome
AT3G15530.1	288	32090.100	8.574	0.237	plasma membrane,vacuole
AT3G15540.1	197	21495.700	4.957	-0.445	nucleus
AT3G15550.1	729	84805.000	6.488	-0.899	nucleus
AT3G15590.1	610	69398.000	8.615	-0.355	mitochondrion
AT3G15620.1	556	63793.600	8.986	-0.458	mitochondrion
AT3G15930.1	687	77688.500	8.136	-0.115	cytosol
AT3G15950.1	772	85020.800	4.329	-0.703	endoplasmic reticulum
AT3G16070.1	150	17594.700	6.235	-0.597	mitochondrion
AT3G16080.1	95	10772.100	12.374	-1.045	cytosol,nucleus
AT3G16420.1	298	32159.900	5.560	-0.303	cytosol
AT3G16460.1	705	72477.700	5.172	-0.375	cytosol
AT3G16510.1	360	39287.600	6.450	-0.618	nucleus
AT3G16670.1	154	15875.800	8.220	0.860	extracellular

Table S-5.2. Subcellular targeting of signifcantly differentially expressed genes using SUBA4

Gene	Amino Acid Residues	Molecular Weight	Isoelectric Point	GRAVY	Location SUBAcon
AT3G16700.1	224	24418.000	8.934	0.042	mitochondrion
AT3G16800.1	351	38603.200	7.832	-0.225	nucleus
AT3G16810.1	641	71607.700	9.645	-0.433	cytosol,nucleus
AT3G16860.1	653	72027.100	8.572	-0.218	plasma membrane
AT3G17120.1	219	23311.900	10.331	-0.453	cytosol
AT3G17130.1	183	19454.600	5.742	0.170	extracellular
AT3G17170.1	314	36277.600	4.234	-1.056	plastid
AT3G17220.1	173	18368.100	9.259	-0.067	extracellular
AT3G17390.1	393	42798.000	5.606	-0.255	plasma membrane,nucleus
AT3G17465.1	324	35406.000	10.405	-0.247	mitochondrion
AT3G17820.1	354	38596.700	5.934	-0.408	cytosol
AT3G17830.1	517	57262.400	9.959	-0.576	plastid
AT3G18070.1	501	57246.800	7.292	-0.420	extracellular
AT3G18080.1	512	58986.600	9.816	-0.483	extracellular
AT3G18130.1	326	35829.400	7.138	-0.175	cytosol
AT3G18580.1	217	24215.000	9.654	-0.420	mitochondrion
AT3G18600.1	568	63820.100	9.836	-0.482	nucleus
AT3G18680.1	339	36265.300	8.478	-0.058	plastid
AT3G18740.1	112	12280.100	10.212	-0.266	cytosol
AT3G18760.1	139	15967.500	9.337	-0.476	cytosol
AT3G18850.1	375	43492.300	9.200	0.118	endoplasmic reticulum
AT3G19050.1	2,771	315080.000	4.863	-0.590	nucleus
AT3G19230.1	519	57264.400	9.128	-0.243	extracellular
AT3G19270.1	468	53925.000	10.166	-0.209	extracellular
AT3G19380.1	421	46058.500	7.342	0.030	golgi,nucleus
AT3G19440.1	477	52968.200	9.953	-0.521	mitochondrion
AT3G19620.1	781	85504.900	8.667	-0.097	extracellular
AT3G19930.1	514	57098.600	8.249	0.559	plasma membrane
AT3G20080.1	523	59360.900	7.262	-0.121	extracellular
AT3G20130.1	515	58712.100	9.087	-0.091	plasma membrane
AT3G20240.1	348	37905.800	9.893	0.208	peroxisome
AT3G20260.1	437	50510.100	5.463	-0.710	cytosol,nucleus
AT3G20370.1	379	43451.400	6.537	-0.323	extracellular
AT3G20395.1	223	24887.600	8.882	0.244	plasma membrane
AT3G20440.1	869	100107.000	5.973	-0.567	plastid
AT3G20460.1	488	53054.200	8.076	0.507	plasma membrane
AT3G20470.1	174	13718.800	10.794	0.207	vacuole
AT3G20540.1	1,034	115569.000	7.867	-0.463	plastid
AT3G20660.1	526	57505.200	6.008	0.391	vacuole
AT3G20830.1	408	45891.900	9.717	-0.394	nucleus
AT3G21090.1	691	77241.900	9.603	0.076	plasma membrane
AT3G21110.1	411	46065.700	6.379	-0.318	plastid
AT3G21230.1	570	62562.700	5.540	-0.033	peroxisome
AT3G21300.1	554	61735.400	7.841	-0.264	mitochondrion
AT3G21310.1	383	44279.800	9.366	-0.152	plasma membrane,endoplasmic reticulum
AT3G21460.1	102	11056.700	8.499	0.454	cytosol
AT3G21470.1	523	58230.900	6.898	0.048	plasma membrane
AT3G21530.1	458	52028.600	9.853	-0.400	mitochondrion
AT3G21540.1	955	106071.000	7.308	-0.335	nucleus
AT3G21670.1	590	65249.500	9.410	0.205	vacuole
AT3G21690.1	506	54954.700	5.190	0.688	vacuole
AT3G21950.1	368	42013.000	5.317	-0.394	cytosol
AT3G22230.1	135	15615.500	10.984	-0.539	cytosol
AT3G22235.1	71	7317.520	4.074	-0.128	mitochondrion
AT3G22240.1	72	7524.880	4.793	-0.244	plasma membrane
AT3G22310.1	610	63613.200	9.872	-0.266	mitochondrion
AT3G22410.1	400	45279.000	10.580	-0.379	cytosol
AT3G22450.1	311	35726.500	9.487	-0.697	mitochondrion
AT3G22540.1	110	12511.900	8.284	-0.644	nucleus
AT3G22750.1	378	42717.200	7.850	-0.467	cytosol
AT3G22790.1	1,728	198863.000	5.003	-0.746	nucleus
AT3G22840.1	195	20325.700	10.384	0.149	plastid
AT3G22961.1	223	25783.000	6.167	-0.572	nucleus
AT3G23090.1	338	37784.000	9.569	-1.155	cytosol
AT3G23170.1	107	11698.000	10.323	-0.404	mitochondrion
AT3G23370.1	811	89453.100	5.546	-0.387	mitochondrion
AT3G23510.1	867	97886.100	6.426	-0.159	plasma membrane
AT3G23560.1	477	51855.200	8.321	0.736	vacuole
AT3G23570.1	239	26531.700	5.171	-0.264	cytosol
AT3G23580.1	341	39372.200	4.502	-0.134	cytosol
AT3G23670.1	1,313	146619.000	5.033	-0.635	nucleus
AT3G23710.1	313	34577.000	8.691	-0.439	plastid
AT3G23730.1	291	33148.400	9.620	-0.384	extracellular
AT3G23830.1	136	14129.500	8.731	-0.330	mitochondrion
AT3G23840.1	420	46431.700	4.987	-0.008	peroxisome
AT3G23890.1	1,473	164116.000	7.616	-0.522	nucleus
AT3G23940.1	608	64917.500	6.152	-0.101	plastid
AT3G23990.1	577	61284.200	5.415	-0.069	mitochondrion
AT3G24000.1	665	75603.900	8.320	-0.261	mitochondrion

Table S-5.2. Subcellular targeting of signifcantly differentially expressed genes using SUBA4

Gene	Amino Acid Residues	Molecular Weight	Isoelectric Point	GRAVY	Location SUBAcon
AT3G24450.1	140	15864.500	8.285	-0.229	cytosol
AT3G24670.1	440	48764.100	8.974	-0.273	extracellular
AT3G25130.1	406	46524.100	4.696	-0.552	plasma membrane
AT3G25520.1	301	34359.900	9.771	-0.748	cytosol
AT3G25882.1	122	13508.900	5.992	-0.842	nucleus
AT3G25900.1	326	35982.000	5.312	-0.170	cytosol
AT3G25940.1	119	13580.100	7.243	-0.665	nucleus
AT3G26125.1	541	62805.700	6.842	-0.296	endoplasmic reticulum
AT3G26410.1	477	54641.600	6.654	-0.332	cytosol,endoplasmic reticulum
AT3G26460.1	152	17774.000	4.808	-0.718	cytosol
AT3G26540.1	700	79199.200	7.567	-0.003	mitochondrion
AT3G26710.1	267	30103.100	10.396	0.030	plastid
AT3G26960.1	174	19280.100	9.330	-0.063	extracellular
AT3G27025.1	289	32990.300	9.730	-0.813	nucleus
AT3G27180.1	518	57848.600	9.584	-0.387	plastid
AT3G27250.1	282	31350.600	4.738	-0.494	cytosol
AT3G27280.1	279	30639.800	7.817	-0.083	mitochondrion
AT3G27500.1	692	79582.700	6.738	-0.381	nucleus
AT3G27550.1	491	57006.200	8.209	-1.241	nucleus
AT3G27620.1	329	37818.600	7.467	-0.332	mitochondrion
AT3G27831.1	77	8374.540	8.215	0.497	extracellular
AT3G27940.1	153	17601.400	9.724	-0.486	nucleus
AT3G28270.1	374	41614.900	4.963	-0.374	plasma membrane
AT3G28345.1	1,240	135649.000	8.171	0.065	vacuole
AT3G28420.1	216	25412.100	8.882	-0.438	plasma membrane
AT3G28500.1	115	11736.000	4.298	-0.022	cytosol
AT3G28700.1	471	51982.800	5.719	-0.324	mitochondrion
AT3G28860.1	1,252	136796.000	8.374	0.128	plasma membrane
AT3G29000.1	194	22697.100	3.985	-0.622	plasma membrane
AT3G29030.1	255	27613.000	9.077	-0.058	extracellular
AT3G29140.1	98	11182.400	4.013	-0.389	cytosol
AT3G29200.1	340	38240.800	5.716	-0.393	plastid
AT3G29370.1	101	11203.700	10.222	-0.413	mitochondrion
AT3G29575.1	231	25244.900	7.980	-0.618	nucleus
AT3G30180.1	465	53817.900	8.245	-0.248	endoplasmic reticulum
AT3G30775.1	499	54958.900	6.877	-0.184	mitochondrion
AT3G42800.1	341	38961.500	10.186	-1.019	nucleus
AT3G43960.1	376	41543.100	4.820	-0.235	extracellular
AT3G44120.1	384	44014.600	7.665	-0.359	cytosol
AT3G44730.1	1,087	121156.000	8.685	-0.572	nucleus
AT3G44750.1	245	26373.500	4.857	-0.898	nucleus
AT3G44970.1	479	54949.300	9.711	-0.173	endoplasmic reticulum
AT3G45030.1	124	13879.100	10.443	-0.394	cytosol
AT3G45160.1	91	9984.880	6.085	-0.511	extracellular
AT3G45300.1	409	44775.700	7.598	-0.201	mitochondrion
AT3G45390.1	604	66658.200	8.583	-0.048	plasma membrane
AT3G45430.1	674	74382.500	9.100	-0.041	plasma membrane
AT3G45650.1	558	61102.600	9.031	0.419	plasma membrane
AT3G45940.1	868	97455.700	6.607	-0.109	extracellular
AT3G46080.1	164	17740.500	9.828	-0.302	nucleus
AT3G46090.1	168	18360.300	9.253	-0.258	nucleus
AT3G46210.1	239	25811.100	7.050	-0.064	nucleus
AT3G46490.1	330	37612.800	6.087	-0.441	cytosol
AT3G46870.1	257	30135.100	9.806	-0.368	mitochondrion
AT3G46950.1	450	51339.400	10.167	-0.123	mitochondrion
AT3G47030.1	414	47312.600	8.355	-0.029	mitochondrion
AT3G47090.1	1,009	111140.000	6.788	0.043	vacuole
AT3G47640.1	240	26945.600	6.516	-0.785	nucleus
AT3G47950.1	960	105724.000	6.482	0.128	plasma membrane
AT3G47960.1	636	71043.500	9.278	0.197	plasma membrane
AT3G48250.1	621	71036.600	8.225	-0.260	mitochondrion
AT3G48260.1	516	58952.100	5.327	-0.451	nucleus
AT3G48290.1	488	56009.300	7.313	-0.099	endoplasmic reticulum
AT3G48350.1	364	40972.900	6.237	-0.576	endoplasmic reticulum
AT3G48360.1	364	41563.900	9.066	-0.339	nucleus
AT3G48390.1	633	70755.500	4.560	-0.162	cytosol
AT3G48500.1	668	78818.400	4.698	-0.964	plastid
AT3G48830.1	881	99382.600	7.674	-0.275	plasma membrane
AT3G49170.1	850	95500.800	6.795	-0.097	plastid
AT3G49180.1	438	48152.200	5.496	-0.224	nucleus
AT3G49220.1	598	65310.500	8.714	-0.168	extracellular
AT3G49240.1	629	71296.900	5.205	-0.432	mitochondrion
AT3G49260.1	471	52097.200	10.536	-0.914	nucleus
AT3G49320.1	354	40693.400	7.186	-0.424	mitochondrion
AT3G49410.1	574	65654.200	4.296	-0.665	nucleus
AT3G49740.1	737	82017.800	6.361	0.033	mitochondrion
AT3G49790.1	366	40341.400	10.131	-0.131	nucleus
AT3G49900.1	517	57950.800	7.235	-0.409	cytosol
AT3G50010.1	769	88295.500	6.203	-0.268	plasma membrane,nucleus

Table S-5.2. Subcellular targeting of signifcantly differentially expressed genes using SUBA4

Gene	Amino Acid Residues	Molecular Weight	Isoelectric Point	GRAVY	Location SUBAcon
AT3G50040.1	421	47951.300	4.872	-0.823	nucleus
AT3G50050.1	632	69752.700	5.755	-0.241	plasma membrane
AT3G50310.1	342	37554.500	4.744	-0.186	cytosol
AT3G50340.1	403	44305.300	8.997	-0.295	mitochondrion
AT3G50700.1	452	47945.800	9.954	-0.463	nucleus
AT3G50890.1	249	28659.500	10.127	-1.038	nucleus
AT3G51220.1	186	21487.800	8.450	-0.723	cytosol
AT3G51290.1	634	70905.100	8.767	-0.590	nucleus
AT3G51325.1	90	10503.900	6.724	0.181	plasma membrane
AT3G51330.1	529	57867.200	4.787	-0.007	extracellular
AT3G51660.1	112	12211.000	9.122	0.353	peroxisome
AT3G52170.1	499	54031.900	4.553	-0.565	plastid
AT3G52310.1	784	86911.700	9.309	0.032	plasma membrane
AT3G52460.1	300	33153.400	7.328	-0.366	plasma membrane
AT3G53190.1	483	53596.500	6.448	-0.219	extracellular
AT3G53220.1	126	14414.900	6.252	-0.634	cytosol
AT3G53250.1	109	12313.900	7.983	-0.216	cytosol
AT3G53460.1	342	36009.300	4.981	-0.488	plastid
AT3G53630.1	194	22208.800	4.597	-0.829	cytosol,peroxisome
AT3G53940.1	365	39763.800	9.999	-0.073	peroxisome
AT3G53980.1	114	11723.400	8.134	0.256	extracellular
AT3G54000.1	352	39185.800	8.144	-0.670	nucleus
AT3G54030.1	490	54792.400	6.509	-0.316	plasma membrane
AT3G54090.1	471	53784.000	6.005	-0.467	plastid
AT3G54260.1	379	44373.300	9.024	-0.460	extracellular
AT3G54400.1	425	45477.700	9.297	0.063	extracellular
AT3G54780.1	675	74718.600	7.393	-0.219	plasma membrane
AT3G54830.1	546	59739.600	5.480	0.205	golgi
AT3G55240.1	95	11091.000	4.640	-0.785	nucleus
AT3G55510.1	594	68370.800	9.123	-0.332	nucleus
AT3G55605.1	258	29014.700	4.304	-0.561	mitochondrion
AT3G55940.1	584	66465.300	5.679	-0.448	plasma membrane
AT3G55990.1	487	56698.300	4.969	-0.438	golgi
AT3G56030.1	351	39660.800	8.552	-0.225	mitochondrion
AT3G56070.1	176	18921.600	7.965	-0.288	mitochondrion
AT3G56290.1	173	19923.500	9.873	-0.841	plastid
AT3G56330.1	433	48475.300	7.950	-0.237	plastid
AT3G56400.1	294	32937.300	6.232	-0.723	nucleus
AT3G56430.1	434	48536.900	10.266	-0.226	mitochondrion
AT3G56570.1	531	59454.800	4.164	-0.560	nucleus
AT3G56710.1	151	16862.600	5.242	-0.768	plastid
AT3G56810.1	332	37096.700	8.937	-0.671	plastid
AT3G56890.1	219	24692.600	4.471	-0.116	cytosol
AT3G56990.1	711	79671.900	7.704	-0.718	nucleus
AT3G57000.1	298	33831.500	7.930	-0.537	cytosol
AT3G57010.1	376	41982.300	6.062	-0.164	endoplasmic reticulum
AT3G57020.1	370	41460.000	7.010	-0.189	endoplasmic reticulum
AT3G57150.1	565	63029.700	9.736	-0.716	nucleus
AT3G57180.1	660	73091.200	6.241	-0.428	plastid
AT3G57190.1	406	45971.400	7.206	-0.298	mitochondrion
AT3G57240.1	341	37633.600	8.568	-0.163	extracellular
AT3G57360.1	254	28108.000	4.484	-0.387	cytosol
AT3G57460.1	356	40332.400	7.054	-0.123	cytosol
AT3G57520.1	773	85148.000	5.490	-0.187	cytosol
AT3G57680.1	519	56208.100	5.753	-0.099	plastid
AT3G57770.1	269	30292.500	6.620	-0.068	cytosol
AT3G57780.1	671	74813.700	4.714	-0.556	nucleus
AT3G58120.1	329	36807.200	6.804	-1.007	nucleus
AT3G58520.1	418	48824.000	9.168	-0.521	mitochondrion
AT3G58660.1	446	49973.200	10.269	-0.626	cytosol,nucleus
AT3G58700.1	182	20862.400	10.484	-0.474	cytosol
AT3G58850.1	118	12872.900	4.296	-0.558	nucleus
AT3G59010.1	529	57516.600	9.193	-0.262	extracellular
AT3G59220.1	287	31604.800	5.192	-0.198	nucleus
AT3G59290.1	1,024	109700.000	5.474	-0.815	nucleus
AT3G59480.1	326	35046.100	4.996	0.037	cytosol
AT3G59680.1	201	23194.300	11.210	-0.683	nucleus
AT3G59820.1	755	85739.700	6.675	-0.512	mitochondrion
AT3G59890.1	349	37871.700	7.307	-0.013	plastid
AT3G59900.1	130	14696.400	10.458	0.185	endoplasmic reticulum
AT3G60290.1	357	40443.200	6.107	-0.310	cytosol
AT3G60330.1	961	105526.000	6.828	0.056	plasma membrane
AT3G60360.1	228	27150.600	10.588	-1.325	nucleus
AT3G60390.1	315	34749.100	8.377	-0.707	nucleus
AT3G60540.1	81	8217.180	11.329	0.321	endoplasmic reticulum
AT3G60900.1	422	43609.700	5.626	0.086	plasma membrane
AT3G60960.1	403	45508.500	6.620	0.017	mitochondrion
AT3G60980.1	412	47370.800	7.834	-0.308	mitochondrion
AT3G61100.1	166	18893.200	4.210	-0.390	cytosol

Table S-5.2. Subcellular targeting of signifcantly differentially expressed genes using SUBA4

Gene	Amino Acid Residues	Molecular Weight	Isoelectric Point	GRAVY	Location SUBAcon
AT3G61380.1	718	80735.400	4.316	-0.588	nucleus
AT3G61460.1	170	20061.100	4.638	-0.121	extracellular
AT3G61520.1	766	86910.900	7.210	-0.155	mitochondrion
AT3G61680.1	649	71739.000	7.086	-0.347	nucleus
AT3G61780.1	1,121	127928.000	5.377	-0.794	plastid
AT3G61810.1	375	42057.000	9.761	-0.051	extracellular
AT3G61820.1	483	51464.000	8.522	0.004	extracellular
AT3G61920.1	187	19939.800	6.229	-0.053	cytosol
AT3G61950.1	358	41032.600	6.745	-0.633	nucleus
AT3G62270.1	703	78618.400	8.617	0.213	plasma membrane
AT3G62550.1	162	18266.000	5.066	-0.182	cytosol
AT3G62570.1	552	61966.600	9.323	-0.331	nucleus
AT3G62870.1	256	29036.100	10.868	-0.568	cytosol
AT3G62890.1	573	64950.200	7.615	-0.060	plastid
AT3G62950.1	103	11312.800	8.887	-0.061	cytosol
AT3G63090.1	404	47813.200	9.814	-0.516	cytosol
AT3G63200.1	384	41489.400	7.799	-0.173	cytosol
AT3G63440.1	533	60003.200	9.115	-0.150	mitochondrion
AT3G63450.1	404	45677.800	7.560	-0.440	cytosol
AT3G63470.1	502	56242.700	8.483	-0.300	extracellular
AT3G66652.1	997	115376.000	5.899	-1.269	nucleus
AT4G00026.1	269	30049.000	10.279	-0.492	mitochondrion
AT4G00390.1	364	39211.200	6.049	-0.765	nucleus
AT4G00480.1	526	59991.100	6.703	-0.580	nucleus
AT4G00620.1	360	38744.000	8.401	-0.033	plastid
AT4G00820.1	534	59998.800	10.906	-1.027	nucleus
AT4G00970.1	665	74891.300	6.267	-0.194	plasma membrane
AT4G01037.1	528	61236.100	6.634	-0.758	plastid
AT4G01060.1	77	8901.500	5.721	-0.795	nucleus
AT4G01200.1	250	27370.600	9.543	-0.321	cytosol
AT4G01380.1	210	23835.200	6.579	-0.247	mitochondrion
AT4G01390.1	300	34274.100	8.151	-0.363	cytosol
AT4G01430.1	365	40460.100	9.547	0.437	plasma membrane
AT4G01540.1	473	53601.600	6.097	-0.627	nucleus
AT4G01580.1	190	22123.600	7.801	-0.558	mitochondrion
AT4G01660.1	623	68631.100	5.544	-0.254	mitochondrion
AT4G01670.1	249	27003.100	6.257	-0.894	nucleus
AT4G01680.1	336	37888.300	7.585	-0.723	nucleus
AT4G01895.1	140	16663.800	3.966	-1.504	nucleus
AT4G01985.1	579	42555.900	13.258	0.266	extracellular
AT4G01990.1	502	56944.600	7.012	-0.314	mitochondrion
AT4G02290.1	516	57304.200	9.250	-0.183	extracellular
AT4G02330.1	573	63947.300	8.625	-0.253	extracellular
AT4G02790.1	372	41724.000	10.450	-0.333	plastid
AT4G02930.1	454	49412.800	6.684	-0.117	mitochondrion
AT4G02990.1	541	61552.600	6.720	-0.313	plastid
AT4G03070.1	322	36913.600	4.678	-0.389	cytosol
AT4G03190.1	585	65651.800	7.882	-0.065	cytosol
AT4G03210.1	290	33143.100	4.914	-0.291	extracellular
AT4G03270.1	302	34670.200	5.789	-0.246	nucleus
AT4G03330.1	305	34485.400	7.666	-0.435	plasma membrane
AT4G03400.1	591	66862.800	5.950	-0.183	cytosol
AT4G03610.1	303	34025.700	5.513	-0.207	cytosol
AT4G04020.1	318	34950.300	5.246	-0.268	plastid
AT4G04180.1	609	67334.900	5.537	-0.404	mitochondrion
AT4G04220.1	811	90843.200	5.381	-0.133	endoplasmic reticulum
AT4G04423.1	156	17860.500	4.159	-0.797	nucleus
AT4G04745.1	146	17222.500	11.618	-0.447	mitochondrion
AT4G04750.1	482	51680.300	5.025	0.617	plasma membrane
AT4G04790.1	821	92840.900	6.478	-0.242	mitochondrion
AT4G04940.1	910	102223.000	6.944	-0.134	nucleus
AT4G05170.1	238	26802.600	4.721	-0.532	nucleus
AT4G05410.1	504	56521.700	6.181	-0.790	nucleus
AT4G06534.1	405	44682.600	9.930	-0.180	extracellular
AT4G06536.1	169	18763.000	7.028	-0.518	peroxisome
AT4G06746.1	150	17200.000	10.552	-0.676	nucleus
AT4G08040.1	460	51801.700	6.786	-0.360	cytosol
AT4G08160.1	752	84556.600	5.779	-0.310	cytosol
AT4G08210.1	686	75829.300	6.349	0.170	cytosol
AT4G08555.1	69	7683.380	10.520	-0.830	nucleus
AT4G08590.1	465	52310.200	4.901	-0.572	nucleus
AT4G08910.1	212	24352.000	6.417	-0.757	nucleus
AT4G09080.1	396	43634.200	8.713	-0.360	plastid
AT4G09160.1	668	75751.500	4.383	-0.670	nucleus
AT4G09420.1	457	51352.400	6.038	-0.236	cytosol
AT4G09730.1	621	68927.900	10.592	-0.518	plastid
AT4G09760.1	346	40352.700	4.750	-0.410	cytosol
AT4G09890.1	87	10167.800	9.818	-1.148	nucleus
AT4G09990.1	290	32839.000	7.209	-0.343	golgi

Table S-5.2. Subcellular targeting of signifcantly differentially expressed genes using SUBA4

Gene	Amino Acid Residues	Molecular Weight	Isoelectric Point	GRAVY	Location SUBAcon
AT4G10290.1	120	14074.800	4.746	-0.503	cytosol
AT4G10310.1	506	57453.600	8.819	0.373	plasma membrane
AT4G10380.1	304	31494.500	8.493	0.507	plasma membrane
AT4G10420.1	322	37155.300	6.499	-0.018	plasma membrane
AT4G10450.1	194	21974.900	10.172	-0.294	cytosol
AT4G10620.1	597	66494.400	9.833	-0.424	mitochondrion
AT4G10650.1	377	42426.100	8.953	-0.285	cytosol
AT4G11060.1	201	22238.600	9.459	-0.356	mitochondrion
AT4G11211.1	21	2403.790	4.308	-0.329	plasma membrane
AT4G11470.1	666	74678.100	6.498	-0.200	plasma membrane
AT4G11630.1	225	25415.800	11.052	-0.449	mitochondrion
AT4G11690.1	566	63789.400	7.871	-0.105	endoplasmic reticulum
AT4G12240.1	364	41911.100	9.425	-0.668	mitochondrion
AT4G12480.1	168	17309.300	9.121	0.242	extracellular
AT4G12600.1	128	14000.100	6.514	-0.005	cytosol,nucleus
AT4G12750.1	1,131	127812.000	7.930	-0.505	nucleus
AT4G13170.1	206	23630.500	11.062	-0.475	cytosol
AT4G13370.1	673	73436.200	10.166	-0.492	cytosol
AT4G13395.1	55	6560.210	10.615	-0.331	mitochondrion
AT4G13560.1	109	11585.100	7.523	-1.181	nucleus
AT4G13570.1	118	13201.200	8.512	0.015	nucleus
AT4G13750.1	2,729	306365.000	6.345	-0.288	nucleus
AT4G13850.1	158	15703.300	7.509	-0.294	mitochondrion
AT4G14130.1	289	32688.800	9.587	-0.325	extracellular
AT4G14200.1	784	84679.600	4.352	-0.719	nucleus
AT4G14430.1	240	25774.300	8.662	0.138	peroxisome
AT4G14550.1	228	25045.100	8.966	-0.510	nucleus
AT4G14690.1	193	20345.800	10.345	0.172	plastid
AT4G14750.1	387	43911.200	10.154	-0.830	nucleus
AT4G14820.1	722	82117.500	6.427	-0.087	plastid
AT4G14860.1	182	20679.300	6.798	-0.464	plastid
AT4G15000.1	135	15608.400	10.960	-0.544	cytosol
AT4G15248.1	117	13562.400	8.218	-0.380	nucleus
AT4G15500.1	475	53498.700	5.166	-0.092	cytosol
AT4G15640.1	390	43912.600	8.849	-0.306	mitochondrion
AT4G15660.1	102	11312.100	8.060	0.297	plasma membrane
AT4G15690.1	102	11205.900	7.346	0.328	plasma membrane
AT4G15770.1	187	20611.800	8.462	-0.150	cytosol
AT4G15850.1	522	57719.000	9.419	-0.204	nucleus
AT4G15910.1	104	10966.100	9.979	-0.254	plastid
AT4G16000.1	89	10351.500	10.828	-0.678	mitochondrion
AT4G16515.1	86	9541.620	10.057	-0.194	endoplasmic reticulum
AT4G16590.1	401	46284.300	9.460	0.119	plasma membrane
AT4G16630.1	789	89359.600	5.326	-0.807	nucleus
AT4G16690.1	262	29015.600	5.504	-0.082	cytosol
AT4G16700.1	453	50562.600	9.682	-0.409	mitochondrion
AT4G16720.1	204	24240.500	11.964	-1.119	cytosol
AT4G16740.1	565	65756.900	7.661	-0.403	cytosol
AT4G16780.1	284	31854.200	9.024	-0.873	nucleus
AT4G16835.1	656	74822.900	8.759	-0.243	mitochondrion
AT4G17030.1	250	27935.300	7.109	-0.148	extracellular
AT4G17460.1	282	31556.400	8.594	-0.770	nucleus
AT4G17483.1	300	33277.200	5.400	-0.008	extracellular
AT4G17670.1	159	18594.400	7.496	-1.056	nucleus
AT4G17680.1	314	35133.600	6.404	-0.522	nucleus
AT4G18100.1	133	15504.100	11.539	-0.715	cytosol
AT4G18170.1	318	35564.900	7.597	-0.914	nucleus
AT4G18290.1	697	80153.900	6.892	-0.176	plasma membrane
AT4G18340.1	397	44164.000	6.693	-0.046	extracellular
AT4G18590.1	106	11716.900	5.035	-0.098	cytosol
AT4G18670.1	857	90840.400	6.707	-0.427	extracellular
AT4G18730.1	182	20862.400	10.484	-0.474	cytosol
AT4G18750.1	871	97703.700	6.708	-0.096	plastid
AT4G18780.1	985	111527.000	7.127	-0.104	plasma membrane,extracellular
AT4G18840.1	545	60845.200	5.303	-0.023	plastid
AT4G18905.1	494	54428.100	4.270	-0.477	nucleus
AT4G18970.1	361	39600.600	5.146	-0.189	extracellular
AT4G19000.1	406	47097.400	8.963	-0.963	nucleus
AT4G19191.1	654	73412.600	6.548	-0.023	mitochondrion
AT4G19230.1	467	53040.300	8.622	-0.192	plasma membrane,extracellular
AT4G19380.1	726	80072.300	7.946	-0.224	cytosol
AT4G19390.1	273	30044.700	9.473	0.381	plastid
AT4G19810.1	379	41130.100	9.033	-0.099	extracellular
AT4G20000.1	208	23253.400	4.798	-0.873	nucleus
AT4G20010.1	371	41731.500	9.414	-0.557	plastid
AT4G20020.1	419	45160.000	7.996	-0.891	mitochondrion
AT4G20090.1	660	74128.100	8.438	-0.045	plastid
AT4G20130.1	483	55613.700	5.277	-0.345	plastid
AT4G20140.1	1,249	137296.000	5.428	-0.106	plasma membrane

Table S-5.2. Subcellular targeting of signifcantly differentially expressed genes using SUBA4

Gene	Amino Acid Residues	Molecular Weight	Isoelectric Point	GRAVY	Location SUBAcon
AT4G20230.1	609	70686.400	6.884	-0.250	plastid
AT4G20940.1	977	105117.000	5.673	-0.090	plasma membrane
AT4G21120.1	594	64850.600	7.901	0.519	plasma membrane
AT4G21140.1	243	27004.200	10.917	-0.637	mitochondrion
AT4G21220.1	304	32332.800	8.215	0.070	mitochondrion
AT4G21400.1	711	79048.900	6.910	-0.039	plasma membrane
AT4G21520.1	425	47545.700	4.518	-0.557	nucleus
AT4G21650.1	766	81484.500	7.428	0.018	extracellular
AT4G21760.1	535	61965.500	6.675	-0.373	vacuole
AT4G21870.1	134	15387.500	4.941	-0.325	cytosol
AT4G21960.1	330	37297.000	7.783	-0.399	extracellular
AT4G21990.1	458	50697.300	7.081	-0.293	plastid
AT4G22010.1	541	60459.200	10.247	-0.232	extracellular
AT4G22270.1	437	49796.600	7.760	0.289	plasma membrane
AT4G22380.1	128	13916.000	7.414	0.021	nucleus
AT4G22390.1	402	46191.200	7.599	-0.112	cytosol
AT4G22470.1	375	38791.600	8.291	-0.031	extracellular
AT4G22620.1	160	18569.100	11.734	-0.434	mitochondrion
AT4G22780.1	449	50692.800	5.997	-0.303	cytosol
AT4G22840.1	409	44209.200	10.311	0.627	plastid
AT4G23130.1	659	73406.000	7.719	-0.084	plasma membrane
AT4G23140.1	674	74504.800	7.527	-0.141	plasma membrane
AT4G23210.1	610	68205.000	8.867	-0.180	plasma membrane
AT4G23220.1	728	82196.000	6.327	0.004	plasma membrane
AT4G23230.1	507	56465.800	8.285	-0.113	plasma membrane
AT4G23620.1	264	29019.600	10.549	-0.199	mitochondrion
AT4G23800.1	456	53233.700	9.953	-1.321	nucleus
AT4G23820.1	444	48637.900	8.659	-0.150	extracellular
AT4G24050.1	332	35842.000	7.152	0.022	cytosol
AT4G24175.1	306	34904.100	5.526	-0.744	plastid
AT4G24180.1	260	27452.000	4.556	0.005	extracellular
AT4G24230.1	364	39530.800	3.877	-0.368	extracellular
AT4G24275.1	126	14395.900	9.464	-1.106	nucleus
AT4G24780.1	408	45016.400	8.238	-0.331	extracellular
AT4G25260.1	201	22174.200	4.752	-0.225	extracellular
AT4G25470.1	216	24265.500	4.752	-0.522	nucleus
AT4G25480.1	216	24237.300	4.867	-0.488	nucleus
AT4G25490.1	213	23830.900	4.739	-0.607	nucleus
AT4G25630.1	320	33655.400	10.695	-0.395	nucleus
AT4G25730.1	821	92272.400	9.336	-0.928	nucleus
AT4G25835.1	506	57618.300	4.993	-0.408	extracellular,endoplasmic reticulum
AT4G25850.1	383	43676.400	7.037	-0.445	cytosol
AT4G25990.1	394	44580.300	8.568	-0.798	nucleus
AT4G26110.1	372	42999.400	4.113	-1.110	nucleus
AT4G26150.1	352	39347.500	9.593	-0.702	nucleus
AT4G26260.1	317	36905.400	4.656	-0.567	cytosol
AT4G26590.1	753	84894.700	9.291	0.332	plasma membrane
AT4G26600.1	671	75546.800	5.734	-0.971	nucleus
AT4G26760.1	578	65208.200	4.747	-0.625	cytosol
AT4G26780.1	327	36118.000	5.036	-0.750	mitochondrion
AT4G26800.1	369	41255.800	9.332	-0.003	cytosol
AT4G27010.1	2,374	266645.000	6.164	0.062	nucleus
AT4G27260.1	612	69287.100	5.781	-0.263	cytosol
AT4G27280.1	130	14503.400	4.278	-0.244	nucleus
AT4G27340.1	619	70573.200	9.117	-0.330	plastid
AT4G27490.1	256	27449.800	4.613	-0.025	cytosol
AT4G27654.1	67	8181.230	7.616	0.984	extracellular
AT4G27657.1	62	6766.350	8.530	0.356	extracellular
AT4G27730.1	736	82365.600	9.051	0.519	plasma membrane
AT4G27900.1	261	29451.900	4.601	-0.503	nucleus
AT4G28070.1	464	52209.800	7.104	-0.124	mitochondrion
AT4G28250.1	264	28426.400	8.854	0.064	extracellular
AT4G28450.1	452	51361.100	9.931	-0.554	nucleus
AT4G28510.1	288	31708.400	9.732	-0.128	mitochondrion
AT4G28780.1	367	39898.900	4.629	0.078	extracellular
AT4G28820.1	173	19153.700	4.666	-0.550	nucleus
AT4G28950.1	209	23043.800	9.603	-0.139	plasma membrane
AT4G29110.1	200	22785.400	10.285	-0.622	nucleus
AT4G29230.1	498	54875.600	7.038	-0.870	nucleus
AT4G29400.1	302	34642.000	5.054	-0.615	mitochondrion
AT4G29410.1	143	15911.500	11.707	-0.599	cytosol
AT4G29510.1	390	43896.000	4.586	-0.312	cytosol
AT4G29880.1	373	41992.500	8.918	-0.140	nucleus
AT4G29905.1	67	7816.630	8.036	-0.054	plasma membrane
AT4G29920.1	1,017	113791.000	6.052	-0.492	plastid
AT4G30020.1	816	87509.400	7.311	-0.088	extracellular
AT4G30130.1	725	81804.200	5.340	-0.601	nucleus
AT4G30150.1	2,009	224606.000	6.941	-0.016	nucleus
AT4G30180.1	158	17810.400	9.528	-0.619	nucleus

Table S-5.2. Subcellular targeting of signifcantly differentially expressed genes using SUBA4

Gene	Amino Acid Residues	Molecular Weight	Isoelectric Point	GRAVY	Location SUBAcon
AT4G30190.1	948	104407.000	6.992	0.097	plasma membrane
AT4G30220.1	88	9864.790	4.047	-0.272	nucleus
AT4G30230.1	260	29181.700	10.899	-0.785	nucleus
AT4G30250.1	519	59514.700	5.783	-0.544	plasma membrane
AT4G30290.1	277	31564.300	9.044	-0.499	extracellular
AT4G30410.1	180	20436.200	11.030	-0.449	nucleus
AT4G30650.1	73	7906.080	4.333	1.142	extracellular
AT4G30660.1	74	8519.750	4.867	0.893	extracellular
AT4G30800.1	159	17932.100	11.411	-0.576	cytosol
AT4G30930.1	270	30909.300	5.488	-0.726	mitochondrion
AT4G30990.1	2,599	294817.000	8.179	-0.063	nucleus
AT4G31120.1	642	71874.200	5.203	-0.234	cytosol
AT4G31210.1	1,284	141571.000	9.903	-0.563	plastid
AT4G31650.1	493	56233.600	10.423	-0.546	nucleus
AT4G31790.1	277	30792.000	4.726	-0.134	cytosol
AT4G31810.1	409	45502.300	4.858	-0.203	mitochondrion
AT4G31840.1	177	18962.500	9.177	0.076	extracellular
AT4G31870.1	233	25775.600	10.078	-0.346	plastid
AT4G32000.1	418	45844.100	9.469	0.067	extracellular
AT4G32270.1	239	27269.100	10.608	-0.419	mitochondrion
AT4G32280.1	251	28611.600	6.281	-0.560	nucleus
AT4G32290.1	384	44044.300	9.169	-0.168	extracellular
AT4G32460.1	365	39820.900	8.201	-0.022	extracellular
AT4G32800.1	221	24858.800	4.621	-0.586	nucleus
AT4G32880.1	833	92001.500	6.236	-0.186	nucleus
AT4G33260.1	447	49506.200	8.178	-0.482	nucleus
AT4G33270.1	457	50553.400	8.579	-0.501	nucleus
AT4G33495.1	409	48289.000	10.030	-0.407	mitochondrion
AT4G33550.1	130	14283.700	8.958	0.319	extracellular
AT4G33790.1	493	56037.900	8.926	0.010	endoplasmic reticulum
AT4G33985.1	154	17026.900	5.979	-0.773	nucleus
AT4G33990.1	823	92419.700	7.504	-0.027	mitochondrion
AT4G34138.1	488	54839.500	5.430	-0.147	plasma membrane
AT4G34290.1	144	15999.500	10.478	-0.288	plastid
AT4G34360.1	248	28713.700	4.405	-0.525	cytosol
AT4G34560.1	221	25284.900	10.656	-0.372	golgi,endoplasmic reticulum
AT4G34770.1	104	11318.700	8.486	0.090	mitochondrion
AT4G34790.1	108	12213.800	9.660	-0.375	plastid
AT4G34900.1	1,353	148771.000	6.705	-0.090	cytosol
AT4G34970.1	141	16370.600	8.032	-0.551	cytosol
AT4G35030.1	321	37223.200	8.888	-0.286	cytosol
AT4G35060.1	153	17163.300	8.316	-0.388	plasma membrane
AT4G35090.1	492	56934.300	7.121	-0.574	peroxisome
AT4G35130.1	804	90790.700	8.197	-0.096	plastid
AT4G35160.1	382	42616.500	5.198	-0.099	cytosol
AT4G35350.1	355	39619.600	5.675	-0.449	vacuole
AT4G35640.1	355	38425.900	5.764	-0.008	cytosol
AT4G35850.1	444	50459.700	7.758	-0.308	mitochondrion
AT4G35900.1	285	31379.100	10.906	-0.970	nucleus
AT4G36130.1	258	27950.000	11.455	-0.454	cytosol
AT4G36180.1	1,136	123672.000	6.305	-0.026	plasma membrane
AT4G36230.1	221	20344.800	7.294	-0.668	extracellular
AT4G36270.1	486	55108.800	7.577	-0.473	cytosol
AT4G36280.1	626	69981.200	7.179	-0.432	cytosol
AT4G36380.1	524	59359.200	7.009	-0.184	golgi,endoplasmic reticulum
AT4G36420.1	179	19514.000	10.343	-0.218	mitochondrion
AT4G36470.1	371	41986.900	5.340	-0.388	cytosol
AT4G36570.1	58	6660.620	9.105	-1.183	nucleus
AT4G36580.1	632	71011.400	9.801	-0.641	plastid
AT4G36770.1	457	50816.800	5.650	-0.072	cytosol
AT4G36850.1	392	43826.000	8.169	0.043	plasma membrane
AT4G37170.1	691	78030.700	7.903	-0.287	mitochondrion
AT4G37190.1	562	62207.200	4.574	-0.308	golgi
AT4G37370.1	497	56201.500	8.725	-0.153	endoplasmic reticulum
AT4G37400.1	501	56639.900	8.523	-0.268	endoplasmic reticulum
AT4G37450.1	209	20490.200	9.842	-0.150	extracellular
AT4G37540.1	240	26613.900	8.508	-0.298	nucleus
AT4G37660.1	167	18220.200	10.084	-0.097	mitochondrion
AT4G37770.1	469	53373.700	8.007	-0.386	cytosol
AT4G37910.1	682	73079.100	5.254	-0.295	mitochondrion
AT4G38010.1	559	62437.400	8.289	0.136	cytosol
AT4G38020.1	352	38462.700	8.269	0.024	plastid
AT4G38150.1	302	33456.100	6.919	-0.471	mitochondrion
AT4G38160.1	333	37890.600	9.335	-0.114	mitochondrion
AT4G38380.1	560	59820.300	10.143	0.541	plastid
AT4G38400.1	265	28644.200	8.248	0.008	extracellular
AT4G38540.1	407	45507.600	6.298	-0.214	golgi
AT4G38560.1	521	58781.200	9.386	-0.771	nucleus
AT4G38620.1	282	31810.100	8.760	-0.653	nucleus

Table S-5.2. Subcellular targeting of signifcantly differentially expressed genes using SUBA4

Gene	Amino Acid Residues	Molecular Weight	Isoelectric Point	GRAVY	Location SUBAcon
AT4G38950.1	836	94469.000	7.486	-0.589	nucleus
AT4G39070.1	242	26780.900	6.493	-0.499	nucleus
AT4G39110.1	878	96510.100	6.010	-0.168	extracellular
AT4G39210.1	521	58032.500	8.559	-0.290	plastid
AT4G39340.1	127	13613.300	4.161	0.237	extracellular
AT4G39400.1	1,196	130551.000	6.378	-0.086	plasma membrane
AT4G39410.1	304	34205.400	7.597	-0.849	nucleus
AT4G39470.1	341	39157.800	9.119	-0.318	plastid
AT4G39670.1	229	26515.300	4.296	-0.322	cytosol
AT4G39675.1	70	8230.830	10.258	-1.083	cytosol
AT4G39830.1	582	66157.700	9.044	-0.345	extracellular
AT4G39880.1	178	19853.200	10.864	-0.633	mitochondrion
AT4G39955.1	328	37642.800	8.842	-0.201	mitochondrion
AT4G40000.1	783	88188.200	6.905	-0.462	nucleus
AT4G40010.1	350	39777.000	4.627	-0.450	cytosol
AT4G40070.1	323	36071.700	8.809	-0.429	plasma membrane,endoplasmic reticulum
AT5G01320.1	603	65468.100	5.638	-0.099	cytosol
AT5G01380.1	323	38274.800	6.523	-1.268	nucleus
AT5G01410.1	309	33218.400	5.990	0.036	cytosol
AT5G01540.1	682	75872.100	9.508	-0.195	plasma membrane
AT5G01740.1	162	18429.000	5.545	-0.173	cytosol
AT5G01820.1	442	50300.600	8.213	-0.335	cytosol
AT5G01840.1	270	30031.700	11.044	-0.805	nucleus
AT5G02050.1	267	29765.100	4.066	-0.507	mitochondrion
AT5G02170.1	526	57541.400	6.243	0.510	plasma membrane
AT5G02200.1	181	20233.100	4.244	-0.492	cytosol,nucleus
AT5G02430.1	905	99899.800	7.588	-0.670	nucleus
AT5G02450.1	108	12190.300	12.132	-0.964	cytosol
AT5G02540.1	331	36193.500	8.584	-0.029	cytosol
AT5G02550.1	76	8181.270	7.880	-1.162	nucleus
AT5G02560.1	153	16219.000	11.481	-0.499	nucleus
AT5G02610.1	123	14332.100	11.604	-0.728	cytosol
AT5G02750.1	283	32151.100	7.273	-0.004	nucleus
AT5G02760.1	370	41336.600	9.147	-0.325	nucleus
AT5G02890.1	353	38805.400	5.341	-0.131	cytosol
AT5G02960.1	142	15736.400	11.112	-0.539	cytosol
AT5G03120.1	76	8354.070	7.070	-0.291	extracellular
AT5G03150.1	503	55203.900	10.205	-0.713	nucleus
AT5G03170.1	246	25593.100	5.844	0.052	extracellular
AT5G03210.1	62	7008.100	3.384	-0.353	plasma membrane
AT5G03240.1	306	34281.400	7.816	-0.435	cytosol
AT5G03350.1	274	30164.000	9.947	-0.244	extracellular
AT5G03470.1	495	57539.600	6.516	-0.351	cytosol
AT5G03545.1	70	8024.120	4.111	0.596	plasma membrane
AT5G03995.1	85	10175.100	9.829	-0.494	cytosol
AT5G04130.1	732	81057.900	9.037	-0.308	mitochondrion
AT5G04250.1	345	39233.500	4.656	-0.649	cytosol
AT5G04770.1	583	62812.100	8.719	0.662	plasma membrane
AT5G04840.1	307	33435.200	7.811	-0.546	nucleus
AT5G04895.1	1,161	130839.000	8.484	-0.353	mitochondrion
AT5G05180.1	432	49881.200	4.499	-0.777	nucleus
AT5G05300.1	102	10555.900	9.719	0.448	extracellular
AT5G05320.1	406	45609.200	9.301	-0.218	plastid,peroxisome
AT5G05840.1	439	48865.300	5.078	-0.388	cytosol
AT5G05960.1	116	12443.500	9.212	0.116	extracellular
AT5G05990.1	259	30070.400	5.183	-0.791	mitochondrion
AT5G06510.1	269	29796.000	8.847	-0.641	nucleus
AT5G06550.1	502	57422.200	5.241	-0.410	mitochondrion
AT5G06620.1	325	36136.300	6.732	-0.079	mitochondrion
AT5G06790.1	209	23893.500	8.602	-0.521	plastid
AT5G06930.1	723	80576.700	5.962	-0.539	plastid
AT5G06990.1	261	28387.700	10.341	-0.325	plastid
AT5G07000.1	347	39655.400	6.323	-0.292	cytosol
AT5G07030.1	455	48696.900	10.059	0.023	extracellular
AT5G07440.1	411	44701.600	6.510	-0.148	mitochondrion
AT5G07800.1	460	52340.100	6.208	-0.392	cytosol
AT5G07860.1	454	50436.200	6.829	-0.244	cytosol
AT5G08130.1	409	45547.800	7.241	-0.812	nucleus
AT5G08180.1	156	16949.100	10.013	-0.201	nucleus
AT5G08185.1	45	5408.650	8.239	-0.007	extracellular
AT5G08305.1	534	59921.400	7.922	-0.119	mitochondrion
AT5G08310.1	832	94076.600	6.652	-0.013	mitochondrion
AT5G08350.1	222	25255.800	10.551	-0.422	mitochondrion
AT5G08400.1	333	37986.100	6.929	-0.353	plasma membrane
AT5G08600.1	822	93476.000	5.307	-1.061	nucleus
AT5G08610.1	850	94191.400	10.060	-0.643	plastid
AT5G08620.1	563	62498.400	10.432	-0.301	nucleus
AT5G09270.1	111	12595.700	9.627	-0.768	nucleus
AT5G09300.1	472	53216.900	6.997	-0.423	mitochondrion

Table S-5.2. Subcellular targeting of signifcantly differentially expressed genes using SUBA4

Gene	Amino Acid Residues	Molecular Weight	Isoelectric Point	GRAVY	Location SUBAcon
AT5G09805.1	99	11047.300	11.326	-0.545	mitochondrion
AT5G09840.1	924	102373.000	7.544	-0.568	mitochondrion
AT5G10140.1	196	21866.500	8.453	-0.393	nucleus
AT5G10695.1	67	7447.130	8.713	0.087	plasma membrane
AT5G11140.1	241	27619.400	6.533	-0.264	cytosol
AT5G11240.1	615	66887.800	6.858	-0.232	nucleus
AT5G11310.1	602	68341.200	8.257	-0.237	mitochondrion
AT5G11410.1	336	38401.400	9.068	-0.378	plastid
AT5G11540.1	585	64964.600	8.393	-0.238	extracellular
AT5G11550.1	314	33307.100	8.496	-0.182	plastid
AT5G11630.1	93	9629.700	11.845	0.049	mitochondrion
AT5G11930.1	148	15710.100	5.114	0.311	mitochondrion
AT5G12020.1	155	17624.300	6.803	-0.617	cytosol
AT5G12050.1	362	41033.600	8.890	-1.119	nucleus
AT5G12220.1	611	69295.200	7.104	-0.437	nucleus
AT5G12940.1	371	39955.200	9.893	0.197	extracellular
AT5G13240.1	224	25997.500	4.306	-0.342	cytosol
AT5G13320.1	575	65131.600	4.639	-0.246	cytosol
AT5G13330.1	212	24288.900	9.115	-1.178	nucleus
AT5G13370.1	595	66982.300	5.427	-0.172	cytosol
AT5G13460.1	443	50823.400	10.612	-0.907	nucleus
AT5G13830.1	224	24334.500	9.564	-0.119	cytosol
AT5G14050.1	546	60991.700	5.280	-0.613	nucleus
AT5G14105.1	76	8438.380	10.428	-0.247	mitochondrion
AT5G14180.1	418	46050.400	7.201	0.005	extracellular
AT5G14230.1	751	81399.000	6.872	-0.025	cytosol
AT5G14470.1	366	40863.300	7.250	-0.162	cytosol
AT5G14520.1	590	67947.800	8.995	-0.542	nucleus
AT5G14580.1	991	107778.000	6.589	-0.271	mitochondrion
AT5G14770.1	938	105322.000	8.204	-0.007	mitochondrion
AT5G14920.1	275	29139.800	10.558	-0.525	extracellular
AT5G15070.1	1,049	118789.000	6.093	-0.473	cytosol
AT5G15150.1	314	36284.100	6.867	-1.065	nucleus
AT5G15160.1	94	10546.300	10.107	-0.763	nucleus
AT5G15230.1	106	11996.800	9.570	-0.379	extracellular
AT5G15300.1	548	62115.200	8.276	-0.234	cytosol
AT5G15410.1	726	83245.900	9.982	-0.014	plasma membrane
AT5G15550.1	433	47340.200	5.608	-0.264	nucleus
AT5G15580.1	927	104094.000	9.582	-0.837	nucleus
AT5G15700.1	1,011	114527.000	8.589	-0.425	plastid
AT5G15750.1	182	21768.600	9.856	-0.644	cytosol
AT5G15780.1	401	42980.100	10.515	-0.126	extracellular
AT5G15800.1	251	28658.300	8.658	-0.746	nucleus
AT5G15860.1	427	47584.200	6.517	-0.138	cytosol
AT5G16060.1	95	10941.200	8.937	-0.638	nucleus
AT5G16250.1	183	19959.500	8.052	0.630	plasma membrane
AT5G16370.1	552	60773.300	6.974	-0.024	peroxisome
AT5G16420.1	535	60936.300	7.535	-0.201	mitochondrion
AT5G16570.1	356	38988.900	4.908	-0.406	cytosol
AT5G16650.1	128	15017.600	6.112	-0.866	cytosol
AT5G16750.1	876	96702.600	5.841	-0.218	nucleus
AT5G16930.1	644	70996.400	10.150	-0.605	mitochondrion
AT5G16980.1	239	26582.200	6.785	-0.059	cytosol
AT5G17240.1	491	55875.400	5.182	-0.320	nucleus
AT5G17270.1	899	101009.000	5.051	-0.214	plasma membrane,nucleus
AT5G17420.1	1,026	115804.000	6.667	-0.205	plasma membrane
AT5G17760.1	505	57462.300	7.343	-0.425	plasma membrane
AT5G18010.1	90	9738.840	9.974	0.051	mitochondrion
AT5G18060.1	90	9865.050	9.635	0.069	mitochondrion
AT5G18300.1	147	17550.700	5.372	-0.921	nucleus
AT5G18360.1	900	102295.000	6.309	-0.142	nucleus
AT5G18362.1	182	20263.200	8.259	-0.425	nucleus
AT5G18430.1	362	40125.600	9.398	-0.002	extracellular
AT5G18690.1	116	11851.200	3.336	0.482	extracellular
AT5G18820.1	575	61196.400	8.149	-0.004	plastid
AT5G19030.1	172	19389.200	10.830	-0.285	plastid
AT5G19300.1	398	44882.200	6.447	-0.679	nucleus
AT5G19530.1	339	38548.800	5.056	-0.288	cytosol
AT5G19600.1	634	70364.400	8.801	0.429	plastid
AT5G20020.1	221	25063.800	6.861	-0.419	nucleus
AT5G20160.1	128	13898.000	7.414	0.036	nucleus
AT5G20250.1	749	83121.000	6.659	-0.269	plastid
AT5G20410.1	468	52729.500	6.752	-0.247	plastid
AT5G20635.1	251	27158.100	8.316	-0.071	nucleus
AT5G20710.1	826	92717.100	8.298	-0.428	extracellular
AT5G20740.1	205	22330.600	7.616	-0.215	extracellular
AT5G20820.1	127	13981.500	6.089	-0.317	cytosol
AT5G22100.1	375	40876.500	7.914	-0.086	mitochondrion
AT5G22300.1	355	38897.500	5.446	-0.104	plasma membrane

Table S-5.2. Subcellular targeting of signifcantly differentially expressed genes using SUBA4

Gene	Amino Acid Residues	Molecular Weight	Isoelectric Point	GRAVY	Location SUBAcon
AT5G22310.1	481	55017.000	8.265	-0.995	nucleus
AT5G22460.1	340	39100.300	7.572	-0.271	extracellular
AT5G22500.1	491	55484.100	8.416	-0.068	golgi
AT5G22580.1	111	12349.700	5.528	0.052	vacuole
AT5G22740.1	534	61561.700	9.401	0.158	golgi
AT5G22860.1	502	56457.400	7.268	-0.159	extracellular
AT5G22920.1	291	33550.800	7.003	-0.648	nucleus
AT5G22930.1	238	27112.600	6.249	-0.601	nucleus
AT5G22940.1	469	53811.700	9.874	-0.198	golgi
AT5G23070.1	282	31227.300	8.282	-0.217	plastid
AT5G23300.1	460	48549.300	9.708	-0.110	mitochondrion
AT5G23400.1	589	64021.900	10.207	0.079	extracellular
AT5G23535.1	159	17499.400	10.764	-0.512	mitochondrion
AT5G23690.1	527	59616.900	7.862	-0.161	mitochondrion
AT5G23800.1	552	63862.500	7.406	-0.581	cytosol
AT5G23870.1	415	45965.900	8.238	-0.093	extracellular
AT5G23930.1	457	51888.700	10.317	-0.166	mitochondrion
AT5G24105.1	63	6574.230	6.498	1.102	extracellular
AT5G24110.1	303	33987.100	6.574	-0.918	nucleus
AT5G24160.1	517	56893.500	8.945	-0.020	plasma membrane
AT5G24240.1	574	64038.700	5.421	-0.291	peroxisome
AT5G24530.1	341	39365.700	5.425	-0.443	mitochondrion
AT5G24660.1	94	10679.600	4.520	-0.691	nucleus
AT5G24850.1	526	60382.100	9.055	-0.512	mitochondrion
AT5G25130.1	496	56734.900	9.475	-0.065	endoplasmic reticulum
AT5G25190.1	181	20607.300	7.602	-0.712	nucleus
AT5G25240.1	131	15089.500	8.831	-0.962	nucleus
AT5G25390.1	186	20814.800	9.597	-0.574	nucleus
AT5G25450.1	122	14596.900	10.206	-0.600	mitochondrion
AT5G25460.1	369	39980.300	7.444	0.050	extracellular
AT5G25800.1	567	62805.000	6.834	-0.219	cytosol
AT5G25980.1	467	53425.400	6.890	-0.407	extracellular
AT5G26180.1	567	63177.900	10.508	-0.378	mitochondrion
AT5G26200.1	342	37030.900	10.451	0.018	peroxisome
AT5G26220.1	216	24574.200	5.027	-0.335	peroxisome
AT5G26230.1	341	36107.900	10.353	-0.575	plastid
AT5G26280.1	350	39447.600	8.925	-0.300	extracellular
AT5G26330.1	187	19688.700	7.615	0.373	extracellular
AT5G26670.1	416	46564.700	8.907	-0.280	extracellular
AT5G26742.1	747	81004.800	7.657	-0.365	plastid
AT5G26800.1	112	12599.700	11.109	-0.115	mitochondrion
AT5G26860.1	940	103936.000	5.300	-0.297	mitochondrion
AT5G27030.1	1,108	122663.000	7.211	-0.292	golgi,plasma membrane
AT5G27110.1	691	77989.500	7.154	-0.023	mitochondrion
AT5G27120.1	533	58758.400	9.950	-0.471	nucleus
AT5G27220.1	1,181	135838.000	5.268	-0.592	cytosol
AT5G27330.1	628	72015.700	5.626	-0.779	endoplasmic reticulum
AT5G27395.1	313	36497.300	10.539	-0.452	mitochondrion
AT5G27440.1	216	24410.600	11.882	0.209	plastid
AT5G27850.1	187	20968.000	11.611	-0.418	cytosol
AT5G28060.1	133	15420.000	11.239	-0.874	cytosol
AT5G28630.1	148	16024.100	4.759	-1.499	nucleus
AT5G28640.1	210	22465.100	6.219	-0.800	nucleus
AT5G35180.1	778	87034.100	7.358	-0.455	plasma membrane
AT5G35510.1	68	8067.630	8.067	-0.604	cytosol
AT5G35670.1	442	49546.600	8.559	-0.860	nucleus
AT5G36910.1	134	14179.100	6.232	0.222	extracellular
AT5G36950.1	586	64729.700	8.125	-0.147	mitochondrion
AT5G37300.1	481	54420.500	9.035	-0.039	cytosol,peroxisome
AT5G37540.1	442	48650.600	9.416	-0.115	extracellular
AT5G37570.1	550	61655.800	7.142	-0.051	mitochondrion
AT5G37950.1	351	39044.300	4.733	0.115	mitochondrion
AT5G38100.1	359	40946.900	5.968	-0.282	cytosol
AT5G38200.1	436	49784.100	5.647	-0.425	cytosol
AT5G38890.1	191	20233.400	7.506	0.021	cytosol
AT5G38970.1	465	53770.700	9.245	-0.244	endoplasmic reticulum
AT5G39050.1	469	51767.800	5.222	-0.076	cytosol
AT5G39350.1	677	75964.400	8.016	-0.034	mitochondrion
AT5G39680.1	710	80848.500	8.141	-0.158	mitochondrion
AT5G39790.1	273	31055.500	7.049	-0.306	plastid
AT5G39840.1	776	88199.100	5.689	-0.302	mitochondrion
AT5G39860.1	92	10515.500	9.362	-0.711	nucleus
AT5G39940.1	480	52074.600	9.776	-0.078	mitochondrion
AT5G39980.1	678	78277.400	8.370	-0.281	plastid
AT5G40020.1	256	28095.500	7.805	-0.141	extracellular
AT5G40330.1	219	24944.800	9.406	-0.596	nucleus
AT5G40480.1	1,923	210677.000	5.889	-0.040	nucleus
AT5G40770.1	277	30401.600	7.889	-0.013	mitochondrion
AT5G40780.1	446	49816.400	8.958	0.484	plasma membrane

Table S-5.2. Subcellular targeting of signifcantly differentially expressed genes using SUBA4

Gene	Amino Acid Residues	Molecular Weight	Isoelectric Point	GRAVY	Location SUBAcon
AT5G41080.1	374	42018.200	4.583	-0.175	cytosol
AT5G41140.1	983	113141.000	4.860	-0.943	nucleus
AT5G41270.1	258	28944.200	11.010	-0.933	nucleus
AT5G41400.1	176	20031.000	4.972	0.010	extracellular
AT5G41520.1	180	19734.400	10.209	-0.697	cytosol
AT5G41550.1	1,085	122071.000	7.521	-0.183	mitochondrion
AT5G41650.1	117	12861.700	8.461	0.117	mitochondrion
AT5G41820.1	687	79145.000	6.137	-0.379	nucleus
AT5G41830.1	463	53585.300	6.403	-0.133	cytosol
AT5G41900.1	471	53648.200	9.869	-0.170	extracellular
AT5G42040.1	233	26733.400	4.756	-0.035	cytosol,nucleus
AT5G42150.1	315	35551.600	9.399	-0.349	mitochondrion
AT5G42280.1	694	80040.500	7.308	-0.228	nucleus
AT5G42720.1	438	47171.600	7.125	-0.020	extracellular
AT5G43020.1	669	73930.300	8.780	-0.051	plasma membrane
AT5G43240.1	512	56966.800	5.302	-0.113	cytosol,nucleus
AT5G43450.1	362	40877.700	4.752	-0.211	cytosol
AT5G43760.1	529	59309.900	9.210	-0.102	plasma membrane
AT5G43990.1	717	79367.000	4.791	-0.383	nucleus
AT5G44010.1	357	40792.300	5.873	-0.171	cytosol
AT5G44420.1	80	8518.450	7.978	0.454	extracellular
AT5G44550.1	197	20748.900	10.224	0.711	plasma membrane
AT5G44572.1	93	9928.170	10.810	-0.218	extracellular
AT5G44578.1	103	11437.700	9.894	-0.472	extracellular
AT5G44785.1	440	49902.200	10.490	-0.644	mitochondrion
AT5G45040.1	175	19211.000	7.211	-0.260	plastid
AT5G45080.1	392	44144.200	8.935	-0.351	cytosol
AT5G45140.1	1,161	130219.000	8.286	-0.245	nucleus
AT5G45340.1	463	52369.500	9.231	-0.177	endoplasmic reticulum
AT5G45775.1	172	19776.100	10.453	-0.440	cytosol
AT5G45840.1	668	75349.500	6.132	-0.234	plasma membrane
AT5G46050.1	582	65275.000	9.389	0.263	vacuole
AT5G46090.1	214	23630.700	4.782	0.369	vacuole
AT5G46100.1	472	52881.800	7.853	-0.053	cytosol
AT5G46330.1	1,173	128832.000	5.573	-0.016	plasma membrane
AT5G46580.1	711	80884.000	8.215	-0.256	plastid
AT5G46690.1	327	36649.400	7.041	-0.542	nucleus
AT5G46830.1	511	57351.300	6.015	-0.475	nucleus
AT5G46920.1	735	85184.500	9.761	-0.544	mitochondrion
AT5G47455.1	100	10357.300	12.507	-0.043	mitochondrion
AT5G47500.1	362	40044.100	8.896	-0.217	extracellular
AT5G47560.1	540	58101.500	6.763	0.708	vacuole
AT5G47800.1	559	63305.900	8.630	-0.363	nucleus
AT5G48030.1	456	49440.500	9.186	-0.520	mitochondrion
AT5G48240.1	309	34480.400	9.328	-1.158	nucleus
AT5G48450.1	621	69097.100	9.178	-0.197	plasma membrane,extracellular
AT5G48460.1	654	73668.900	8.519	-0.204	cytosol
AT5G48470.1	397	44016.000	5.981	-0.433	plastid
AT5G48530.1	195	23775.800	9.229	-1.406	mitochondrion
AT5G48540.1	263	28996.800	8.670	-0.129	extracellular
AT5G48657.1	245	28209.700	9.717	-0.675	cytosol,nucleus
AT5G48900.1	417	46730.300	8.676	-0.316	extracellular
AT5G48910.1	646	73262.900	7.120	-0.184	plastid
AT5G48920.1	205	22751.100	7.284	-0.602	nucleus
AT5G49120.1	150	17170.500	9.259	-0.724	plastid
AT5G49170.1	185	21433.300	10.183	-0.668	nucleus
AT5G49410.1	145	16922.000	11.224	-0.681	cytosol
AT5G49500.1	497	55266.000	9.691	-0.255	cytosol
AT5G49520.1	399	44727.900	6.514	-1.085	nucleus
AT5G49800.1	242	27426.800	8.056	-0.358	nucleus
AT5G49910.1	718	77000.800	4.916	-0.359	plastid
AT5G50150.1	420	47036.500	9.168	-0.427	plasma membrane
AT5G50330.1	479	54632.600	9.666	-0.261	cytosol
AT5G50335.1	74	8462.240	9.509	-0.674	nucleus
AT5G50740.1	283	32082.600	8.047	-1.067	nucleus
AT5G50810.1	77	8750.630	7.128	-0.331	mitochondrion
AT5G50820.1	193	22778.800	4.684	-0.882	nucleus
AT5G51030.1	314	35189.700	5.942	-0.327	cytosol
AT5G51190.1	221	24578.100	9.727	-0.612	nucleus
AT5G51220.1	281	32116.000	9.863	-0.247	mitochondrion
AT5G51310.1	325	37126.600	4.908	-0.504	cytosol
AT5G51330.1	639	72735.100	10.011	-0.788	nucleus
AT5G51440.1	210	23469.900	9.598	-0.558	mitochondrion
AT5G51540.1	706	79928.900	6.869	-0.388	mitochondrion
AT5G51670.1	474	53171.000	9.542	-0.249	plastid
AT5G51720.1	108	11627.100	9.704	-0.319	plastid
AT5G51790.1	204	22996.700	10.240	-0.518	nucleus
AT5G52470.1	308	32831.500	10.799	-0.392	nucleus
AT5G52850.1	893	98845.300	7.965	0.007	mitochondrion

Table S-5.2. Subcellular targeting of signifcantly differentially expressed genes using SUBA4

Gene	Amino Acid Residues	Molecular Weight	Isoelectric Point	GRAVY	Location SUBAcon
AT5G53070.1	221	25353.000	10.148	-0.466	mitochondrion
AT5G53090.1	375	41945.900	8.225	-0.134	cytosol
AT5G53210.1	364	40171.600	4.983	-0.513	nucleus
AT5G53770.1	530	59014.300	7.847	-0.464	nucleus
AT5G53920.1	371	40368.300	4.535	0.141	plastid
AT5G54095.1	135	14232.300	4.022	-0.756	extracellular
AT5G54100.1	401	43609.500	9.519	-0.176	mitochondrion
AT5G54190.1	405	43865.400	9.906	-0.166	plastid
AT5G54580.1	156	17091.200	10.132	-0.374	mitochondrion
AT5G54620.1	431	48604.900	9.283	0.137	plasma membrane
AT5G54690.1	535	60883.800	9.497	-0.145	golgi
AT5G55010.1	109	12732.400	9.159	-0.129	cytosol
AT5G55140.1	109	12360.000	11.201	-0.481	mitochondrion
AT5G55280.1	433	45567.300	7.505	-0.042	plastid
AT5G55400.1	714	79792.100	4.879	-0.250	cytosol
AT5G55570.1	143	15742.200	11.261	-0.210	plastid
AT5G55580.1	496	57204.900	9.155	-0.511	plastid
AT5G55730.1	424	44851.800	6.721	-0.039	extracellular
AT5G55930.1	755	85353.000	8.470	0.361	plasma membrane
AT5G56090.1	457	50130.200	10.713	0.160	mitochondrion
AT5G56120.1	236	27176.400	9.148	0.084	plasma membrane
AT5G56220.1	973	108405.000	8.680	-0.243	peroxisome
AT5G56490.1	577	64127.900	6.946	-0.089	extracellular
AT5G56870.1	724	80595.300	8.882	-0.238	extracellular
AT5G56890.1	1,113	119251.000	9.165	-0.358	plasma membrane
AT5G56960.1	466	52747.800	9.729	-0.567	nucleus
AT5G57010.1	495	56153.900	9.879	-0.676	cytosol
AT5G57080.1	62	6522.040	10.017	0.008	extracellular
AT5G57120.1	330	37583.500	6.048	-1.465	nucleus
AT5G57280.1	289	32388.300	8.208	-0.604	nucleus
AT5G57390.1	558	60309.300	7.926	-0.636	nucleus
AT5G57450.1	304	33733.400	8.754	-0.183	nucleus
AT5G57640.1	226	24920.400	3.964	-0.932	nucleus
AT5G57655.1	287	32409.600	7.887	-0.350	endoplasmic reticulum
AT5G57760.1	78	9088.580	10.645	-0.446	cytosol
AT5G57770.1	406	44871.600	8.445	-0.368	cytosol
AT5G57780.1	167	19439.800	11.462	-0.573	cytosol
AT5G57785.1	73	8489.750	12.382	-0.073	mitochondrion
AT5G57870.1	780	85576.600	8.434	-0.448	cytosol,nucleus
AT5G57970.1	347	38651.700	10.262	-0.468	nucleus
AT5G58210.1	380	40850.200	4.741	-0.432	mitochondrion
AT5G58370.1	446	50646.400	10.657	-0.706	mitochondrion
AT5G58540.1	484	53655.500	5.322	-0.141	mitochondrion
AT5G58550.1	925	105483.000	5.488	-0.258	cytosol
AT5G58690.1	578	66256.300	7.363	-0.518	cytosol
AT5G58770.1	310	35944.900	5.918	-0.394	plastid
AT5G59070.1	505	56688.900	9.078	-0.231	endoplasmic reticulum
AT5G59200.1	544	61359.200	6.309	-0.079	plastid
AT5G59340.1	260	29185.000	9.308	-0.764	nucleus
AT5G59440.1	263	29551.200	8.452	-0.373	cytosol,mitochondrion,nucleus
AT5G59660.1	852	94473.100	8.416	-0.227	plasma membrane
AT5G59720.1	161	18135.500	7.700	-0.657	peroxisome
AT5G59980.1	581	64082.200	5.923	-0.393	nucleus
AT5G60100.1	495	55289.100	7.619	-0.983	nucleus
AT5G60490.1	249	26368.200	4.873	0.028	plasma membrane
AT5G60540.1	255	27439.900	4.961	-0.005	cytosol
AT5G60670.1	166	17843.800	9.542	-0.278	cytosol
AT5G60720.1	691	77819.200	9.528	-0.523	plastid
AT5G60730.1	391	42942.200	9.348	-0.088	mitochondrion
AT5G60840.1	207	23156.200	3.495	-0.700	nucleus
AT5G60870.1	445	47333.900	6.236	-0.173	mitochondrion
AT5G60930.1	1,294	145231.000	7.145	-0.759	nucleus
AT5G61030.1	309	29986.600	4.629	-0.465	mitochondrion
AT5G61100.1	227	25579.900	4.758	-0.607	nucleus
AT5G61350.1	842	92692.300	6.321	-0.143	plasma membrane
AT5G61360.1	210	24472.000	8.506	-0.469	nucleus
AT5G61370.1	487	55551.900	9.961	-0.281	mitochondrion
AT5G61430.1	336	38474.500	8.201	-0.671	nucleus
AT5G61600.1	241	26826.400	6.687	-0.693	nucleus
AT5G61800.1	499	56052.000	8.468	-0.001	mitochondrion
AT5G61820.1	475	53074.200	6.392	-0.276	extracellular
AT5G61880.1	113	12311.700	9.820	-0.273	mitochondrion
AT5G61940.1	1,094	124654.000	5.146	-0.445	nucleus
AT5G62165.1	210	24674.800	9.957	-0.805	nucleus
AT5G62170.1	703	79220.800	10.284	-0.795	nucleus
AT5G62190.1	671	72894.900	9.852	-0.409	nucleus
AT5G62220.1	517	59648.500	8.420	-0.418	plastid
AT5G62230.1	966	106493.000	7.084	0.042	plasma membrane
AT5G62280.1	236	26011.100	7.238	-0.201	cytosol

Table S-5.2. Subcellular targeting of signifcantly differentially expressed genes using SUBA4

Gene	Amino Acid Residues	Molecular Weight	Isoelectric Point	GRAVY	Location SUBAcon
AT5G62290.1	229	25604.200	3.795	-0.601	nucleus
AT5G62370.1	982	110274.000	7.643	0.063	mitochondrion
AT5G62440.1	202	22546.500	5.742	-0.943	nucleus
AT5G62550.1	487	53427.400	9.698	-0.859	nucleus
AT5G62720.1	243	25828.900	10.731	0.521	plastid
AT5G62730.1	589	65246.400	8.574	0.369	vacuole
AT5G62920.1	186	21240.000	6.951	-0.238	nucleus
AT5G62990.1	494	56791.200	7.792	-0.463	plastid
AT5G63160.1	365	41482.800	9.441	-0.318	cytosol,nucleus
AT5G63180.1	432	47897.300	6.882	-0.392	extracellular
AT5G63290.1	484	54049.400	5.859	-0.264	plastid
AT5G63420.1	911	100559.000	8.390	-0.388	plastid
AT5G63580.1	250	28484.000	4.509	-0.356	cytosol
AT5G63650.1	360	41556.100	4.974	-0.652	nucleus
AT5G64120.1	328	34891.700	8.269	-0.016	extracellular
AT5G64310.1	131	12638.100	6.703	0.307	extracellular
AT5G64330.1	746	81877.800	7.479	-0.359	golgi
AT5G64420.1	1,306	146123.000	4.984	-0.360	nucleus
AT5G64490.1	187	21010.700	8.086	0.243	plasma membrane
AT5G64650.1	160	18339.300	11.212	-0.766	mitochondrion
AT5G64670.1	281	31201.500	11.758	-0.498	mitochondrion
AT5G64680.1	203	22534.300	9.848	-0.907	nucleus
AT5G64710.1	841	94059.800	8.280	-0.504	plastid
AT5G64780.1	175	19992.200	6.393	-0.843	nucleus
AT5G64810.1	194	22045.100	5.340	-0.974	nucleus
AT5G64816.1	130	14442.300	8.424	-0.260	plastid
AT5G64870.1	479	52836.400	7.292	-0.332	golgi,vacuole
AT5G65010.1	578	65033.300	6.431	-0.337	golgi
AT5G65070.1	200	22854.800	8.904	-0.596	nucleus
AT5G65310.1	312	34792.400	4.754	-0.707	nucleus
AT5G65380.1	486	52974.800	7.997	0.719	plasma membrane
AT5G65390.1	130	12510.800	3.952	0.252	extracellular
AT5G65850.1	392	45439.600	9.324	-0.105	mitochondrion
AT5G66052.1	67	7028.400	7.345	0.731	plasma membrane
AT5G66310.1	1,063	121431.000	5.469	-0.654	cytosol
AT5G66330.1	418	45334.200	4.860	0.114	extracellular
AT5G66420.1	655	70037.300	5.949	0.015	cytosol
AT5G66500.1	532	58913.700	8.170	0.083	mitochondrion
AT5G66540.1	524	59747.700	4.226	-1.097	nucleus
AT5G66630.1	702	80250.200	6.302	-0.292	cytosol,plasma membrane
AT5G66640.1	450	51311.300	5.559	-0.505	nucleus
AT5G66860.1	249	27338.300	10.011	-0.124	mitochondrion
AT5G66960.1	792	91005.900	6.674	-0.471	mitochondrion
AT5G67020.1	394	43630.800	9.562	-0.286	mitochondrion
AT5G67180.1	352	39596.100	8.988	-0.794	nucleus
AT5G67450.1	245	26472.500	7.891	-0.785	nucleus
AT5G67480.1	372	42463.800	9.406	-0.326	nucleus
AT5G67520.1	310	34066.600	9.286	-0.411	plastid
AT5G67620.1	182	19707.600	10.021	-0.619	nucleus
ATCG00340.1	734	82479.800	7.424	0.120	plastid
ATCG00350.1	750	83235.300	7.117	0.252	plastid
ATMG00040.1	315	34176.600	6.589	-0.149	mitochondrion
ATMG00110.1	206	23080.300	8.622	0.330	mitochondrion
ATMG00140.1	167	19072.100	7.092	-0.273	mitochondrion
ATMG00160.1	260	29377.600	5.508	0.234	mitochondrion
ATMG00670.1	275	30212.300	4.652	-0.052	mitochondrion
ATMG00690.1	240	27681.700	11.714	-0.435	mitochondrion
ATMG01090.1	262	29638.400	6.598	0.004	mitochondrion
ATMG01130.1	106	11759.000	4.854	-0.283	mitochondrion
ATMG01170.1	349	39741.700	6.843	0.744	mitochondrion
ATMG01200.1	294	33611.700	4.665	-0.149	mitochondrion
ATMG01220.1	113	12933.700	10.979	-0.362	mitochondrion
ATMG01370.1	111	12893.200	10.918	0.314	mitochondrion
ATMG01410.1	204	22815.700	9.959	0.206	mitochondrion

Table S-5.3 AgriGO Gene ontology analysis and REVIGO summary

GO term	Ontology	Description	Number	Z-Score	FDR
GO:0005737	C	cytoplasm	449	7.8	5.90E-13
GO:0005622	C	intracellular	621	7.7	7.90E-13
GO:0044444	C	cytoplasmic part	419	7.6	9.10E-13
GO:0044424	C	intracellular part	600	7.3	4.10E-12
GO:0043232	C	intracellular non-membrane-bounded organelle	136	7.3	4.10E-12
GO:0043228	C	non-membrane-bounded organelle	136	7.3	4.10E-12
GO:0044446	C	intracellular organelle part	181	7.2	7.50E-12
GO:0044422	C	organelle part	182	7.1	9.20E-12
GO:0005739	C	mitochondrion	116	7.1	9.20E-12
GO:0043229	C	intracellular organelle	540	6.9	3.10E-11
GO:0043226	C	organelle	541	6.9	3.50E-11
GO:0030529	C	ribonucleoprotein complex	91	6.4	1.30E-09
GO:0043231	C	intracellular membrane-bounded organelle	477	5.9	2.30E-08
GO:0043227	C	membrane-bounded organelle	478	5.9	2.50E-08
GO:0005840	C	ribosome	78	5.8	2.90E-08
GO:0032991	C	macromolecular complex	154	5.8	3.20E-08
GO:0012505	C	endomembrane system	188	-5.4	3.10E-07
GO:0033279	C	ribosomal subunit	59	5.3	5.70E-07
GO:0009536	C	plastid	188	5.2	8.00E-07
GO:0031974	C	membrane-enclosed lumen	73	5.2	9.30E-07
GO:0070013	C	intracellular organelle lumen	71	5.1	1.40E-06
GO:0043233	C	organelle lumen	71	5.1	1.40E-06
GO:0005730	C	nucleolus	50	4.8	4.40E-06
GO:0009507	C	chloroplast	175	4.8	6.10E-06
GO:0044445	C	cytosolic part	48	4.7	7.00E-06
GO:0022626	C	cytosolic ribosome	53	4.7	7.30E-06
GO:0015934	C	large ribosomal subunit	46	4.7	9.80E-06
GO:0005829	C	cytosol	71	4.6	1.20E-05
GO:0031981	C	nuclear lumen	58	4.4	3.70E-05
GO:0044428	C	nuclear part	64	4.3	5.10E-05
GO:0022625	C	cytosolic large ribosomal subunit	35	4	0.00017
GO:0009505	C	plant-type cell wall	25	-3.7	0.00046
GO:0044429	C	mitochondrial part	22	3.3	0.0024
GO:0031225	C	anchored to membrane	26	-3.1	0.0039
GO:0031975	C	envelope	27	2.9	0.0076
GO:0031967	C	organelle envelope	27	2.9	0.0076
GO:0031980	C	mitochondrial lumen	10	2.8	0.0092
GO:0005759	C	mitochondrial matrix	10	2.8	0.0092
GO:0080008	C	CUL4 RING ubiquitin ligase complex	16	2.8	0.012
GO:0031224	C	intrinsic to membrane	48	-2.7	0.013
GO:0030312	C	external encapsulating structure	43	-2.7	0.014
GO:0005618	C	cell wall	43	-2.7	0.014
GO:0044435	C	plastid part	39	2.7	0.014
GO:0009526	C	plastid envelope	14	2.5	0.021
GO:0015935	C	small ribosomal subunit	13	2.5	0.022
GO:0031461	C	cullin-RING ubiquitin ligase complex	17	2.4	0.025
GO:0000151	C	ubiquitin ligase complex	17	2.4	0.025
GO:0022627	C	cytosolic small ribosomal subunit	12	2.4	0.03
GO:0009941	C	chloroplast envelope	12	2.3	0.036
GO:0005576	C	extracellular region	16	-2.3	0.038
GO:0019866	C	organelle inner membrane	15	2.2	0.041
GO:0048046	C	apoplast	11	-2.2	0.041
GO:0005886	C	plasma membrane	104	-2.2	0.048
GO:0003735	F	structural constituent of ribosome	77	5.8	8.30E-07
GO:0005198	F	structural molecule activity	83	5.3	6.00E-06
GO:0003723	F	RNA binding	64	5.1	1.50E-05
GO:0016301	F	kinase activity	92	-4.8	5.70E-05
GO:0003700	F	transcription factor activity	139	-4.3	0.00045
GO:0030599	F	pectinesterase activity	12	-4.1	0.00064
GO:0004091	F	carboxylesterase activity	27	-4	0.0011
GO:0016773	F	phosphotransferase activity, alcohol group as acceptor	54	-3.5	0.0068
GO:0004386	F	helicase activity	23	3.4	0.0092
GO:0004518	F	nuclease activity	15	3.3	0.01
GO:0030528	F	transcription regulator activity	151	-3.3	0.01
GO:0008026	F	ATP-dependent helicase activity	22	3.2	0.011
GO:0070035	F	purine NTP-dependent helicase activity	22	3.2	0.011
GO:0004674	F	protein serine/threonine kinase activity	39	-3.2	0.012
GO:0004672	F	protein kinase activity	47	-3.2	0.012
GO:0050660	F	FAD binding	12	-3.1	0.012
GO:0016772	F	transferase activity, transferring phosphorus-containing groups	112	-3	0.017
GO:0015238	F	drug transmembrane transporter activity	11	3	0.017
GO:0016798	F	hydrolase activity, acting on glycosyl bonds	43	-3	0.018
GO:0016779	F	nucleotidyltransferase activity	19	3	0.018
GO:0016887	F	ATPase activity	45	2.9	0.02
GO:0003824	F	catalytic activity	604	-2.9	0.02
GO:0016741	F	transferase activity, transferring one-carbon groups	32	2.8	0.022
GO:0008168	F	methyltransferase activity	32	2.8	0.022
GO:0015297	F	antiporter activity	15	2.7	0.031
GO:0016740	F	transferase activity	213	-2.6	0.042
GO:0003899	F	DNA-directed RNA polymerase activity	10	2.6	0.043
GO:0005516	F	calmodulin binding	15	-2.5	0.05
GO:0006412	P	translation	85	6	5.30E-07
GO:0042254	P	ribosome biogenesis	47	5.4	5.20E-06
GO:0006396	P	RNA processing	45	5.4	5.20E-06
GO:0022613	P	ribonucleoprotein complex biogenesis	47	5.4	5.20E-06
GO:0065007	P	biological regulation	237	-4.9	5.40E-05
GO:0044085	P	cellular component biogenesis	73	4.6	0.00018

Table S-5.3 AgriGO Gene ontology analysis and REVIGO summary

GO:0050794	P	regulation of cellular process	186	-4.4	0.00033
GO:0034660	P	ncRNA metabolic process	25	4.3	0.00046
GO:0034470	P	ncRNA processing	24	4.3	0.00048
GO:0023052	P	signaling	83	-4.2	0.00071
GO:0050789	P	regulation of biological process	197	-4.1	0.0008
GO:0006468	P	protein amino acid phosphorylation	55	-4.1	0.0008
GO:0006464	P	protein modification process	67	-4.1	0.00094
GO:0043687	P	post-translational protein modification	59	-4	0.00096
GO:0071554	P	cell wall organization or biogenesis	26	-4	0.00097
GO:0009733	P	response to auxin stimulus	43	-3.9	0.0015
GO:0010467	P	gene expression	245	3.9	0.0015
GO:0006793	P	phosphorus metabolic process	64	-3.7	0.0022
GO:0006796	P	phosphate metabolic process	64	-3.7	0.0022
GO:0023060	P	signal transmission	61	-3.7	0.0022
GO:0071555	P	cell wall organization	18	-3.8	0.0022
GO:0023046	P	signaling process	61	-3.7	0.0022
GO:0016072	P	rRNA metabolic process	19	3.7	0.0023
GO:0006364	P	rRNA processing	19	3.7	0.0023
GO:0007165	P	signal transduction	59	-3.7	0.0025
GO:0080090	P	regulation of primary metabolic process	109	-3.6	0.0028
GO:0016310	P	phosphorylation	60	-3.6	0.0028
GO:0060255	P	regulation of macromolecule metabolic process	107	-3.6	0.003
GO:0010468	P	regulation of gene expression	107	-3.6	0.003
GO:0006629	P	lipid metabolic process	51	-3.5	0.0039
GO:0044255	P	cellular lipid metabolic process	29	-3.5	0.0039
GO:0045449	P	regulation of transcription	105	-3.5	0.0039
GO:0019219	P	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	105	-3.5	0.0039
GO:0009889	P	regulation of biosynthetic process	110	-3.4	0.0039
GO:0042545	P	cell wall modification	15	-3.5	0.0039
GO:0010556	P	regulation of macromolecule biosynthetic process	105	-3.5	0.0039
GO:0019222	P	regulation of metabolic process	117	-3.4	0.0039
GO:0031326	P	regulation of cellular biosynthetic process	110	-3.4	0.0039
GO:0051171	P	regulation of nitrogen compound metabolic process	108	-3.4	0.0046
GO:0008610	P	lipid biosynthetic process	23	-3.3	0.0074
GO:0009719	P	response to endogenous stimulus	85	-3.2	0.0074
GO:0048589	P	developmental growth	21	-3.2	0.0075
GO:0031323	P	regulation of cellular metabolic process	114	-3.2	0.0075
GO:0040007	P	growth	24	-3.2	0.0085
GO:0009725	P	response to hormone stimulus	81	-3	0.016
GO:0006721	P	terpenoid metabolic process	10	-2.9	0.018
GO:0006753	P	nucleoside phosphate metabolic process	11	2.9	0.019
GO:0009416	P	response to light stimulus	54	-2.9	0.019
GO:0009451	P	RNA modification	11	2.9	0.019
GO:0009314	P	response to radiation	54	-2.9	0.019
GO:0009117	P	nucleotide metabolic process	11	2.9	0.019
GO:0010033	P	response to organic substance	99	-2.9	0.02
GO:0009664	P	plant-type cell wall organization	10	-2.9	0.02
GO:0071669	P	plant-type cell wall organization or biogenesis	16	-2.9	0.021
GO:0009165	P	nucleotide biosynthetic process	10	2.8	0.026
GO:0008361	P	regulation of cell size	21	-2.7	0.026
GO:0000902	P	cell morphogenesis	18	-2.7	0.026
GO:0043412	P	macromolecule modification	79	-2.7	0.026
GO:0009790	P	embryonic development	42	2.7	0.026
GO:0006996	P	organelle organization	34	2.8	0.026
GO:0032535	P	regulation of cellular component size	22	-2.8	0.026
GO:0090066	P	regulation of anatomical structure size	22	-2.8	0.026
GO:0007242	P	intracellular signaling cascade	34	-2.8	0.026
GO:0055086	P	nucleobase, nucleoside and nucleotide metabolic process	13	2.7	0.029
GO:0044267	P	cellular protein metabolic process	179	2.7	0.03
GO:0016049	P	cell growth	20	-2.7	0.031
GO:0019748	P	secondary metabolic process	32	-2.6	0.033
GO:0006720	P	isoprenoid metabolic process	11	-2.6	0.033
GO:0009826	P	unidimensional cell growth	15	-2.6	0.035
GO:0060560	P	developmental growth involved in morphogenesis	15	-2.6	0.035
GO:0009653	P	anatomical structure morphogenesis	38	-2.6	0.035
GO:0009553	P	embryo sac development	11	2.6	0.036
GO:0006350	P	transcription	115	-2.5	0.039
GO:0006457	P	protein folding	21	2.5	0.04
GO:0016070	P	RNA metabolic process	119	2.5	0.04
GO:0009639	P	response to red or far red light	17	-2.5	0.04
GO:0007167	P	enzyme linked receptor protein signaling pathway	12	-2.5	0.04
GO:0007169	P	transmembrane receptor protein tyrosine kinase signaling pathway	12	-2.5	0.04
GO:0009793	P	embryonic development ending in seed dormancy	37	2.5	0.04
GO:0043933	P	macromolecular complex subunit organization	16	2.5	0.04
GO:0032989	P	cellular component morphogenesis	19	-2.5	0.04
GO:0023034	P	intracellular signaling pathway	16	-2.5	0.041
GO:0010876	P	lipid localization	12	-2.5	0.041
GO:0006869	P	lipid transport	12	-2.5	0.041
GO:0009605	P	response to external stimulus	27	-2.4	0.047

REVIGO Molecular Function

GO term	**Ontology**	**Description**	**Number**	**Z-Score**	**FDR**	
GO:0003735	F	structural constituent of ribosome	77	5.8	8.30E-07	6.080921908
GO:0005198	F	structural molecule activity	83	5.3	6.00E-06	5.22184875
GO:0003723	F	RNA binding	64	5.1	1.50E-05	4.823908741
GO:0003700	F	transcription factor activity	139	-4.3	0.00045	3.346787486
GO:0030599	F	pectinesterase activity	12	-4.1	0.00064	3.193820026

Table S-5.3 AgriGO Gene ontology analysis and REVIGO summary

GO:0004091	F	carboxylesterase activity	27	-4	0.0011	2.958607315
GO:0004386	F	helicase activity	23	3.4	0.0092	2.036212173
GO:0030528	F	transcription regulator activity	151	-3.3	0.01	2
GO:0070035	F	purine NTP-dependent helicase activity	22	3.2	0.011	1.958607315
GO:0004674	F	protein serine/threonine kinase activity	39	-3.2	0.012	1.920818754
GO:0050660	F	FAD binding	12	-3.1	0.012	1.920818754
GO:0016772	F	transferase activity, transferring phosphorus-containing groups	112	-3	0.017	1.769551079
GO:0015238	F	drug transmembrane transporter activity	11	3	0.017	1.769551079
GO:0016798	F	hydrolase activity, acting on glycosyl bonds	43	-3	0.018	1.744727495
GO:0003824	F	catalytic activity	604	-2.9	0.02	1.698970004
GO:0016887	F	ATPase activity	45	2.9	0.02	1.698970004
GO:0016741	F	transferase activity, transferring one-carbon groups	32	2.8	0.022	1.657577319
GO:0008168	F	methyltransferase activity	32	2.8	0.022	1.657577319
GO:0016740	F	transferase activity	213	-2.6	0.042	1.37675071
GO:0005516	F	calmodulin binding	15	-2.5	0.05	1.301029996
GO:0016301	F	kinase activity	92	-4.8	5.70E-05	
GO:0016773	F	phosphotransferase activity, alcohol group as acceptor	54	-3.5	0.0068	
GO:0004672	F	protein kinase activity	47	-3.2	0.012	
GO:0008026	F	ATP-dependent helicase activity	22	3.2	0.011	
GO:0016779	F	nucleotidyltransferase activity	19	3	0.018	
GO:0004518	F	nuclease activity	15	3.3	0.01	
GO:0015297	F	antiporter activity	15	2.7	0.031	
GO:0003899	F	DNA-directed RNA polymerase activity	10	2.6	0.043	

REVIGO Cellular Component

GO term	Ontology	Description	Number	Z-Score	FDR	
GO:0005737	C	cytoplasm	449	7.8	5.90E-13	12.22914799
GO:0005622	C	intracellular	621	7.7	7.90E-13	12.10237291
GO:0043228	C	non-membrane-bounded organelle	136	7.3	4.10E-12	11.38721614
GO:0005739	C	mitochondrion	116	7.1	9.20E-12	11.03621217
GO:0043229	C	intracellular organelle	540	6.9	3.10E-11	10.50863831
GO:0043226	C	organelle	541	6.9	3.50E-11	10.45593196
GO:0030529	C	ribonucleoprotein complex	91	6.4	1.30E-09	8.886056648
GO:0043231	C	intracellular membrane-bounded organelle	477	5.9	2.30E-08	7.638272164
GO:0043227	C	membrane-bounded organelle	478	5.9	2.50E-08	7.602059991
GO:0032991	C	macromolecular complex	154	5.8	3.20E-08	7.494850022
GO:0012505	C	endomembrane system	188	-5.4	3.10E-07	6.508638306
GO:0033279	C	ribosomal subunit	59	5.3	5.70E-07	6.244125144
GO:0009536	C	plastid	188	5.2	8.00E-07	6.096910013
GO:0031974	C	membrane-enclosed lumen	73	5.2	9.30E-07	6.031517051
GO:0005730	C	nucleolus	50	4.8	4.40E-06	5.356547324
GO:0005829	C	cytosol	71	4.6	1.20E-05	4.920818754
GO:0009505	C	plant-type cell wall	25	-3.7	0.00046	3.337242168
GO:0031225	C	anchored to membrane	26	-3.1	0.0039	2.408935393
GO:0031975	C	envelope	27	2.9	0.0076	2.119186408
GO:0031980	C	mitochondrial lumen	10	2.8	0.0092	2.036212173
GO:0080008	C	CUL4 RING ubiquitin ligase complex	16	2.8	0.012	1.920818754
GO:0031224	C	intrinsic to membrane	48	-2.7	0.013	1.886056648
GO:0030312	C	external encapsulating structure	43	-2.7	0.014	1.853871964
GO:0009526	C	plastid envelope	14	2.5	0.021	1.677780705
GO:0005576	C	extracellular region	16	-2.3	0.038	1.420216403
GO:0048046	C	apoplast	11	-2.2	0.041	1.387216143
GO:0044444	C	cytoplasmic part	419	7.6	9.10E-13	12.04095861
GO:0044424	C	intracellular part	600	7.3	4.10E-12	11.38721614
GO:0043232	C	intracellular non-membrane-bounded organelle	136	7.3	4.10E-12	11.38721614
GO:0044446	C	intracellular organelle part	181	7.2	7.50E-12	11.12493874
GO:0044422	C	organelle part	182	7.1	9.20E-12	11.03621217
GO:0005840	C	ribosome	78	5.8	2.90E-08	7.537602002
GO:0070013	C	intracellular organelle lumen	71	5.1	1.40E-06	5.853871964
GO:0043233	C	organelle lumen	71	5.1	1.40E-06	5.853871964
GO:0009507	C	chloroplast	175	4.8	6.10E-06	5.214670165
GO:0044445	C	cytosolic part	48	4.7	7.00E-06	5.15490196
GO:0022626	C	cytosolic ribosome	53	4.7	7.30E-06	5.13667714
GO:0015934	C	large ribosomal subunit	46	4.7	9.80E-06	5.008773924
GO:0031981	C	nuclear lumen	58	4.4	3.70E-05	4.431798276
GO:0044428	C	nuclear part	64	4.3	5.10E-05	4.292429824
GO:0022625	C	cytosolic large ribosomal subunit	35	4	0.00017	3.769551079
GO:0044429	C	mitochondrial part	22	3.3	0.0024	2.619788758
GO:0031967	C	organelle envelope	27	2.9	0.0076	2.119186408
GO:0005759	C	mitochondrial matrix	10	2.8	0.0092	2.036212173
GO:0005618	C	cell wall	43	-2.7	0.014	1.853871964
GO:0044435	C	plastid part	39	2.7	0.014	1.853871964
GO:0015935	C	small ribosomal subunit	13	2.5	0.022	1.657577319
GO:0031461	C	cullin-RING ubiquitin ligase complex	17	2.4	0.025	1.602059991
GO:0000151	C	ubiquitin ligase complex	17	2.4	0.025	1.602059991
GO:0022627	C	cytosolic small ribosomal subunit	12	2.4	0.03	1.522878745
GO:0009941	C	chloroplast envelope	12	2.3	0.036	1.443697499
GO:0019866	C	organelle inner membrane	15	2.2	0.041	1.387216143
GO:0005886	C	plasma membrane	104	-2.2	0.048	1.318758763

REVIGO Cellular Component

GO term	Ontology	Description	Number	Z-Score	FDR	
GO:0006412	P	translation	85	6	5.30E-07	6.27572413
GO:0042254	P	ribosome biogenesis	47	5.4	5.20E-06	5.283996656
GO:0065007	P	biological regulation	237	-4.9	5.40E-05	4.26760624
GO:0034660	P	ncRNA metabolic process	25	4.3	0.00046	3.337242168
GO:0023052	P	signaling	83	-4.2	0.00071	3.148741651
GO:0043687	P	post-translational protein modification	59	-4	0.00096	3.017728767

Table S-5.3 AgriGO Gene ontology analysis and REVIGO summary

GO:0071554	P	cell wall organization or biogenesis	26	-4	0.00097	3.013228266
GO:0010467	P	gene expression	245	3.9	0.0015	2.823908741
GO:0009733	P	response to auxin stimulus	43	-3.9	0.0015	2.823908741
GO:0006793	P	phosphorus metabolic process	64	-3.7	0.0022	2.657577319
GO:0006629	P	lipid metabolic process	51	-3.5	0.0039	2.408935393
GO:0009719	P	response to endogenous stimulus	85	-3.2	0.0074	2.13076828
GO:0048589	P	developmental growth	21	-3.2	0.0075	2.124938737
GO:0009117	P	nucleotide metabolic process	11	2.9	0.019	1.721246399
GO:0009416	P	response to light stimulus	54	-2.9	0.019	1.721246399
GO:0043412	P	macromolecule modification	79	-2.7	0.026	1.585026652
GO:0032535	P	regulation of cellular component size	22	-2.8	0.026	1.585026652
GO:0019748	P	secondary metabolic process	32	-2.6	0.033	1.48148606
GO:0009553	P	embryo sac development	11	2.6	0.036	1.443697499
GO:0006457	P	protein folding	21	2.5	0.04	1.397940009
GO:0007169	P	transmembrane receptor protein tyrosine kinase signaling pathway	12	-2.5	0.04	1.397940009
GO:0006869	P	lipid transport	12	-2.5	0.041	1.387216143
GO:0009605	P	response to external stimulus	27	-2.4	0.047	1.327902142
GO:0050794	P	regulation of cellular process	186	-4.4	0.00033	3.48148606
GO:0034470	P	ncRNA processing	24	4.3	0.00048	3.318758763
GO:0040007	P	growth	24	-3.2	0.0085	2.070581074
GO:0009664	P	plant-type cell wall organization	10	-2.9	0.02	1.698970004
GO:0009725	P	response to hormone stimulus	81	-3	0.016	1.795880017
GO:0010033	P	response to organic substance	99	-2.9	0.02	1.698970004
GO:0023046	P	signaling process	61	-3.7	0.0022	2.657577319
GO:0006350	P	transcription	115	-2.5	0.039	1.408935393
GO:0009653	P	anatomical structure morphogenesis	38	-2.6	0.035	1.455931956
GO:0016049	P	cell growth	20	-2.7	0.031	1.508638306
GO:0000902	P	cell morphogenesis	18	-2.7	0.026	1.585026652
GO:0042545	P	cell wall modification	15	-3.5	0.0039	2.408935393
GO:0071555	P	cell wall organization	18	-3.8	0.0022	2.657577319
GO:0044085	P	cellular component biogenesis	73	4.6	0.00018	3.744727495
GO:0032989	P	cellular component morphogenesis	19	-2.5	0.04	1.397940009
GO:0044255	P	cellular lipid metabolic process	29	-3.5	0.0039	2.408935393
GO:0044267	P	cellular protein metabolic process	179	2.7	0.03	1.522878745
GO:0060560	P	developmental growth involved in morphogenesis	15	-2.6	0.035	1.455931956
GO:0009790	P	embryonic development	42	2.7	0.026	1.585026652
GO:0009793	P	embryonic development ending in seed dormancy	37	2.5	0.04	1.397940009
GO:0007167	P	enzyme linked receptor protein signaling pathway	12	-2.5	0.04	1.397940009
GO:0007242	P	intracellular signaling cascade	34	-2.8	0.026	1.585026652
GO:0023034	P	intracellular signaling pathway	16	-2.5	0.041	1.387216143
GO:0006720	P	isoprenoid metabolic process	11	-2.6	0.033	1.48148606
GO:0008610	P	lipid biosynthetic process	23	-3.3	0.0074	2.13076828
GO:0010876	P	lipid localization	12	-2.5	0.041	1.387216143
GO:0043933	P	macromolecular complex subunit organization	16	2.5	0.04	1.397940009
GO:0055086	P	nucleobase, nucleoside and nucleotide metabolic process	13	2.7	0.029	1.537602002
GO:0006753	P	nucleoside phosphate metabolic process	11	2.9	0.019	1.721246399
GO:0009165	P	nucleotide biosynthetic process	10	2.8	0.026	1.585026652
GO:0006996	P	organelle organization	34	2.8	0.026	1.585026652
GO:0006796	P	phosphate metabolic process	64	-3.7	0.0022	2.657577319
GO:0016310	P	phosphorylation	60	-3.6	0.0028	2.552841969
GO:0071669	P	plant-type cell wall organization or biogenesis	16	-2.9	0.021	1.677780705
GO:0006468	P	protein amino acid phosphorylation	55	-4.1	0.0008	3.096910013
GO:0006464	P	protein modification process	67	-4.1	0.00094	3.026872146
GO:0090066	P	regulation of anatomical structure size	22	-2.8	0.026	1.585026652
GO:0050789	P	regulation of biological process	197	-4.1	0.0008	3.096910013
GO:0009889	P	regulation of biosynthetic process	110	-3.4	0.0039	2.408935393
GO:0008361	P	regulation of cell size	21	-2.7	0.026	1.585026652
GO:0031326	P	regulation of cellular biosynthetic process	110	-3.4	0.0039	2.408935393
GO:0031323	P	regulation of cellular metabolic process	114	-3.2	0.0075	2.124938737
GO:0010468	P	regulation of gene expression	107	-3.6	0.003	2.522878745
GO:0010556	P	regulation of macromolecule biosynthetic process	105	-3.5	0.0039	2.408935393
GO:0060255	P	regulation of macromolecule metabolic process	107	-3.6	0.003	2.522878745
GO:0019222	P	regulation of metabolic process	117	-3.4	0.0039	2.408935393
GO:0051171	P	regulation of nitrogen compound metabolic process	108	-3.4	0.0046	2.337242168
GO:0019219	P	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	105	-3.5	0.0039	2.408935393
GO:0080090	P	regulation of primary metabolic process	109	-3.6	0.0028	2.552841969
GO:0045449	P	regulation of transcription	105	-3.5	0.0039	2.408935393
GO:0009314	P	response to radiation	54	-2.9	0.019	1.721246399
GO:0009639	P	response to red or far red light	17	-2.5	0.04	1.397940009
GO:0022613	P	ribonucleoprotein complex biogenesis	47	5.4	5.20E-06	5.283996656
GO:0016070	P	RNA metabolic process	119	2.5	0.04	1.397940009
GO:0009451	P	RNA modification	11	2.9	0.019	1.721246399
GO:0006396	P	RNA processing	45	5.4	5.20E-06	5.283996656
GO:0016072	P	rRNA metabolic process	19	3.7	0.0023	2.638272164
GO:0006364	P	rRNA processing	19	3.7	0.0023	2.638272164
GO:0007165	P	signal transduction	59	-3.7	0.0025	2.602059991
GO:0023060	P	signal transmission	61	-3.7	0.0022	2.657577319
GO:0006721	P	terpenoid metabolic process	10	-2.9	0.018	1.744727495
GO:0009826	P	unidimensional cell growth	15	-2.6	0.035	1.455931956

Table S-5.3 2022 differentially expressed genes were entered in AgriGO Parametric Analysis of Gene Set Enrichment (PAGE) using the log2FC (lpa66/WT) values and default settings. Gray rows represent redundant gene ontologies determined by REVIGO using small or tiny similarity, FDR values are calcuted by AgriGO, referencing *Arabidopsis thaliana* GO term database and default SimRel semantic similarity setting. Yellow rows represent manually curated vague or redundant terms.

Table S-5.4 Polar lipid lipidomics anlaysis of lpa66 mutants and wild type plants

			wild type	wild type	wild type	wild type	wild type	wild type		*lpa66*	*lpa66*	*lpa66*	*lpa66*	*lpa66*	*lpa66*	
Mass	**Compound Formula**	**Compound Name**	**Sample01**	**Sample02**	**Sample03**	**Sample04**	**Sample05**	**ave**	**stdev**	**Sample06**	**Sample07**	**Sample08**	**Sample09**	**Sample10**	**ave**	**stdev**
926.6	C49H80O15	**DGDG(34:6)**	1.536	1.434	1.298	1.339	1.389	1.399	0.092	2.098	2.294	2.227	2.227	1.986	2.166	0.123
928.6	C49H82O15	**DGDG(34:5)**	0.379	0.387	0.335	0.360	0.394	0.371	0.024	0.353	0.389	0.353	0.391	0.349	0.367	0.021
930.6	C49H84O15	**DGDG(34:4)**	0.143	0.126	0.132	0.142	0.133	0.135	0.007	0.096	0.115	0.107	0.128	0.100	0.109	0.013
932.6	C49H86O15	**DGDG(34:3)**	2.909	2.558	2.586	2.788	2.436	2.655	0.190	2.438	2.364	2.841	2.554	2.470	2.533	0.185
934.6	C49H88O15	**DGDG(34:2)**	0.353	0.366	0.328	0.435	0.291	0.354	0.053	0.186	0.210	0.178	0.243	0.211	0.205	0.025
936.6	C49H90O15	**DGDG(34:1)**	0.214	0.194	0.190	0.217	0.173	0.198	0.018	0.123	0.136	0.114	0.143	0.141	0.132	0.012
954.6	C51H84O15	**DGDG(36:6)**	11.709	11.595	11.335	11.839	11.845	11.665	0.211	14.093	14.122	16.302	15.249	13.062	14.566	1.241
956.6	C51H86O15	**DGDG(36:5)**	0.588	0.590	0.581	0.701	0.619	0.616	0.050	0.303	0.349	0.296	0.425	0.457	0.366	0.073
958.6	C51H88O15	**DGDG(36:4)**	0.213	0.222	0.193	0.219	0.217	0.213	0.012	0.139	0.139	0.172	0.163	0.158	0.154	0.015
960.6	C51H90O15	**DGDG(36:3)**	0.181	0.182	0.179	0.218	0.183	0.189	0.016	0.131	0.122	0.158	0.150	0.144	0.141	0.014
962.6	C51H92O15	**DGDG(36:2)**	0.008	0.008	0.006	0.015	0.008	0.009	0.004	0.001	0.006	0.000	0.007	0.009	0.005	0.004
964.7	C51H94O15	**DGDG(36:1)**	0.000	0.002	0.003	0.003	0.001	0.002	0.001	0.000	0.000	0.005	0.002	0.001	0.002	0.002
982.6	C53H88O15	**DGDG(38:6)**	0.068	0.077	0.071	0.066	0.075	0.071	0.005	0.091	0.089	0.099	0.125	0.063	0.093	0.022
984.6	C53H90O15	**DGDG(38:5)**	0.017	0.017	0.021	0.022	0.018	0.019	0.002	0.010	0.006	0.007	0.010	0.008	0.008	0.002
986.6	C53H92O15	**DGDG(38:4)**	0.007	0.007	0.009	0.004	0.009	0.007	0.002	0.007	0.007	0.007	0.012	0.005	0.008	0.003
988.7	C53H94O15	**DGDG(38:3)**	0.005	0.003	0.003	0.002	0.004	0.003	0.001	0.002	0.002	0.001	0.001	0.001	0.001	0.001
Total DGDG		**Total DGDG**	**18.332**	**17.768**	**17.271**	**18.371**	**17.796**	**17.907**	**0.456**	**20.071**	**20.349**	**22.866**	**21.828**	**19.166**	**20.856**	**1.476**
764.5	C43H70O10	**MGDG(34:6)**	82.659	77.365	75.542	84.174	87.510	81.450	4.930	91.279	90.755	101.138	93.059	81.632	91.573	6.951
766.5	C43H72O10	**MGDG(34:5)**	10.255	10.202	10.171	11.684	10.691	10.601	0.641	9.317	9.066	9.419	9.317	8.389	9.102	0.419
768.5	C43H74O10	**MGDG(34:4)**	1.870	1.809	2.037	2.439	1.544	1.940	0.331	0.901	0.789	0.656	1.041	0.917	0.861	0.146
770.5	C43H76O10	**MGDG(34:3)**	0.961	0.813	0.898	1.114	0.731	0.903	0.147	0.734	0.698	0.921	0.898	0.654	0.781	0.121
772.6	C43H78O10	**MGDG(34:2)**	0.239	0.248	0.250	0.333	0.174	0.249	0.057	0.138	0.135	0.138	0.159	0.137	0.141	0.010
774.6	C43H80O10	**MGDG(34:1)**	0.154	0.110	0.135	0.153	0.082	0.127	0.031	0.089	0.083	0.100	0.122	0.053	0.090	0.025
792.5	C45H74O10	**MGDG(36:6)**	15.701	15.337	16.896	18.257	17.770	16.792	1.267	16.999	16.448	20.412	19.449	17.471	18.156	1.695
794.5	C45H76O10	**MGDG(36:5)**	1.088	1.118	1.117	1.324	0.984	1.126	0.124	0.789	0.772	0.863	1.095	0.862	0.876	0.129
796.6	C45H78O10	**MGDG(36:4)**	0.461	0.469	0.469	0.582	0.439	0.484	0.056	0.324	0.319	0.348	0.370	0.394	0.351	0.031
798.6	C45H80O10	**MGDG(36:3)**	0.075	0.077	0.083	0.104	0.079	0.084	0.012	0.036	0.044	0.049	0.056	0.042	0.045	0.008
800.6	C45H82O10	**MGDG(36:2)**	0.005	0.003	0.008	0.001	0.003	0.004	0.003	0.002	0.000	0.002	0.002	0.003	0.002	0.001
802.6	C45H84O10	**MGDG(36:1)**	0.000	0.001	0.000	0.002	0.000	0.001	0.001	0.001	0.000	0.000	0.000	0.000	0.000	0.000
820.6	C47H78O10	**MGDG(38:6)**	0.051	0.032	0.041	0.029	0.036	0.038	0.009	0.056	0.051	0.057	0.109	0.033	0.061	0.028
822.6	C47H80O10	**MGDG(38:5)**	0.019	0.023	0.021	0.020	0.019	0.020	0.001	0.017	0.013	0.012	0.016	0.013	0.014	0.002
824.6	C47H82O10	**MGDG(38:4)**	0.017	0.016	0.012	0.021	0.019	0.017	0.003	0.021	0.018	0.017	0.022	0.011	0.018	0.004
826.6	C47H84O10	**MGDG(38:3)**	0.003	0.001	0.001	0.000	0.000	0.001	0.001	0.001	0.000	0.001	0.001	0.000	0.001	0.001
Total MGDG		**Total MGDG**	**113.558**	**107.623**	**107.681**	**120.239**	**120.083**	**113.837**	**6.257**	**120.705**	**119.190**	**134.133**	**125.716**	**110.612**	**122.071**	**8.664**
738.5	C38H73O10P	**PG(32:1)**	0.621	0.601	0.547	0.559	0.563	0.578	0.031	0.946	0.970	1.116	1.053	0.825	0.982	0.111
740.5	C38H75O10P	**PG(32:0)**	0.286	0.289	0.314	0.345	0.281	0.303	0.027	0.180	0.219	0.207	0.250	0.198	0.211	0.026
760.5	C40H71O10P	**PG(34:4)**	7.152	7.339	6.764	6.578	6.844	6.935	0.306	9.291	9.031	10.001	9.221	8.396	9.188	0.575
762.5	C40H73O10P	**PG(34:3)**	3.849	4.164	4.680	4.804	4.445	4.389	0.388	2.416	2.173	2.135	2.497	2.670	2.378	0.225
764.5	C40H75O10P	**PG(34:2)**	2.312	2.367	2.604	2.763	2.312	2.472	0.203	1.487	1.494	1.394	1.602	1.480	1.492	0.074
766.5	C40H77O10P	**PG(34:1)**	1.259	1.247	1.480	1.565	1.105	1.331	0.187	0.848	0.781	0.774	1.000	0.812	0.843	0.093
768.5	C40H79O10P	**PG(34:0)**	0.071	0.088	0.113	0.132	0.096	0.100	0.023	0.042	0.057	0.044	0.061	0.047	0.050	0.008
784.5	C42H71O10P	**PG(36:6)**	0.038	0.053	0.063	0.053	0.045	0.051	0.009	0.038	0.030	0.033	0.035	0.024	0.032	0.006
786.5	C42H73O10P	**PG(36:5)**	0.034	0.029	0.048	0.046	0.039	0.039	0.008	0.026	0.026	0.020	0.014	0.022	0.022	0.005
788.5	C42H75O10P	**PG(36:4)**	0.036	0.054	0.049	0.051	0.040	0.046	0.008	0.037	0.034	0.035	0.033	0.025	0.033	0.005
790.5	C42H77O10P	**PG(36:3)**	0.024	0.034	0.037	0.039	0.039	0.035	0.006	0.021	0.020	0.020	0.022	0.023	0.021	0.001
792.5	C42H79O10P	**PG(36:2)**	0.031	0.032	0.027	0.035	0.032	0.031	0.003	0.016	0.019	0.014	0.018	0.016	0.017	0.002
794.6	C42H81O10P	**PG(36:1)**	0.007	0.005	0.004	0.001	0.002	0.004	0.002	0.004	0.000	0.002	0.000	0.000	0.001	0.002
Total PG		**Total PG**	**15.722**	**16.303**	**16.729**	**16.971**	**15.844**	**16.314**	**0.542**	**15.350**	**14.855**	**15.797**	**15.808**	**14.537**	**15.269**	**0.566**
500.3	C22H43O9P	**LPG(16:1)**	0.000	0.000	0.000	0.005	0.000	0.001	0.002	0.000	0.000	0.000	0.000	0.000	0.000	0.000
502.3	C22H45O9P	**LPG(16:0)**	0.024	0.007	0.003	0.015	0.005	0.011	0.009	0.000	0.002	0.010	0.020	0.003	0.007	0.008
524.3	C24H43O9P	**LPG(18:3)**	0.057	0.039	0.058	0.011	0.056	0.044	0.020	0.093	0.057	0.060	0.058	0.038	0.061	0.020
526.3	C24H45O9P	**LPG(18:2)**	0.001	0.005	0.002	0.000	0.000	0.002	0.002	0.005	0.000	0.000	0.000	0.000	0.001	0.002
528.3	C24H47O9P	**LPG(18:1)**	0.011	0.001	0.002	0.006	0.000	0.004	0.005	0.002	0.000	0.000	0.000	0.000	0.000	0.001
Total LysoPG		**Total LysoPG**	**0.093**	**0.052**	**0.065**	**0.037**	**0.060**	**0.062**	**0.020**	**0.100**	**0.059**	**0.071**	**0.078**	**0.040**	**0.070**	**0.022**
494.3	C24H48O7PN	**LPC(16:1)**	0.004	0.002	0.000	0.000	0.001	0.002	0.002	0.001	0.000	0.000	0.000	0.000	0.000	0.000
496.3	C24H50O7PN	**LPC(16:0)**	0.017	0.016	0.008	0.010	0.008	0.012	0.004	0.012	0.010	0.011	0.011	0.009	0.011	0.001
518.3	C26H48O7PN	**LPC(18:3)**	0.029	0.017	0.014	0.012	0.021	0.019	0.007	0.019	0.020	0.016	0.020	0.016	0.018	0.002
520.3	C26H50O7PN	**LPC(18:2)**	0.030	0.025	0.019	0.022	0.031	0.025	0.005	0.016	0.022	0.018	0.015	0.016	0.018	0.003
522.3	C26H52O7PN	**LPC(18:1)**	0.008	0.007	0.003	0.002	0.009	0.006	0.003	0.004	0.003	0.006	0.003	0.004	0.004	0.001
524.4	C26H54O7PN	**LPC(18:0)**	0.005	0.005	0.002	0.000	0.000	0.002	0.002	0.001	0.000	0.000	0.000	0.001	0.000	0.000
Total LysoPC		**Total LysoPC**	**0.093**	**0.071**	**0.046**	**0.048**	**0.070**	**0.066**	**0.019**	**0.052**	**0.056**	**0.051**	**0.048**	**0.046**	**0.051**	**0.004**
452.3	C21H42O7PN	**LPE(16:1)**	0.001	0.000	0.000	0.000	0.001	0.000	0.001	0.000	0.000	0.001	0.000	0.000	0.000	0.001
454.3	C21H44O7PN	**LPE(16:0)**	0.061	0.063	0.079	0.066	0.083	0.070	0.010	0.075	0.061	0.082	0.070	0.057	0.069	0.010
476.3	C23H42O7PN	**LPE(18:3)**	0.035	0.037	0.028	0.023	0.035	0.032	0.006	0.040	0.041	0.039	0.032	0.020	0.034	0.009
478.3	C23H44O7PN	**LPE(18:2)**	0.050	0.049	0.042	0.039	0.050	0.046	0.005	0.041	0.055	0.040	0.047	0.037	0.044	0.007
480.3	C23H46O7PN	**LPE(18:1)**	0.007	0.002	0.008	0.003	0.004	0.005	0.003	0.004	0.006	0.000	0.002	0.001	0.003	0.002
Total LysoPE		**Total LysoPE**	**0.155**	**0.151**	**0.157**	**0.130**	**0.173**	**0.153**	**0.015**	**0.159**	**0.163**	**0.164**	**0.152**	**0.114**	**0.150**	**0.021**
734.6	C40H80O8PN	**PC(32:0)**	0.021	0.021	0.012	0.016	0.017	0.018	0.004	0.018	0.012	0.020	0.016	0.016	0.016	0.003
754.5	C42H76O8PN	**PC(34:4)**	0.276	0.281	0.274	0.281	0.293	0.281	0.007	0.278	0.283	0.254	0.278	0.270	0.273	0.012
756.5	C42H78O8PN	**PC(34:3)**	5.742	5.370	5.633	5.327	5.301	5.475	0.200	6.622	6.676	7.046	6.964	6.643	6.790	0.199
758.6	C42H80O8PN	**PC(34:2)**	6.512	6.997	7.276	7.639	6.578	7.000	0.475	4.895	4.736	4.399	5.015	5.806	4.970	0.522
760.6	C42H82O8PN	**PC(34:1)**	0.706	0.867	0.965	0.972	0.685	0.839	0.138	0.773	0.674	0.546	0.676	0.692	0.672	0.081
778.5	C44H76O8PN	**PC(36:6)**	3.468	3.334	3.767	3.375	3.813	3.551	0.224	4.623	4.888	5.059	4.903	4.239	4.742	0.322
780.5	C44H78O8PN	**PC(36:5)**	5.937	6.431	6.856	6.570	6.628	6.484	0.342	5.781	5.982	5.721	6.424	5.999	5.981	0.276
782.6	C44H80O8PN	**PC(36:4)**	5.451	6.229	6.870	6.860	6.051	6.292	0.597	4.603	4.402	3.676	4.618	4.581	4.376	0.401
784.6	C44H82O8PN	**PC(36:3)**	1.555	1.835	2.045	2.172	1.696	1.861	0.251	1.578	1.504	1.192	1.547	1.623	1.489	0.172
786.6	C44H84O8PN	**PC(36:2)**	0.633	0.773	0.817	0.960	0.813	0.799	0.117	0.548	0.511	0.380	0.573	0.686	0.540	0.110
788.6	C44H86O8PN	**PC(36:1)**	0.100	0.135	0.117	0.110	0.107	0.114	0.013	0.115	0.126	0.109	0.110	0.126	0.117	0.009
806.6	C46H80O8PN	**PC(38:6)**	0.036	0.031	0.029	0.019	0.030	0.029	0.006	0.038	0.038	0.047	0.037	0.043	0.041	0.004
808.6	C46H82O8PN	**PC(38:5)**	0.096	0.089	0.081	0.081	0.085	0.087	0.006	0.092	0.084	0.078	0.073	0.070	0.079	0.009
810.6	C46H84O8PN	**PC(38:4)**	0.128	0.144	0.135	0.125	0.155	0.138	0.012	0.117	0.123	0.120	0.131	0.109	0.120	0.008
812.6	C46H86O8PN	**PC(38:3)**	0.124	0.135	0.148	0.129	0.124	0.132	0.010	0.119	0.128	0.112	0.135	0.114	0.122	0.010
814.6	C46H88O8PN	**PC(38:2)**	0.072	0.067	0.054	0.053	0.051	0.059	0.009	0.047	0.054	0.044	0.052	0.048	0.049	0.004
836.6	C48H86O8PN	**PC(40:5)**	0.008	0.008	0.008	0.006	0.006	0.007	0.001	0.008	0.008	0.009	0.010	0.006	0.008	0.002
838.6	C48H88O8PN	**PC(40:4)**	0.011	0.011	0.007	0.010	0.013	0.010	0.002	0.008	0.007	0.006	0.014	0.009	0.009	0.003
840.6	C48H90O8PN	**PC(40:3)**	0.010	0.009	0.007	0.011	0.010	0.010	0.002	0.008	0.005	0.011	0.010	0.011	0.009	0.003
842.7	C48H92O8PN	**PC(40:2)**	0.010	0.008	0.011	0.009	0.010	0.010	0.001	0.011	0.005	0.008	0.009	0.007	0.008	0.002
Total PC		**Total PC**	**30.898**	**32.777**	**35.113**	**34.724**	**32.466**	**33.196**	**1.732**	**30.277**	**30.246**	**28.838**	**31.598**	**31.097**	**30.411**	**1.049**
686.5	C37H68O8PN	**PE(32:3)**	0.009	0.012	0.010	0.011	0.014	0.011	0.002	0.030	0.027	0.026	0.021	0.018	0.024	0.005
688.5	C37H70O8PN	**PE(32:2)**	0.010	0.014	0.019	0.019	0.017	0.016	0.004	0.018	0.014	0.014	0.013	0.010	0.014	0.003
690.5	C37H72O8PN	**PE(32:1)**	0.017	0.017	0.018	0.014	0.013	0.016	0.002	0.022	0.020	0.020	0.018	0.016	0.019	0.002
692.5	C37H74O8PN	**PE(32:0)**	0.003	0.006	0.002	0.005	0.002	0.004	0.002	0.005	0.006	0.003	0.006	0.002	0.004	0.002
712.5	C39H70O8PN	**PE(34:4)**	0.038	0.045	0.048	0.049	0.050	0.046	0.005	0.046	0.052	0.051	0.050	0.031	0.046	0.009

Table S-5.4 Polar lipid lipidomics anlaysis of lpa66 mutants and wild type plants

			wild type	wild type	wild type	wild type	wild type	wild type		*lpa66*	*lpa66*	*lpa66*	*lpa66*	*lpa66*	*lpa66*	
Mass	**Compound Formula**	**Compound Name**	**Sample01**	**Sample02**	**Sample03**	**Sample04**	**Sample05**	**ave**	**stdev**	**Sample06**	**Sample07**	**Sample08**	**Sample09**	**Sample10**	**ave**	**stdev**
714.5	C39H72O8PN	**PE(34:3)**	1.969	2.510	2.605	2.461	2.424	2.394	0.247	3.172	3.237	3.291	3.195	2.489	3.077	0.332
716.5	C39H74O8PN	**PE(34:2)**	2.528	3.473	3.634	3.582	3.285	3.300	0.452	2.947	3.042	2.814	3.063	2.453	2.864	0.250
718.5	C39H76O8PN	**PE(34:1)**	0.064	0.083	0.104	0.094	0.073	0.084	0.016	0.077	0.082	0.065	0.084	0.061	0.074	0.010
736.5	C41H70O8PN	**PE(36:6)**	0.454	0.571	0.676	0.620	0.583	0.581	0.082	0.703	0.703	0.683	0.683	0.523	0.659	0.077
738.5	C41H72O8PN	**PE(36:5)**	1.398	1.814	2.047	1.907	1.746	1.783	0.243	1.702	1.670	1.594	1.765	1.370	1.620	0.153
740.5	C41H74O8PN	**PE(36:4)**	1.176	1.551	1.626	1.634	1.434	1.484	0.190	1.176	1.202	1.100	1.304	1.004	1.157	0.112
742.5	C41H76O8PN	**PE(36:3)**	0.398	0.470	0.532	0.522	0.461	0.477	0.054	0.446	0.433	0.404	0.451	0.389	0.424	0.027
744.5	C41H78O8PN	**PE(36:2)**	0.174	0.215	0.231	0.268	0.229	0.223	0.034	0.179	0.214	0.185	0.250	0.176	0.201	0.031
746.6	C41H80O8PN	**PE(36:1)**	0.008	0.008	0.008	0.011	0.008	0.009	0.001	0.008	0.011	0.010	0.003	0.002	0.007	0.004
764.5	C43H74O8PN	**PE(38:6)**	0.013	0.015	0.013	0.009	0.013	0.013	0.003	0.013	0.019	0.018	0.014	0.013	0.015	0.003
766.5	C43H76O8PN	**PE(38:5)**	0.028	0.028	0.030	0.032	0.030	0.030	0.002	0.037	0.036	0.027	0.035	0.024	0.032	0.006
768.5	C43H78O8PN	**PE(38:4)**	0.040	0.048	0.049	0.047	0.052	0.047	0.004	0.040	0.038	0.034	0.034	0.030	0.035	0.004
770.6	C43H80O8PN	**PE(38:3)**	0.032	0.042	0.048	0.047	0.045	0.043	0.006	0.037	0.043	0.033	0.040	0.032	0.037	0.005
798.6	C45H84O8PN	**PE(40:3)**	0.039	0.045	0.044	0.044	0.052	0.045	0.005	0.040	0.048	0.038	0.046	0.042	0.043	0.004
800.6	C45H86O8PN	**PE(40:2)**	0.091	0.111	0.105	0.109	0.129	0.109	0.013	0.097	0.080	0.078	0.103	0.078	0.087	0.012
824.6	C47H86O8PN	**PE(42:4)**	0.041	0.043	0.042	0.043	0.050	0.044	0.004	0.043	0.048	0.052	0.060	0.035	0.048	0.009
826.6	C47H88O8PN	**PE(42:3)**	0.188	0.194	0.191	0.185	0.202	0.192	0.006	0.170	0.175	0.200	0.203	0.145	0.179	0.024
828.6	C47H90O8PN	**PE(42:2)**	0.162	0.175	0.174	0.183	0.180	0.175	0.008	0.156	0.162	0.164	0.190	0.132	0.161	0.020
Total PE		**Total PE**	**8.884**	**11.494**	**12.256**	**11.897**	**11.092**	**11.124**	**1.326**	**11.161**	**11.361**	**10.906**	**11.632**	**9.073**	**10.827**	**1.016**
822.5	C41H73O13P	**PI(32:3)**	0.059	0.055	0.051	0.051	0.055	0.054	0.004	0.097	0.109	0.121	0.123	0.099	0.110	0.012
824.5	C41H75O13P	**PI(32:2)**	0.020	0.020	0.018	0.020	0.019	0.020	0.001	0.023	0.018	0.021	0.026	0.019	0.021	0.003
826.5	C41H77O13P	**PI(32:1)**	0.018	0.020	0.014	0.020	0.017	0.018	0.003	0.017	0.029	0.025	0.042	0.028	0.028	0.009
828.5	C41H79O13P	**PI(32:0)**	0.007	0.007	0.005	0.007	0.005	0.006	0.001	0.006	0.007	0.004	0.005	0.003	0.005	0.002
848.5	C43H75O13P	**PI(34:4)**	0.048	0.044	0.046	0.046	0.050	0.047	0.002	0.056	0.062	0.059	0.057	0.047	0.056	0.006
850.5	C43H77O13P	**PI(34:3)**	3.019	2.815	2.742	2.771	2.789	2.827	0.110	4.066	4.207	4.650	4.506	3.752	4.236	0.356
852.5	C43H79O13P	**PI(34:2)**	2.997	3.127	3.078	3.358	3.023	3.117	0.144	2.621	2.566	2.446	2.661	2.503	2.559	0.087
854.5	C43H81O13P	**PI(34:1)**	0.056	0.066	0.103	0.096	0.071	0.078	0.020	0.071	0.101	0.059	0.092	0.082	0.081	0.017
872.5	C45H75O13P	**PI(36:6)**	0.151	0.142	0.156	0.142	0.151	0.148	0.006	0.270	0.294	0.313	0.276	0.205	0.272	0.041
874.5	C45H77O13P	**PI(36:5)**	0.144	0.153	0.163	0.165	0.162	0.157	0.009	0.153	0.151	0.137	0.153	0.143	0.147	0.007
876.5	C45H79O13P	**PI(36:4)**	0.133	0.152	0.169	0.187	0.155	0.159	0.020	0.114	0.112	0.081	0.107	0.097	0.102	0.013
878.5	C45H81O13P	**PI(36:3)**	0.135	0.165	0.175	0.206	0.178	0.172	0.026	0.145	0.144	0.117	0.135	0.149	0.138	0.013
880.6	C45H83O13P	**PI(36:2)**	0.101	0.127	0.127	0.172	0.156	0.137	0.028	0.076	0.073	0.057	0.081	0.100	0.078	0.015
882.6	C45H85O13P	**PI(36:1)**	0.012	0.012	0.011	0.015	0.008	0.012	0.002	0.010	0.009	0.010	0.015	0.010	0.011	0.002
Total PI		**Total PI**	**6.900**	**6.907**	**6.857**	**7.256**	**6.838**	**6.952**	**0.173**	**7.724**	**7.882**	**8.100**	**8.279**	**7.237**	**7.844**	**0.400**
756.5	C40H70O10PN	**PS(34:4)**	0.003	0.002	0.000	0.002	0.004	0.002	0.002	0.000	0.000	0.008	0.000	0.002	0.002	0.003
758.5	C40H72O10PN	**PS(34:3)**	0.129	0.153	0.163	0.163	0.188	0.159	0.021	0.204	0.206	0.219	0.205	0.165	0.200	0.020
760.5	C40H74O10PN	**PS(34:2)**	0.107	0.128	0.126	0.153	0.159	0.135	0.021	0.132	0.137	0.123	0.135	0.089	0.123	0.020
762.5	C40H76O10PN	**PS(34:1)**	0.002	0.004	0.006	0.003	0.000	0.003	0.002	0.000	0.004	0.002	0.004	0.004	0.003	0.002
780.5	C42H70O10PN	**PS(36:6)**	0.003	0.007	0.008	0.005	0.007	0.006	0.002	0.009	0.008	0.008	0.007	0.007	0.008	0.001
782.5	C42H72O10PN	**PS(36:5)**	0.015	0.013	0.017	0.017	0.015	0.015	0.001	0.012	0.019	0.017	0.019	0.014	0.016	0.003
784.5	C42H74O10PN	**PS(36:4)**	0.011	0.013	0.013	0.012	0.011	0.012	0.001	0.012	0.012	0.009	0.013	0.013	0.012	0.002
786.5	C42H76O10PN	**PS(36:3)**	0.038	0.046	0.048	0.057	0.057	0.049	0.008	0.045	0.043	0.041	0.050	0.040	0.044	0.004
788.5	C42H78O10PN	**PS(36:2)**	0.025	0.031	0.033	0.045	0.045	0.036	0.009	0.035	0.032	0.028	0.033	0.028	0.031	0.003
790.6	C42H80O10PN	**PS(36:1)**	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
808.5	C44H74O10PN	**PS(38:6)**	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.000	0.000	0.000
810.5	C44H76O10PN	**PS(38:5)**	0.000	0.000	0.002	0.002	0.001	0.001	0.001	0.001	0.000	0.001	0.000	0.002	0.001	0.001
812.5	C44H78O10PN	**PS(38:4)**	0.003	0.005	0.005	0.009	0.006	0.006	0.002	0.005	0.002	0.001	0.001	0.000	0.002	0.002
814.6	C44H80O10PN	**PS(38:3)**	0.022	0.037	0.035	0.051	0.043	0.038	0.010	0.029	0.031	0.026	0.035	0.034	0.031	0.003
816.6	C44H82O10PN	**PS(38:2)**	0.028	0.032	0.033	0.044	0.042	0.036	0.007	0.033	0.027	0.026	0.030	0.031	0.029	0.003
818.6	C44H84O10PN	**PS(38:1)**	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.002	0.000	0.000	0.001	0.001	0.001
840.6	C46H82O10PN	**PS(40:4)**	0.002	0.000	0.003	0.001	0.003	0.002	0.001	0.002	0.002	0.002	0.003	0.002	0.002	0.000
842.6	C46H84O10PN	**PS(40:3)**	0.039	0.049	0.043	0.056	0.060	0.049	0.009	0.079	0.077	0.074	0.080	0.093	0.081	0.007
844.6	C46H86O10PN	**PS(40:2)**	0.039	0.046	0.044	0.055	0.061	0.049	0.009	0.065	0.063	0.062	0.071	0.072	0.067	0.005
846.6	C46H88O10PN	**PS(40:1)**	0.000	0.003	0.004	0.003	0.001	0.002	0.001	0.002	0.002	0.004	0.000	0.003	0.002	0.002
868.6	C48H86O10PN	**PS(42:4)**	0.033	0.034	0.026	0.031	0.032	0.031	0.003	0.052	0.049	0.062	0.060	0.063	0.057	0.006
870.6	C48H88O10PN	**PS(42:3)**	0.124	0.139	0.119	0.142	0.152	0.135	0.013	0.232	0.269	0.291	0.280	0.292	0.273	0.025
872.6	C48H90O10PN	**PS(42:2)**	0.076	0.099	0.082	0.101	0.104	0.092	0.012	0.156	0.160	0.180	0.182	0.177	0.171	0.012
874.6	C48H92O10PN	**PS(42:1)**	0.002	0.000	0.001	0.000	0.000	0.001	0.001	0.002	0.000	0.000	0.000	0.002	0.001	0.001
898.6	C50H92O10PN	**PS(44:3)**	0.003	0.009	0.002	0.009	0.004	0.005	0.003	0.013	0.016	0.015	0.012	0.014	0.014	0.002
900.7	C50H94O10PN	**PS(44:2)**	0.012	0.012	0.010	0.008	0.014	0.011	0.002	0.020	0.017	0.019	0.018	0.016	0.018	0.002
Total PS		**Total PS**	**0.722**	**0.865**	**0.821**	**0.967**	**1.012**	**0.877**	**0.116**	**1.138**	**1.178**	**1.221**	**1.238**	**1.160**	**1.187**	**0.042**
666.5	C35H69O8P	**PA(32:0)**	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.002	0.000	0.000	0.000	0.001	0.001	0.001
682.4	C37H61O8P	**PA(34:6)**	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.000	0.000	0.001
684.4	C37H63O8P	**PA(34:5)**	0.001	0.000	0.000	0.001	0.000	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000
686.4	C37H65O8P	**PA(34:4)**	0.010	0.010	0.007	0.001	0.007	0.007	0.004	0.012	0.024	0.015	0.021	0.008	0.016	0.007
688.5	C37H67O8P	**PA(34:3)**	0.190	0.083	0.073	0.064	0.112	0.104	0.051	0.151	0.268	0.166	0.215	0.117	0.183	0.059
690.5	C37H69O8P	**PA(34:2)**	0.247	0.125	0.104	0.106	0.156	0.147	0.059	0.129	0.244	0.137	0.188	0.120	0.164	0.052
692.5	C37H71O8P	**PA(34:1)**	0.016	0.009	0.009	0.010	0.009	0.011	0.003	0.002	0.016	0.006	0.007	0.005	0.007	0.005
710.4	C39H65O8P	**PA(36:6)**	0.048	0.017	0.009	0.016	0.024	0.023	0.015	0.027	0.067	0.035	0.041	0.020	0.038	0.018
712.5	C39H67O8P	**PA(36:5)**	0.125	0.039	0.030	0.037	0.069	0.060	0.040	0.055	0.134	0.065	0.091	0.044	0.078	0.036
714.5	C39H69O8P	**PA(36:4)**	0.134	0.041	0.046	0.046	0.081	0.070	0.039	0.037	0.107	0.048	0.076	0.037	0.061	0.030
716.5	C39H71O8P	**PA(36:3)**	0.036	0.007	0.012	0.016	0.020	0.018	0.011	0.017	0.042	0.014	0.027	0.017	0.023	0.012
718.5	C39H73O8P	**PA(36:2)**	0.016	0.008	0.007	0.008	0.008	0.009	0.004	0.005	0.011	0.003	0.011	0.007	0.007	0.004
Total PA		**Total PA**	**0.823**	**0.341**	**0.294**	**0.305**	**0.486**	**0.450**	**0.223**	**0.436**	**0.914**	**0.490**	**0.680**	**0.376**	**0.579**	**0.219**
Total		**Total**	**196.179**	**194.352**	**197.289**	**210.945**	**205.922**	**200.938**	**7.147**	**207.174**	**206.254**	**222.636**	**217.058**	**193.458**	**209.316**	**11.212**

Table S-5.4 Samples are represented in normalized signal per mass dry weight.

Table S-5.5 Oxylipin lipidomics analysis of wild type, *lpa66* mutants, and *dot4* mutants.

	chemical formula	**adduct**	**WT1**	**WT2**	**WT3**	**WT4**	**WT5**	***lpa66* 1**	***lpa66* 2**	***lpa66* 3**	***lpa66* 4**	***lpa66* 5**	***dot4* 1**	***dot4* 2**	***dot4* 3**	***dot4* 4**	***dot4* 5**	***dot4* 6**
acDGDG(18:4-O/34:6)	C37H61O5	[M+NH4]+	0.005	0.006	0.005	0.005	0.004	0.007	0.007	0.007	0.007	0.005	0.004	0.003	0.003	0.004	0.004	0.003
acDGDG(18:4-O/34:7-O)	C37H59O6	[M+NH4]+	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.001	0.001	0.002	0.001	0.001
acDGDG(18:4-O/34:8-2O)	C37H57O7	[M+NH4]+	0.004	0.005	0.004	0.005	0.003	0.004	0.004	0.005	0.005	0.004	0.002	0.003	0.002	0.002	0.002	0.002
acMGDG(16:3/34:6)	C37H61O5	[M+NH4]+	0.004	0.004	0.003	0.003	0.003	0.006	0.007	0.007	0.007	0.006	0.004	0.004	0.004	0.004	0.004	0.004
acMGDG(16:0/34:6)	C37H61O5	[M+NH4]+	0.013	0.011	0.008	0.012	0.007	0.012	0.013	0.018	0.014	0.009	0.012	0.007	0.008	0.009	0.005	0.005
acMGDG(16:0/34:7-O)	C37H59O6	[M+NH4]+	0.003	0.003	0.003	0.003	0.002	0.004	0.005	0.005	0.005	0.004	0.003	0.003	0.003	0.004	0.003	0.003
acMGDG(18:3/34:6)	C37H61O5	[M+NH4]+	0.009	0.007	0.006	0.009	0.006	0.007	0.010	0.009	0.008	0.007	0.012	0.008	0.005	0.006	0.005	0.006
acMGDG(16:3/36:6)	C39H65O5	[M+NH4]+	0.006	0.005	0.005	0.005	0.004	0.007	0.007	0.008	0.007	0.006	0.006	0.010	0.005	0.005	0.004	0.005
acMGDG(18:2/34:6)	C37H61O5	[M+NH4]+	0.004	0.004	0.003	0.004	0.003	0.004	0.004	0.004	0.005	0.004	0.003	0.003	0.002	0.003	0.003	0.002
acMGDG(16:1/36:6)	C37H57O7	[M+NH4]+	0.011	0.010	0.007	0.009	0.005	0.008	0.007	0.009	0.010	0.012	0.003	0.005	0.003	0.004	0.003	0.004
acMGDG(18:1/34:6)	C37H61O5	[M+NH4]+	0.004	0.005	0.004	0.004	0.010	0.004	0.004	0.004	0.004	0.003	0.006	0.005	0.004	0.006	0.005	0.004
acMGDG(16:0/36:6)	C37H57O7	[M+NH4]+	0.006	0.002	0.004	0.003	0.003	0.009	0.007	0.010	0.023	0.009	0.013	0.030	0.023	0.014	0.016	0.021
acMGDG(18:0/34:6)	C37H61O5	[M+NH4]+	0.007	0.005	0.004	0.005	0.003	0.005	0.005	0.008	0.006	0.004	0.004	0.003	0.003	0.003	0.002	0.002
acMGDG(18:4-O/34:6)	C37H61O5	[M+NH4]+	0.005	0.007	0.004	0.005	0.005	0.006	0.005	0.006	0.007	0.005	0.003	0.003	0.004	0.004	0.004	0.004
acMGDG(18:3/34:7-O)	C37H59O6	[M+NH4]+	0.005	0.004	0.003	0.014	0.003	0.004	0.005	0.004	0.005	0.003	0.005	0.005	0.004	0.007	0.005	0.004
acMGDG(16:4-O/36:6)	C39H65O5	[M+NH4]+	0.004	0.003	0.005	0.005	0.002	0.004	0.005	0.007	0.009	0.007	0.012	0.016	0.018	0.012	0.013	0.014
acMGDG(18:3-O/34:6)	C37H61O5	[M+NH4]+	0.004	0.004	0.003	0.003	0.003	0.004	0.004	0.004	0.004	0.003	0.002	0.002	0.002	0.003	0.002	0.002
acMGDG(18:2/34:7-O)	C37H59O6	[M+NH4]+	0.004	0.003	0.004	0.003	0.002	0.004	0.004	0.003	0.004	0.003	0.002	0.001	0.001	0.002	0.001	0.001
acMGDG(16:3-O/36:6)	C39H65O5	[M+NH4]+	0.004	0.002	0.002	0.003	0.001	0.002	0.004	0.003	0.004	0.002	0.002	0.002	0.001	0.001	0.001	0.001
acMGDG(18:4-O/34:7-O)	C37H59O6	[M+NH4]+	0.004	0.002	0.002	0.003	0.002	0.003	0.003	0.002	0.004	0.002	0.002	0.004	0.002	0.003	0.002	0.003
acMGDG(18:3/36:6)	C39H65O5	[M+NH4]+	0.008	0.006	0.005	0.005	0.005	0.010	0.012	0.012	0.013	0.008	0.019	0.020	0.009	0.010	0.010	0.011
acMGDG(18:4-2O/34:6)	C37H61O5	[M+NH4]+	0.004	0.004	0.003	0.003	0.003	0.003	0.004	0.004	0.004	0.003	0.002	0.001	0.001	0.002	0.001	0.001
acMGDG(18:3-O/34:7-O)	C37H59O6	[M+NH4]+	0.004	0.003	0.003	0.003	0.002	0.003	0.003	0.003	0.003	0.003	0.003	0.002	0.002	0.002	0.002	0.002
acMGDG(18:2/34:8-2O)	C37H57O7	[M+NH4]+	0.007	0.010	0.005	0.008	0.004	0.007	0.008	0.009	0.013	0.004	0.014	0.012	0.009	0.011	0.009	0.009
acMGDG(18:3/34:7-2O)	C37H59O7	[M+NH4]+	0.002	0.003	0.001	0.005	0.001	0.003	0.002	0.002	0.003	0.002	0.001	0.001	0.001	0.002	0.001	0.001
acMGDG(18:3-2O/34:6)	C37H61O5	[M+NH4]+	0.003	0.003	0.003	0.003	0.003	0.003	0.004	0.005	0.004	0.003	0.008	0.005	0.003	0.008	0.004	0.003
acMGDG(16:3-2O/34:8-2O)	C37H57O7	[M+NH4]+	0.003	0.004	0.003	0.003	0.004	0.005	0.004	0.004	0.006	0.004	0.023	0.018	0.009	0.020	0.013	0.010
acMGDG(18:0/36:6)	C39H65O5	[M+NH4]+	0.005	0.002	0.003	0.003	0.001	0.003	0.002	0.004	0.004	0.002	0.001	0.002	0.002	0.002	0.000	0.002
acMGDG(16:0/36:8-2O)	C39H61O7	[M+NH4]+	0.002	0.001	0.000	0.001	0.001	0.003	0.002	0.004	0.005	0.003	0.003	0.008	0.004	0.004	0.003	0.005
acMGDG(18:4-O/34:8-2O)	C37H57O7	[M+NH4]+	0.010	0.005	0.004	0.004	0.005	0.035	0.025	0.040	0.151	0.041	0.071	0.308	0.158	0.071	0.097	0.127
acMGDG(16:4-O/36:8-2O)	C39H61O7	[M+NH4]+	0.002	0.002	0.002	0.002	0.001	0.001	0.001	0.001	0.002	0.001	0.003	0.003	0.002	0.002	0.003	0.001
acMGDG(18:3/36:7-O)	C39H63O6	[M+NH4]+	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.002	0.001	0.002	0.002	0.001	0.001	0.001	0.001
acMGDG(18:4-2O/34:7-O)	C37H59O6	[M+NH4]+	0.002	0.002	0.003	0.002	0.002	0.002	0.003	0.002	0.002	0.002	0.002	0.001	0.001	0.001	0.001	0.001
acMGDG(18:3-O/36:6)	C39H65O5	[M+NH4]+	0.005	0.006	0.003	0.003	0.004	0.006	0.005	0.007	0.006	0.007	0.010	0.011	0.007	0.012	0.009	0.007
acMGDG(16:3-O/36:8-2O)	C39H61O7	[M+NH4]+	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
acMGDG(18:4-3O/34:6)	C37H61O5	[M+NH4]+	0.004	0.004	0.003	0.003	0.003	0.004	0.004	0.005	0.004	0.003	0.002	0.003	0.002	0.003	0.002	0.002
acMGDG(18:2-O/36:6)	C39H65O5	[M+NH4]+	0.007	0.008	0.004	0.007	0.005	0.007	0.008	0.009	0.009	0.007	0.013	0.012	0.006	0.014	0.008	0.009
acMGDG(18:3-3O/34:6)	C37H61O5	[M+NH4]+	0.004	0.003	0.002	0.003	0.003	0.004	0.003	0.004	0.005	0.003	0.002	0.002	0.001	0.002	0.002	0.002
acMGDG(18:5-2O/36:6)	C39H65O5	[M+NH4]+	0.004	0.003	0.002	0.002	0.003	0.004	0.004	0.004	0.009	0.004	0.008	0.017	0.005	0.006	0.006	0.011
acMGDG(18:4-O/36:7-O)	C39H63O6	[M+NH4]+	0.001	0.001	0.001	0.001	0.001	0.003	0.003	0.003	0.012	0.004	0.014	0.029	0.009	0.010	0.010	0.020
acMGDG(18:3/36:8-2O)	C39H61O7	[M+NH4]+	0.002	0.002	0.001	0.002	0.001	0.004	0.003	0.003	0.005	0.002	0.004	0.004	0.002	0.001	0.001	0.002
acMGDG(18:4-2O/34:8-2O)	C37H57O7	[M+NH4]+	0.004	0.003	0.002	0.003	0.002	0.003	0.004	0.006	0.008	0.003	0.007	0.011	0.007	0.007	0.005	0.008
acMGDG(18:3-O/36:7-O)	C39H63O6	[M+NH4]+	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
acMGDG(18:4-O/36:6-O)	C39H65O6	[M+NH4]+	0.002	0.001	0.001	0.001	0.001	0.002	0.001	0.002	0.003	0.002	0.002	0.003	0.002	0.001	0.002	0.002
acMGDG(18:2/36:8-2O)	C39H61O7	[M+NH4]+	0.003	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.004	0.002	0.003	0.004	0.002	0.003	0.003	0.003
acMGDG(18:4-3O/34:7-O)	C37H59O6	[M+NH4]+	0.002	0.002	0.002	0.003	0.002	0.002	0.002	0.002	0.002	0.002	0.001	0.001	0.001	0.002	0.001	0.001
acMGDG(18:3-2O/36:6)	C39H65O5	[M+NH4]+	0.007	0.012	0.005	0.006	0.003	0.008	0.008	0.010	0.013	0.004	0.031	0.023	0.014	0.035	0.015	0.012
acMGDG(18:3-O/36:6-O)	C39H65O6	[M+NH4]+	0.003	0.003	0.003	0.005	0.003	0.005	0.004	0.002	0.004	0.004	0.004	0.011	0.004	0.007	0.003	0.004
acMGDG(16:3-2O/36:8-2O)	C39H61O7	[M+NH4]+	0.001	0.001	0.001	0.001	0.001	0.001	0.000	0.001	0.002	0.001	0.002	0.003	0.001	0.001	0.001	0.001
acMGDG(18:3-3O/34:7-O)	C37H59O6	[M+NH4]+	0.003	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.001	0.001	0.001	0.002	0.001	0.001
acMGDG(18:4-O/36:8-2O)	C39H61O7	[M+NH4]+	0.003	0.002	0.002	0.001	0.002	0.009	0.005	0.009	0.029	0.009	0.013	0.059	0.025	0.012	0.012	0.022
acMGDG(18:4-O/36:8-2O) (alt)	C39H59O6	[M+NH4]+	0.003	0.002	0.001	0.001	0.001	0.003	0.002	0.003	0.010	0.003	0.006	0.021	0.009	0.004	0.005	0.008
acMGDG(18:3-O/36:8-2O)	C39H61O7	[M+NH4]+	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.002	0.002	0.001	0.002	0.002	0.001	0.001	0.001	0.001
acMGDG(18:4-3O/36:6)	C39H65O5	[M+NH4]+	0.002	0.002	0.002	0.002	0.001	0.002	0.003	0.003	0.003	0.002	0.002	0.004	0.002	0.002	0.002	0.002
acMGDG(18:2-O/36:8-2O)	C39H61O7	[M+NH4]+	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
acMGDG(18:4-O/36:6-2O)	C39H65O7	[M+NH4]+	0.001	0.002	0.001	0.001	0.000	0.001	0.001	0.001	0.001	0.002	0.002	0.003	0.001	0.002	0.001	0.001
acMGDG(18:2-3O/36:6)	C39H65O5	[M+NH4]+	0.002	0.002	0.002	0.002	0.002	0.003	0.002	0.003	0.004	0.002	0.003	0.003	0.003	0.006	0.004	0.003
acMGDG(18:5-2O/36:8-2O)	C39H61O7	[M+NH4]+	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.002	0.004	0.001	0.002	0.002	0.003
acMGDG(18:4-2O/36:8-2O)	C39H61O7	[M+NH4]+	0.000	0.001	0.000	0.001	0.000	0.001	0.000	0.001	0.001	0.001	0.002	0.002	0.002	0.001	0.001	0.001
acMGDG(18:3-2O/36:8-2O)	C39H61O7	[M+NH4]+	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.002	0.003	0.001	0.002	0.003	0.001	0.002	0.001	0.002
acMGDG(18:3-3O/36:8-2O)	C39H61O7	[M+NH4]+	0.001	0.001	0.001	0.001	0.000	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.000	0.001
Campesterol-Glc(16:0)	C28H47	[M+NH4]+	0.015	0.013	0.015	0.017	0.013	0.026	0.031	0.037	0.032	0.035	0.019	0.018	0.019	0.025	0.019	0.018
Stigmasterol-Glc(16:0)	C29H47	[M+NH4]+	0.012	0.009	0.008	0.008	0.010	0.018	0.020	0.019	0.017	0.022	0.012	0.013	0.012	0.014	0.011	0.011
Sitosterol-Glc(16:0)	C29H49	[M+NH4]+	0.110	0.096	0.084	0.094	0.087	0.213	0.216	0.272	0.246	0.214	0.097	0.109	0.106	0.122	0.102	0.112
Campesterol-Glc(18:3)	C28H47	[M+NH4]+	0.009	0.010	0.012	0.010	0.011	0.025	0.024	0.024	0.022	0.021	0.010	0.010	0.012	0.010	0.009	0.012
Campesterol-Glc(18:2)	C28H47	[M+NH4]+	0.010	0.011	0.012	0.012	0.011	0.017	0.016	0.017	0.017	0.019	0.011	0.010	0.011	0.013	0.010	0.011
Stigmasterol-Glc(18:3)	C29H47	[M+NH4]+	0.006	0.008	0.007	0.008	0.007	0.012	0.016	0.018	0.014	0.020	0.009	0.008	0.007	0.009	0.006	0.007
Campesterol-Glc(18:4-O)	C28H47	[M+NH4]+	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.000	0.000	0.001	0.000	0.000
Stigmasterol-Glc(18:2)	C29H47	[M+NH4]+	0.007	0.007	0.007	0.007	0.008	0.010	0.011	0.010	0.011	0.014	0.008	0.006	0.007	0.008	0.006	0.007
Sitosterol-Glc(18:3)	C29H49	[M+NH4]+	0.073	0.067	0.067	0.067	0.068	0.160	0.177	0.178	0.181	0.147	0.059	0.059	0.065	0.065	0.057	0.064
Sitosterol-Glc(18:2)	C29H49	[M+NH4]+	0.079	0.080	0.079	0.091	0.082	0.127	0.124	0.122	0.138	0.130	0.066	0.066	0.061	0.080	0.060	0.067
Stigmasterol-Glc(18:4-O)	C29H47	[M+NH4]+	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.000	0.001	0.000	0.001
Sitosterol-Glc(18:4-O)	C29H49	[M+NH4]+	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.002	0.002	0.002	0.001	0.001	0.001	0.001	0.001	0.001
DAG(16:0/18:3)	C19H37O3	[M+NH4]+	0.011	0.011	0.011	0.011	0.011	0.014	0.014	0.013	0.013	0.012	0.011	0.012	0.010	0.010	0.011	0.012
DAG(18:3/18:3)	C21H35O3	[M+NH4]+	0.006	0.007	0.006	0.006	0.007	0.009	0.009	0.008	0.008	0.007	0.006	0.005	0.005	0.006	0.006	0.006
DAG(18:2/18:3)	C21H37O3	[M+NH4]+	0.007	0.008	0.008	0.009	0.008	0.007	0.007	0.006	0.007	0.007	0.007	0.006	0.007	0.007	0.007	0.007
DGDG(34:0)	C37H73O5	[M+NH4]+	0.090	0.085	0.058	0.097	0.052	0.047	0.066	0.056	0.072	0.041	0.067	0.040	0.035	0.028	0.041	0.044
DGDG(36:0)	C39H77O5	[M+NH4]+	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
GlcCer(34:1)-2	C34H68O4N	[M+H]+	0.738	0.781	0.723	0.727	0.703	0.793	0.892	0.874	0.882	0.817	0.518	0.439	0.430	0.546	0.466	0.459
GlcCer(34:1)-3	C34H68O5N	[M+H]+	1.060	1.093	0.978	0.921	0.869	1.341	1.514	1.580	1.517	1.385	0.741	0.602	0.556	0.725	0.599	0.594
GlcCer(40:1)-3	C40H80O5N	[M+H]+	0.328	0.362	0.371	0.386	0.348	0.372	0.363	0.348	0.393	0.374	0.276	0.229	0.221	0.266	0.217	0.223
GlcCer(42:2)-3	C42H82O5N	[M+H]+	1.779	1.850	1.767	1.777	1.635	1.909	1.876	1.920	1.963	1.762	1.750	1.593	1.489	1.848	1.580	1.538
MGDG(34:0)	C37H73O5	[M+NH4]+	0.053	0.050	0.042	0.056	0.020	0.026	0.075	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.079	0.020
MGDG(36:0)	C39H77O5	[M+NH4]+	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.008	0.011	0.000	0.000	0.039	0.007	0.000	0.000	0.000
NAE(16:0)	C2H8ON	[M+H]+	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
NAPE(18:3/34:3)	C37H65O4	[M+NH4]+	0.002	0.002	0.002	0.002	0.002	0.003	0.003	0.003	0.003	0.003	0.002	0.002	0.002	0.002	0.002	0.002
NAPE(18:3/36:6)	C39H63O4	[M+NH4]+	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
PE(24:0)	C27H51O4	[M+H]+	0.000	0.013	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
PE(40:0)	C43H83O4	[M+H]+	0.005	0.000	0.032	0.005	0.081	0.011	0.003	0.000	0.015	0.059	0.044	0.021	0.029	0.025	0.027	0.020
Sitosterol(18:3)	C29H49	[M+NH4]+	0.006	0.002	0.002	0.001	0.002	0.004	0.004	0.007	0.005	0.005	0.008	0.014	0.015	0.018	0.012	0.017
Sitosterol(18:2)	C29H49	[M+NH4]+	0.004	0.001	0.001	0.001	0.001	0.002	0.002	0.004	0.003	0.003	0.007	0.011	0.010	0.012	0.010	0.012
Campesterol-Glc	C28H47	[M+NH4]+	0.125	0.096	0.093	0.088	0.091	0.118	0.134	0.153	0.143	0.089	0.143	0.135	0.135	0.169	0.148	0.137
Stigmasterol-Glc	C29H47	[M+NH4]+	0.096	0.071	0.069	0.052	0.066	0.080	0.094	0.103	0.100	0.070	0.158	0.129	0.111	0.139	0.131	0.119
Sitosterol-Glc	C29H49	[M+NH4]+	0.908	0.711	0.650	0.628	0.639	0.932	1.021	1.117	1.222	0.674	0.932	0.938	0.836	0.990	0.992	0.912
TAG(16:0/34:6)	C37H59O4	[M+NH4]+	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.001	0.000	0.001	0.000	0.000
TAG(17:1/34:2)	C37H67O4	[M+NH4]+	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TAG(18:3/34:6)	C37H59O4	[M+NH4]+	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.000	0.002	0.000	0.000
TAG(18:3/34:2)	C37H67O4	[M+NH4]+	0.003	0.002	0.002	0.002	0.002	0.003	0.002	0.002	0.002	0.002	0.007	0.006	0.005	0.015	0.005	0.005
TAG(18:3/36:6)	C39H63O4	[M+NH4]+	0.015	0.014	0.016	0.016	0.015	0.021	0.019	0.016	0.017	0.014	0.016	0.012	0.013	0.015	0.014	0.015
TAG(18:3/36:5)	C39H65O4	[M+NH4]+	0.020	0.020	0.021	0.024	0.020	0.018	0.017	0.012	0.015	0.014	0.021	0.016	0.019	0.021	0.019	0.020
TAG(18:2/36:5)	C39H65O4	[M+NH4]+	0.012	0.012	0.014	0.015	0.013	0.008	0.008	0.006	0.008	0.007	0.015	0.012	0.012	0.016	0.013	0.014
acPG(16:1/36:8-2O)	C42H66O12P	[M-H]-	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
DGDG(18:3/7:1-O)	C7H11O3	[M+OAc]-	0.006	0.007	0.007	0.005	0.003	0.005	0.006	0.007	0.005	0.004	0.007	0.005	0.004	0.004	0.003	0.004
DGDG(9:1-O/16:3)	C9H15O3	[M+OAc]-	0.011	0.012	0.017	0.011	0.006	0.013	0.013	0.010	0.008	0.008	0.009	0.007	0.006	0.010	0.006	0.005
DGDG(18:3/7:1-2O)	C7H11O4	[M+OAc]-	0.005	0.004	0.010	0.004	0.003	0.003	0.006	0.004	0.005	0.004	0.008	0.004	0.004	0.006	0.003	0.004
DGDG(9:1-2O/16:3)	C9H15O4	[M+OAc]-	0.005	0.005	0.012	0.008	0.003	0.003	0.006	0.006	0.004	0.004	0.007	0.003	0.003	0.006	0.003	0.004
DGDG(9:1-O/18:3)	C9H15O3	[M+OAc]-	0.018	0.019	0.023	0.014	0.007	0.016	0.017	0.018	0.014	0.009	0.023	0.013	0.010	0.017	0.012	0.010
DGDG(9:1-2O/18:3)	C9H15O4	[M+OAc]-	0.005	0.005	0.009	0.006	0.002	0.005	0.006	0.006	0.004	0.004	0.007	0.004	0.003	0.006	0.003	0.002
DGDG(18:0/16:1)	C18H35O2	[M+OAc]-	0.024	0.022	0.027	0.026	0.015	0.022	0.012	0.016	0.018	0.018	0.025	0.014	0.005	0.027	0.009	0.020
DGDG(18:0/16:0)	C18H35O2	[M+OAc]-	0.088	0.029	0.067	0.078	0.044	0.059	0.059	0.029	0.066	0.015	0.018	0.010	0.045	0.004	0.056	0.004

Table S-5.5 Oxylipin lipidomics analysis of wild type, *lpa66* mutants, and *dot4* mutants.

	chemical formula	adduct	WT1	WT2	WT3	WT4	WT5	*lpa66 1*	*lpa66 2*	*lpa66 3*	*lpa66 4*	*lpa66 5*	*dot4 1*	*dot4 2*	*dot4 3*	*dot4 4*	*dot4 5*	*dot4 6*
DGDG(18:0/18:0)	$C_{18}H_{35}O_2$	[M+OAc]-	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
DGDG(18:3/16:3)	$C_{18}H_{29}O_2$	[M+OAc]-	3.012	3.032	2.435	2.384	2.389	3.908	4.264	3.989	3.804	3.563	3.526	2.661	2.311	3.132	2.707	2.592
DGDG(18:3/16:2)	$C_{18}H_{29}O_2$	[M+OAc]-	0.531	0.586	0.496	0.488	0.453	0.395	0.417	0.368	0.419	0.361	0.549	0.374	0.297	0.403	0.332	0.327
DGDG(18:3/16:1)	$C_{18}H_{29}O_2$	[M+OAc]-	1.146	1.086	2.402	0.990	0.715	0.952	1.445	1.071	0.776	1.113	1.602	0.810	0.665	1.261	0.644	0.725
DGDG(18:3/16:0)	$C_{18}H_{29}O_2$	[M+OAc]-	6.936	5.980	5.947	6.085	5.147	5.808	5.414	6.582	5.301	5.348	5.801	4.030	3.044	4.631	3.692	3.472
DGDG(18:1/16:0)	$C_{16}H_{31}O_2$	[M+OAc]-	0.534	0.525	0.485	0.532	0.392	0.323	0.344	0.303	0.368	0.369	0.525	0.287	0.205	0.301	0.259	0.232
DGDG(18:0/16:0)	$C_{16}H_{31}O_2$	[M+OAc]-	0.120	0.072	0.079	0.051	0.058	0.064	0.063	0.083	0.046	0.080	0.065	0.066	0.010	0.096	0.000	0.049
DGDG(18:4-O/16:3)	$C_{18}H_{27}O_3$	[M+OAc]-	0.004	0.003	0.004	0.002	0.002	0.003	0.004	0.003	0.005	0.003	0.002	0.002	0.001	0.002	0.002	0.001
DGDG(16:0/18:4-O)	$C_{18}H_{27}O_3$	[M+OAc]-	0.016	0.013	0.018	0.011	0.007	0.018	0.019	0.016	0.030	0.009	0.012	0.011	0.006	0.020	0.007	0.006
DGDG(16:0/18:3-O)	$C_{18}H_{29}O_3$	[M+OAc]-	0.066	0.055	0.070	0.058	0.025	0.063	0.057	0.056	0.058	0.034	0.026	0.035	0.017	0.036	0.029	0.028
DGDG(18:4-O/16:4-O)	$C_{16}H_{23}O_3$	[M+OAc]-	0.143	0.156	0.146	0.135	0.124	0.169	0.168	0.180	0.176	0.154	0.122	0.107	0.090	0.130	0.095	0.103
DGDG(18:3/18:3)	$C_{18}H_{29}O_2$	[M+OAc]-	38.764	40.181	36.067	35.476	34.587	44.617	43.666	47.565	44.159	41.192	32.211	28.187	24.409	31.598	25.476	27.020
DGDG(18:2/18:3)	$C_{18}H_{29}O_2$	[M+OAc]-	0.591	0.712	0.586	0.639	0.570	0.270	0.221	0.180	0.271	0.261	0.425	0.316	0.219	0.355	0.226	0.258
DGDG(18:1/18:3)	$C_{18}H_{29}O_2$	[M+OAc]-	0.490	0.478	0.457	0.411	0.389	0.400	0.431	0.432	0.421	0.403	0.709	0.538	0.426	0.581	0.488	0.485
DGDG(18:2/18:2)	$C_{18}H_{31}O_2$	[M+OAc]-	0.349	0.366	0.365	0.449	0.328	0.252	0.246	0.259	0.252	0.310	0.339	0.229	0.176	0.278	0.204	0.207
DGDG(18:3-2O/16:3)	$C_{18}H_{27}O_3$	[M+OAc]-	0.033	0.033	0.024	0.018	0.024	0.040	0.051	0.047	0.047	0.038	0.020	0.021	0.010	0.026	0.011	0.014
DGDG(18:0/18:3)	$C_{18}H_{29}O_2$	[M+OAc]-	3.706	1.129	1.126	2.692	2.303	3.072	1.705	3.561	1.729	2.379	2.070	1.155	0.692	1.103	0.541	0.864
DGDG(16:0/18:3-2O)	$C_{18}H_{27}O_3$	[M+OAc]-	0.072	0.062	0.055	0.032	0.044	0.057	0.075	0.074	0.062	0.056	0.012	0.013	0.009	0.018	0.009	0.009
DGDG(18:4-O/18:3)	$C_{18}H_{27}O_3$	[M+OAc]-	0.046	0.043	0.044	0.033	0.026	0.059	0.064	0.063	0.066	0.033	0.039	0.028	0.022	0.041	0.030	0.030
DGDG(18:4-O/18:4-O)	$C_{18}H_{27}O_3$	[M+OAc]-	0.040	0.013	0.018	0.010	0.014	0.072	0.062	0.055	0.225	0.037	0.011	0.011	0.010	0.046	0.004	0.009
DGDG(20:3/18:3)	$C_{18}H_{29}O_2$	[M+OAc]-	0.275	0.256	0.240	0.214	0.173	0.258	0.296	0.282	0.310	0.179	0.364	0.310	0.167	0.398	0.159	0.172
DGDG(20:2/18:3)	$C_{18}H_{29}O_2$	[M+OAc]-	0.082	0.094	0.087	0.077	0.058	0.073	0.086	0.084	0.090	0.068	0.103	0.085	0.047	0.091	0.052	0.061
DGDG(20:1/18:3)	$C_{18}H_{29}O_2$	[M+OAc]-	0.205	0.238	0.147	0.112	0.173	0.214	0.241	0.265	0.279	0.198	0.129	0.120	0.067	0.112	0.075	0.099
DGDG(18:4-O/18:4-2O)	$C_{18}H_{27}O_3$	[M+OAc]-	0.019	0.015	0.021	0.012	0.010	0.014	0.017	0.016	0.019	0.016	0.016	0.033	0.009	0.056	0.008	0.007
DGMG(16:0)	$C_{16}H_{31}O_2$	[M+OAc]-	1.771	1.682	2.103	1.567	1.722	2.137	2.497	2.317	1.965	1.822	3.130	2.219	1.788	2.323	1.813	2.167
DGMG(16:4-O)	$C_{16}H_{23}O_3$	[M+OAc]-	0.006	0.006	0.007	0.005	0.004	0.006	0.008	0.006	0.008	0.005	0.016	0.008	0.006	0.012	0.006	0.006
DGMG(18:3)	$C_{18}H_{29}O_2$	[M+OAc]-	0.494	0.073	0.061	0.051	0.297	0.102	0.431	0.096	0.200	0.104	2.627	1.299	0.591	0.704	0.252	0.839
DGMG(18:4-O)	$C_{18}H_{27}O_3$	[M+OAc]-	0.012	0.011	0.017	0.011	0.008	0.011	0.014	0.012	0.017	0.010	0.011	0.006	0.004	0.012	0.006	0.006
LPA(14:0)	$C_3H_6O_5P$	[M-H]-	0.000	0.000	0.000	0.000	0.004	0.000	0.000	0.000	0.000	0.000	0.002	0.004	0.003	0.001	0.008	0.006
LPA(16:0)	$C_3H_6O_5P$	[M-H]-	0.028	0.017	0.039	0.016	0.019	0.021	0.029	0.017	0.033	0.020	0.016	0.021	0.011	0.010	0.004	0.006
LPA(18:0)	$C_3H_6O_5P$	[M-H]-	0.014	0.006	0.004	0.026	0.000	0.005	0.014	0.006	0.005	0.005	0.000	0.000	0.000	0.000	0.000	0.000
LPC(13:0)	$C_{13}H_{25}O_2$	[M+OAc]-	0.238	0.268	0.159	0.229	0.131	0.226	0.208	0.205	0.219	0.145	0.162	0.179	0.183	0.158	0.206	0.187
LPC(16:0)	$C_{16}H_{31}O_2$	[M+OAc]-	0.013	0.007	0.006	0.020	0.009	0.011	0.010	0.010	0.009	0.010	0.011	0.008	0.004	0.009	0.007	0.005
LPC(18:3)	$C_{18}H_{29}O_2$	[M+OAc]-	0.019	0.008	0.007	0.007	0.011	0.010	0.014	0.014	0.016	0.011	0.019	0.011	0.009	0.019	0.009	0.010
LPC(18:2)	$C_{18}H_{31}O_2$	[M+OAc]-	0.021	0.011	0.009	0.010	0.013	0.009	0.012	0.010	0.013	0.011	0.024	0.013	0.010	0.022	0.010	0.011
LPC(18:1)	$C_{18}H_{33}O_2$	[M+OAc]-	0.003	0.002	0.002	0.002	0.002	0.002	0.003	0.002	0.003	0.002	0.004	0.003	0.002	0.004	0.002	0.002
LPC(19:0)	$C_{19}H_{37}O_2$	[M+OAc]-	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
LPE(14:0)	$C_{14}H_{27}O_2$	[M-H]-	0.075	0.086	0.063	0.075	0.038	0.064	0.071	0.081	0.072	0.046	0.068	0.077	0.069	0.065	0.064	0.066
LPE(16:0)	$C_{16}H_{31}O_2$	[M-H]-	0.014	0.005	0.004	0.006	0.008	0.012	0.010	0.014	0.010	0.007	0.007	0.004	0.004	0.009	0.004	0.004
LPE(18:3)	$C_{18}H_{29}O_2$	[M-H]-	0.008	0.004	0.003	0.005	0.006	0.007	0.009	0.009	0.010	0.004	0.010	0.006	0.005	0.012	0.005	0.007
LPE(18:2)	$C_{18}H_{31}O_2$	[M-H]-	0.013	0.007	0.007	0.006	0.010	0.008	0.011	0.011	0.011	0.005	0.014	0.010	0.009	0.019	0.008	0.010
LPE(18:1)	$C_{18}H_{33}O_2$	[M-H]-	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.003	0.001	0.006	0.001	0.001	0.002	0.001	0.001
LPE(18:0)	$C_{18}H_{35}O_2$	[M-H]-	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
LPG(14:0)	$C_{14}H_{27}O_2$	[M-H]-	0.063	0.083	0.058	0.059	0.000	0.059	0.065	0.061	0.064	0.007	0.052	0.055	0.057	0.051	0.061	0.060
LPG(18:0)	$C_{18}H_{35}O_2$	[M-H]-	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
LPI(18:3)	$C_6H_{10}O_8P$	[M-H]-	0.020	0.013	0.014	0.013	0.010	0.013	0.021	0.019	0.016	0.013	0.017	0.008	0.006	0.016	0.006	0.007
MGDG(18:3/7:1-O)	$C_7H_{11}O_3$	[M+OAc]-	0.003	0.004	0.003	0.003	0.001	0.003	0.003	0.004	0.003	0.001	0.002	0.002	0.001	0.002	0.002	0.002
MGDG(9:1-O/16:3)	$C_9H_{15}O_3$	[M+OAc]-	0.011	0.011	0.009	0.007	0.003	0.011	0.009	0.012	0.008	0.004	0.007	0.006	0.006	0.006	0.006	0.005
MGDG(18:3/7:1-2O)	$C_7H_{11}O_4$	[M+OAc]-	0.001	0.001	0.001	0.001	0.000	0.001	0.001	0.001	0.001	0.001	0.001	0.000	0.001	0.001	0.000	0.000
MGDG(9:1-2O/16:3)	$C_9H_{15}O_4$	[M+OAc]-	0.001	0.001	0.002	0.003	0.000	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.000	0.001	0.001	0.000
MGDG(9:1-O/18:3)	$C_9H_{15}O_3$	[M+OAc]-	0.005	0.004	0.005	0.004	0.002	0.004	0.004	0.005	0.004	0.002	0.003	0.002	0.002	0.003	0.002	0.003
MGDG(9:1-2O/18:3)	$C_9H_{15}O_4$	[M+OAc]-	0.001	0.001	0.002	0.003	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.000	0.000
MGDG(12:3-O/18:3)	$C_{18}H_{29}O_2$	[M-H]-	0.007	0.004	0.006	0.004	0.003	0.005	0.011	0.007	0.007	0.005	0.009	0.005	0.004	0.006	0.003	0.004
MGDG(18:3/16:3)	$C_{18}H_{29}O_2$	[M+OAc]-	65.955	63.068	57.596	60.533	54.036	64.722	68.263	66.860	65.068	57.549	53.682	49.135	50.404	48.014	55.873	51.414
MGDG(18:3/16:2)	$C_{18}H_{29}O_2$	[M+OAc]-	1.956	2.183	2.177	2.482	1.632	1.052	1.031	0.780	1.036	0.889	1.258	1.084	1.089	1.041	1.091	1.097
MGDG(18:3/16:1)	$C_{18}H_{29}O_2$	[M+OAc]-	0.960	0.856	0.962	1.024	0.555	0.445	0.450	0.392	0.521	0.464	0.638	0.459	0.458	0.377	0.488	0.449
MGDG(18:3/16:0)	$C_{18}H_{29}O_2$	[M+OAc]-	0.434	0.349	0.398	0.398	0.239	0.349	0.384	0.480	0.424	0.281	0.303	0.252	0.251	0.263	0.273	0.254
MGDG(16:0/16:0)	$C_{16}H_{31}O_2$	[M+OAc]-	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
MGDG(18:0/16:0)	$C_{18}H_{35}O_2$	[M+OAc]-	0.061	0.065	0.039	0.044	0.040	0.057	0.048	0.020	0.034	0.021	0.000	0.000	0.063	0.036	0.025	0.043
MGDG(18:3/16:4-O)	$C_{16}H_{23}O_3$	[M+OAc]-	0.030	0.027	0.027	0.024	0.019	0.030	0.032	0.034	0.032	0.019	0.022	0.020	0.020	0.023	0.023	0.023
MGDG(18:4-O/16:3)	$C_{18}H_{27}O_3$	[M+OAc]-	0.042	0.031	0.026	0.023	0.019	0.042	0.092	0.048	0.080	0.024	0.023	0.018	0.015	0.041	0.013	0.021
MGDG(18:3/17:0)	$C_{17}H_{33}O_2$	[M+OAc]-	0.035	0.034	0.033	0.036	0.030	0.023	0.022	0.022	0.022	0.020	0.022	0.017	0.019	0.017	0.020	0.019
MGDG(18:4-O/16:4-O)	$C_{16}H_{23}O_3$	[M+OAc]-	0.036	0.010	0.006	0.007	0.011	0.059	0.066	0.043	0.168	0.028	0.004	0.014	0.009	0.043	0.003	0.007
MGDG(18:4-O/16:4-O)(2)	$C_{18}H_{27}O_3$	[M+OAc]-	0.072	0.028	0.024	0.023	0.032	0.112	0.125	0.089	0.320	0.062	0.016	0.027	0.022	0.080	0.012	0.024
MGDG(18:3/18:3)	$C_{18}H_{29}O_2$	[M+OAc]-	12.793	12.231	12.143	13.161	10.568	11.955	11.150	12.910	11.843	10.709	8.601	8.886	9.156	8.349	8.877	8.998
MGDG(18:2/18:3)	$C_{18}H_{29}O_2$	[M+OAc]-	1.502	1.557	1.606	1.696	1.411	1.203	1.189	1.325	1.359	1.213	1.104	1.021	1.036	1.107	1.054	1.063
MGDG(18:3-O/16:4-O)	$C_{18}H_{29}O_3$	[M+OAc]-	0.003	0.002	0.002	0.004	0.002	0.002	0.003	0.003	0.002	0.001	0.002	0.001	0.001	0.002	0.002	0.002
MGDG(18:4-O/16:3-O)	$C_{18}H_{27}O_3$	[M+OAc]-	0.002	0.002	0.002	0.001	0.002	0.002	0.008	0.002	0.005	0.001	0.004	0.002	0.001	0.003	0.001	0.001
MGDG(18:3-2O/16:3)	$C_{18}H_{27}O_3$	[M+OAc]-	0.346	0.362	0.222	0.196	0.256	0.364	0.407	0.399	0.421	0.299	0.069	0.101	0.092	0.067	0.077	0.083
MGDG(18:0/18:3)	$C_{18}H_{29}O_2$	[M+OAc]-	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
MGDG(18:0/18:0)	$C_{18}H_{35}O_2$	[M+OAc]-	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.014	0.005	0.000	0.000	0.000	0.000
MGDG(18:5-2O/16:4-O)	$C_{16}H_{23}O_3$	[M+OAc]-	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.000	0.001	0.001	0.001
MGDG(18:4-O/18:3)	$C_{18}H_{27}O_3$	[M+OAc]-	0.013	0.011	0.012	0.010	0.007	0.015	0.018	0.018	0.021	0.008	0.008	0.007	0.005	0.009	0.006	0.007
MGDG(18:4-2O/16:4-O)	$C_{16}H_{23}O_3$	[M+OAc]-	0.002	0.001	0.002	0.001	0.001	0.002	0.003	0.002	0.004	0.001	0.001	0.001	0.001	0.002	0.001	0.001
MGDG(18:4-O/18:2)	$C_{18}H_{27}O_3$	[M+OAc]-	0.006	0.002	0.003	0.002	0.003	0.004	0.009	0.003	0.009	0.002	0.003	0.003	0.000	0.006	0.000	0.001
MGDG(18:3-2O/16:4-O)	$C_{16}H_{23}O_3$	[M+OAc]-	0.004	0.003	0.002	0.001	0.002	0.004	0.008	0.004	0.010	0.002	0.001	0.001	0.001	0.004	0.001	0.001
MGDG(18:3-2O/16:4-O)	$C_{18}H_{27}O_3$	[M+OAc]-	0.009	0.006	0.005	0.004	0.006	0.008	0.015	0.009	0.019	0.006	0.002	0.003	0.003	0.008	0.001	0.003
MGDG(18:4-O/18:4-O)	$C_{18}H_{27}O_3$	[M+OAc]-	0.019	0.005	0.007	0.006	0.007	0.031	0.035	0.029	0.112	0.016	0.005	0.013	0.005	0.021	0.002	0.005
MGDG(20:3/18:3)	$C_{18}H_{29}O_2$	[M+OAc]-	0.068	0.061	0.065	0.055	0.050	0.055	0.059	0.061	0.055	0.050	0.049	0.042	0.044	0.039	0.043	0.036
MGDG(18:4-O/18:3-O)	$C_{18}H_{27}O_3$	[M+OAc]-	0.002	0.002	0.002	0.001	0.002	0.003	0.003	0.003	0.002	0.002	0.001	0.001	0.001	0.002	0.001	0.001
MGDG(20:2/18:3)	$C_{18}H_{29}O_2$	[M+OAc]-	0.026	0.028	0.033	0.028	0.017	0.027	0.033	0.027	0.030	0.016	0.058	0.042	0.049	0.049	0.054	0.049
MGDG(20:1/18:3)	$C_{18}H_{29}O_2$	[M+OAc]-	0.151	0.145	0.108	0.098	0.117	0.144	0.149	0.169	0.166	0.118	0.044	0.053	0.046	0.044	0.050	0.048
MGDG(18:3-2O/18:3) AND SQDG(18:4-O/18:4-O)	$C_{18}H_{27}O_3$	[M+OAc]-	0.123	0.116	0.089	0.075	0.098	0.118	0.127	0.144	0.143	0.103	0.018	0.034	0.030	0.023	0.026	0.027
MGDG(18:5-2O/18:4-O)	$C_{18}H_{27}O_3$	[M+OAc]-	0.002	0.002	0.003	0.002	0.001	0.002	0.003	0.002	0.002	0.002	0.001	0.001	0.000	0.001	0.001	0.001
MGDG(18:4-O/18:4-2O)	$C_{18}H_{27}O_3$	[M+OAc]-	0.002	0.001	0.001	0.001	0.001	0.002	0.003	0.002	0.005	0.001	0.001	0.001	0.001	0.002	0.000	0.001
MGDG(18:4-O/18:3-2O)	$C_{18}H_{27}O_3$	[M+OAc]-	0.004	0.002	0.001	0.002	0.002	0.002	0.003	0.004	0.004	0.002	0.001	0.001	0.001	0.003	0.001	0.001
MGDG(18:3-2O/18:3-O)	$C_{18}H_{27}O_3$	[M+OAc]-	0.002	0.002	0.002	0.001	0.001	0.001	0.002	0.002	0.002	0.001	0.001	0.001	0.001	0.002	0.000	0.000
MGDG(18:4-O/18:4-3O)	$C_{18}H_{27}O_3$	[M+OAc]-	0.003	0.002	0.002	0.002	0.002	0.002	0.005	0.002	0.004	0.001	0.001	0.001	0.001	0.002	0.001	0.001
MGDG(18:4-O/18:3-3O)	$C_{18}H_{27}O_3$	[M+OAc]-	0.001	0.001	0.002	0.001	0.001	0.001	0.002	0.001	0.002	0.001	0.001	0.001	0.001	0.002	0.001	0.001
MGDG(18:4-O/18:3-4O)	$C_{18}H_{27}O_3$	[M+OAc]-	0.002	0.001	0.004	0.001	0.001	0.001	0.003	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001
MGMG(16:3)	$C_{16}H_{25}O_2$	[M+OAc]-	0.111	0.036	0.035	0.026	0.036	0.036	0.102	0.060	0.099	0.035	0.040	0.023	0.022	0.028	0.024	0.024
MGMG(16:0)	$C_{16}H_{31}O_2$	[M+OAc]-	0.068	0.024	0.018	0.042	0.038	0.043	0.041	0.067	0.029	0.057	0.008	0.008	0.001	0.005	0.002	0.004
MGMG(18:3)	$C_{18}H_{29}O_2$	[M+OAc]-	0.044	0.025	0.022	0.019	0.020	0.022	0.031	0.031	0.041	0.018	0.025	0.024	0.020	0.029	0.024	0.022
MGMG(18:4-O)	$C_{18}H_{27}O_3$	[M+OAc]-	0.012	0.018	0.021	0.010	0.010	0.006	0.007	0.005	0.009	0.010	0.002	0.002	0.001	0.002	0.001	0.000
NAPE(18:3/34:3)	$C_{18}H_{29}O_2$	[M-H]-	0.003	0.000	0.000	0.001	0.000	0.004	0.000	0.003	0.003	0.003	0.001	0.001	0.003	0.000	0.002	0.002
NAPE(18:3/36:6)	$C_{18}H_{29}O_2$	[M-H]-	0.012	0.010	0.010	0.011	0.011	0.012	0.013	0.014	0.013	0.011	0.010	0.008	0.007	0.009	0.007	0.008
PA(14:0/14:0)	$C_{14}H_{27}O_2$	[M-H]-	0.064	0.085	0.058	0.063	0.025	0.057	0.068	0.056	0.048	0.030	0.057	0.062	0.059	0.065	0.068	0.057
PA(16:3/18:3)	$C_{18}H_{29}O_2$	[M-H]-	0.002	0.001	0.001	0.001	0.001	0.002	0.003	0.003	0.003	0.001	0.003	0.003	0.001	0.004	0.001	0.002
PA(16:1/18:3)	$C_{18}H_{29}O_2$	[M-H]-	0.009	0.008	0.007	0.005	0.005	0.009	0.012	0.011	0.009	0.005	0.010	0.008	0.005	0.007	0.005	0.006
PA(16:0/18:3)	$C_{16}H_{31}O_2$	[M-H]-	0.280	0.123	0.097	0.160	0.175	0.199	0.332	0.231	0.264	0.153	0.416	0.271	0.179	0.245	0.113	0.225
PA(16:0/18:2)	$C_{16}H_{31}O_2$	[M-H]-	0.280	0.108	0.087	0.107	0.174	0.131	0.244	0.143	0.179	0.100	0.431	0.292	0.162	0.252	0.099	0.219
PA(16:0/18:1)	$C_{16}H_{31}O_2$	[M-H]-	0.038	0.016	0.011	0.018	0.018	0.018	0.028	0.019	0.015	0.015	0.039	0.023	0.015	0.020	0.009	0.015
PA(18:3/18:3)	$C_{18}H_{29}O_2$	[M-H]-	0.116	0.040	0.031	0.025	0.067	0.060	0.150	0.074	0.102	0.043	0.271	0.165	0.106	0.113	0.054	0.152
PA(18:2/18:3)	$C_{18}H_{29}O_2$	[M-H]-	0.129	0.042	0.032	0.036	0.078	0.048	0.110	0.049	0.067	0.039	0.268	0.179	0.112	0.138	0.056	0.136
PA(18:1/18:3)	$C_{18}H_{29}O_2$	[M-H]-	0.030	0.010	0.008	0.007	0.011	0.011	0.029	0.014	0.014	0.007	0.048	0.032	0.022	0.020	0.013	0.026
PA(18:2/18:2)	$C_{18}H_{31}O_2$	[M-H]-	0.171	0.055	0.041	0.047	0.097	0.047	0.107	0.050	0.077	0.046	0.375	0.272	0.158	0.219	0.091	0.223
PA(18:0/18:3)	$C_{18}H_{29}O_2$	[M-H]-	0.034	0.005	0.004	0.005	0.015	0.010	0.030	0.010	0.013	0.007	0.013	0.008	0.005	0.006	0.004	0.007
PA(18:0/18:2)	$C_{18}H_{31}O_2$	[M-H]-	0.049	0.007	0.006	0.007	0.021	0.008	0.026	0.007	0.011	0.006	0.016	0.011	0.007	0.008	0.005	0.008
PA(20:0/20:0)	$C_{20}H_{39}O_2$	[M-H]-	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
PC(12:0/12:0)	$C_{12}H_{23}O_2$	[M+OAc]-	0.062	0.092	0.035	0.064	0.000	0.037	0.058	0.056	0.048	0.000	0.045	0.046	0.016	0.030	0.035	0.024

Table S-5.5 Oxylipin lipidomics analysis of wild type, *lpa66* mutants, and *dot4* mutants.

	chemical formula	adduct	WT1	WT2	WT3	WT4	WT5	*lpa66* 1	*lpa66* 2	*lpa66* 3	*lpa66* 4	*lpa66* 5	*dot4* 1	*dot4* 2	*dot4* 3	*dot4* 4	*dot4* 5	*dot4* 6
PC(16:0/16:3)	C16H31O2	[M+OAc]-	0.048	0.038	0.150	0.044	0.039	0.050	0.079	0.051	0.040	0.067	0.047	0.026	0.029	0.041	0.027	0.027
PC(16:0/16:1)	C16H31O2	[M+OAc]-	0.203	0.145	0.507	0.178	0.173	0.180	0.291	0.200	0.141	0.284	0.249	0.149	0.147	0.236	0.157	0.159
PC(16:0/16:0)	C16H31O2	[M+OAc]-	0.256	0.195	0.642	0.269	0.197	0.175	0.251	0.165	0.135	0.282	0.285	0.174	0.160	0.265	0.165	0.178
PC(18:3/16:3)	C18H29O2	[M+OAc]-	0.400	0.313	0.422	0.302	0.349	0.502	0.538	0.547	0.496	0.516	0.399	0.361	0.375	0.376	0.428	0.366
PC(16:1/18:3)	C18H29O2	[M+OAc]-	0.548	0.433	1.392	0.493	0.477	0.531	0.874	0.546	0.387	0.750	0.638	0.377	0.417	0.634	0.438	0.442
PC(16:0/18:3)	C16H31O2	[M+OAc]-	1.251	1.112	1.241	1.094	1.361	1.528	1.553	1.618	1.519	1.755	1.152	1.145	1.214	1.258	1.279	1.229
PC(16:0/18:2)	C16H31O2	[M+OAc]-	1.297	1.270	1.559	1.418	1.463	1.047	1.000	0.906	1.010	1.320	1.193	1.112	1.137	1.146	1.237	1.116
PC(16:0/18:1)	C16H31O2	[M+OAc]-	0.273	0.256	0.406	0.336	0.247	0.265	0.220	0.188	0.213	0.255	0.216	0.150	0.181	0.199	0.186	0.195
PC(16:0/18:3-O)	C18H29O3	[M+OAc]-	0.028	0.018	0.030	0.019	0.014	0.028	0.025	0.024	0.027	0.017	0.013	0.011	0.012	0.013	0.012	0.013
PC(18:3/18:3)	C18H29O2	[M+OAc]-	2.762	2.474	2.971	2.556	3.277	3.908	4.042	4.031	3.699	3.891	2.455	2.414	2.746	2.728	3.027	2.808
PC(18:2/18:3)	C18H29O2	[M+OAc]-	2.899	2.836	3.186	3.046	3.609	3.108	3.165	2.884	3.145	3.556	2.667	2.683	2.902	2.902	3.031	2.832
PC(18:1/18:3)	C18H29O2	[M+OAc]-	0.639	0.623	0.872	0.690	0.742	0.827	0.794	0.661	0.711	0.809	0.731	0.669	0.686	0.648	0.784	0.752
PC(18:2/18:2)	C18H31O2	[M+OAc]-	3.533	3.795	4.469	4.377	4.531	2.470	2.440	1.987	2.542	3.327	3.621	3.423	3.459	3.677	3.678	3.502
PC(18:0/18:3)	C18H29O2	[M+OAc]-	0.313	0.294	0.463	0.354	0.424	0.395	0.384	0.354	0.392	0.545	0.302	0.252	0.273	0.292	0.270	0.259
PC(18:0/18:2)	C18H31O2	[M+OAc]-	0.345	0.378	0.509	0.443	0.499	0.309	0.283	0.206	0.272	0.421	0.366	0.315	0.318	0.334	0.331	0.308
PC(16:0/18:3-2O)	C18H27O3	[M+OAc]-	0.014	0.012	0.013	0.007	0.013	0.015	0.017	0.016	0.015	0.020	0.003	0.004	0.004	0.004	0.004	0.004
PC(18:3/18:3-O)	C18H29O3	[M+OAc]-	0.021	0.019	0.023	0.018	0.014	0.026	0.026	0.026	0.026	0.015	0.011	0.013	0.013	0.012	0.012	0.012
PC(18:2/18:3-O)	C18H29O3	[M+OAc]-	0.019	0.018	0.018	0.018	0.012	0.017	0.018	0.017	0.019	0.012	0.009	0.013	0.012	0.011	0.011	0.010
PC(20:3/18:3)	C18H29O2	[M+OAc]-	0.028	0.024	0.054	0.023	0.027	0.033	0.039	0.033	0.028	0.038	0.041	0.026	0.027	0.031	0.027	0.028
PC(20:2/18:3)	C18H29O2	[M+OAc]-	0.039	0.036	0.064	0.033	0.039	0.043	0.052	0.040	0.026	0.053	0.058	0.042	0.048	0.060	0.052	0.047
PC(18:3/18:3-2O)	C18H27O3	[M+OAc]-	0.011	0.012	0.009	0.006	0.013	0.015	0.017	0.017	0.018	0.016	0.003	0.004	0.004	0.004	0.003	0.003
PC(20:1/18:3)	C18H29O2	[M+OAc]-	0.077	0.079	0.103	0.068	0.097	0.126	0.126	0.118	0.118	0.140	0.074	0.063	0.069	0.074	0.068	0.059
PC(20:1/18:3)	C20H37O2	[M+OAc]-	0.015	0.015	0.018	0.014	0.019	0.016	0.015	0.013	0.014	0.017	0.011	0.010	0.010	0.011	0.010	0.010
PC(18:2/18:3-2O)	C18H27O3	[M+OAc]-	0.010	0.010	0.007	0.006	0.010	0.010	0.011	0.010	0.011	0.013	0.002	0.004	0.003	0.004	0.003	0.003
PC(20:0/18:3)	C18H29O2	[M+OAc]-	0.038	0.042	0.042	0.028	0.039	0.047	0.055	0.047	0.048	0.052	0.097	0.059	0.061	0.078	0.078	0.067
PC(20:0/18:2)	C18H31O2	[M+OAc]-	0.042	0.049	0.061	0.033	0.055	0.038	0.048	0.031	0.039	0.054	0.040	0.032	0.033	0.039	0.035	0.034
PC(22:2/18:3)	C18H29O2	[M+OAc]-	0.020	0.020	0.036	0.021	0.019	0.024	0.029	0.022	0.021	0.027	0.037	0.030	0.032	0.037	0.032	0.031
PC(22:1/18:3)	C18H29O2	[M+OAc]-	0.026	0.027	0.033	0.023	0.024	0.036	0.036	0.034	0.032	0.039	0.053	0.028	0.027	0.041	0.027	0.024
PC(22:0/18:3)	C18H29O2	[M+OAc]-	0.016	0.016	0.029	0.016	0.015	0.022	0.023	0.020	0.020	0.023	0.021	0.017	0.017	0.019	0.015	0.015
PC(22:0/18:2)	C18H31O2	[M+OAc]-	0.019	0.021	0.039	0.024	0.020	0.020	0.022	0.018	0.020	0.022	0.031	0.020	0.021	0.026	0.020	0.018
PC(24:1/24:1)	C24H45O2	[M+OAc]-	0.000	0.000	0.000	0.000	0.025	0.000	0.000	0.000	0.000	0.036	0.000	0.000	0.000	0.000	0.000	0.000
PE(12:0/12:0)	C12H23O2	[M-H]-	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
PE(16:0/16:3)	C16H31O2	[M-H]-	0.006	0.003	0.004	0.006	0.005	0.007	0.007	0.009	0.006	0.006	0.004	0.003	0.003	0.004	0.003	0.003
PE(16:0/16:1)	C16H31O2	[M-H]-	0.010	0.004	0.004	0.006	0.005	0.008	0.008	0.012	0.007	0.006	0.006	0.005	0.005	0.005	0.004	0.005
PE(16:0/16:0)	C16H31O2	[M-H]-	0.003	0.002	0.002	0.003	0.002	0.003	0.003	0.003	0.002	0.002	0.003	0.002	0.002	0.002	0.002	0.002
PE(16:1/18:3)	C18H29O2	[M-H]-	0.012	0.012	0.014	0.013	0.016	0.015	0.016	0.016	0.015	0.014	0.015	0.014	0.015	0.015	0.015	0.016
PE(16:0/18:3)	C18H29O2	[M-H]-	0.815	0.853	1.007	0.942	1.118	1.270	1.379	1.469	1.317	1.096	1.006	0.911	1.026	1.022	1.058	1.058
PE(16:0/18:2)	C18H31O2	[M-H]-	1.288	1.460	1.668	1.683	1.867	1.457	1.549	1.507	1.524	1.280	1.422	1.301	1.385	1.415	1.428	1.402
PE(16:0/18:3-O)	C18H29O3	[M-H]-	0.014	0.016	0.015	0.013	0.010	0.020	0.025	0.028	0.026	0.007	0.011	0.015	0.021	0.014	0.018	0.016
PE(18:2-O/16:0)	C18H31O3	[M-H]-	0.007	0.006	0.008	0.008	0.005	0.008	0.007	0.007	0.008	0.004	0.003	0.004	0.003	0.003	0.002	0.003
PE(18:3/18:3)	C18H29O2	[M-H]-	0.286	0.317	0.405	0.353	0.405	0.459	0.463	0.495	0.426	0.381	0.457	0.425	0.476	0.439	0.496	0.532
PE(18:2/18:3)	C18H29O2	[M-H]-	0.425	0.475	0.539	0.532	0.575	0.556	0.552	0.591	0.590	0.543	0.653	0.630	0.679	0.643	0.698	0.709
PE(18:1/18:3)	C18H29O2	[M-H]-	0.092	0.096	0.118	0.117	0.112	0.114	0.111	0.104	0.109	0.115	0.184	0.173	0.191	0.158	0.202	0.203
PE(18:2/18:2)	C18H31O2	[M-H]-	0.769	0.851	0.916	0.942	0.981	0.731	0.733	0.759	0.784	0.800	1.152	1.096	1.081	1.099	1.132	1.144
PE(18:0/18:3)	C18H29O2	[M-H]-	0.145	0.110	0.134	0.117	0.183	0.184	0.189	0.198	0.179	0.305	0.075	0.067	0.067	0.071	0.068	0.072
PE(18:0/18:2)	C18H31O2	[M-H]-	0.195	0.165	0.201	0.193	0.271	0.181	0.189	0.169	0.180	0.321	0.098	0.084	0.083	0.089	0.090	0.086
PE(16:0/18:3-2O)	C18H27O3	[M-H]-	0.002	0.003	0.002	0.001	0.003	0.004	0.005	0.005	0.004	0.003	0.001	0.002	0.001	0.002	0.001	0.001
PE(18:3/18:3-O)	C18H29O3	[M-H]-	0.006	0.007	0.006	0.006	0.005	0.009	0.010	0.013	0.012	0.005	0.004	0.007	0.010	0.006	0.008	0.007
PE(18:2/18:3-O)	C18H29O3	[M-H]-	0.009	0.010	0.008	0.008	0.008	0.010	0.012	0.016	0.015	0.006	0.007	0.011	0.014	0.010	0.011	0.010
PE(16:0/18:3-3O)	C18H29O5	[M-H]-	0.003	0.004	0.003	0.003	0.003	0.004	0.003	0.004	0.005	0.005	0.054	0.043	0.035	0.042	0.041	0.053
PE(20:2/18:3)	C18H29O2	[M-H]-	0.061	0.046	0.061	0.049	0.076	0.065	0.064	0.061	0.060	0.110	0.029	0.026	0.027	0.028	0.029	0.027
PE(20:1/18:3)	C18H29O2	[M-H]-	0.017	0.015	0.021	0.015	0.021	0.020	0.020	0.018	0.017	0.027	0.012	0.011	0.011	0.012	0.013	0.013
PE(18:3/18:3-2O)	C18H27O3	[M-H]-	0.001	0.001	0.001	0.001	0.001	0.002	0.002	0.002	0.002	0.001	0.000	0.001	0.001	0.001	0.001	0.001
PE(18:2/18:3-2O)	C18H27O3	[M-H]-	0.001	0.002	0.001	0.001	0.002	0.001	0.002	0.002	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001
PE(20:0/18:3)	C18H29O2	[M-H]-	0.009	0.008	0.007	0.008	0.015	0.012	0.009	0.010	0.013	0.022	0.007	0.007	0.009	0.008	0.008	0.009
PE(20:0/18:2)	C18H31O2	[M-H]-	0.019	0.020	0.021	0.021	0.027	0.017	0.019	0.019	0.019	0.024	0.015	0.012	0.012	0.013	0.013	0.012
PE(18:3/18:3-3O)	C18H29O5	[M-H]-	0.002	0.002	0.002	0.002	0.001	0.003	0.002	0.003	0.003	0.003	0.024	0.021	0.018	0.020	0.019	0.026
PE(18:2/18:3-3O)	C18H29O5	[M-H]-	0.003	0.003	0.002	0.002	0.002	0.003	0.002	0.003	0.003	0.004	0.037	0.034	0.026	0.032	0.028	0.039
PE(22:0/18:3)	C18H29O2	[M-H]-	0.017	0.017	0.020	0.020	0.023	0.022	0.023	0.021	0.022	0.023	0.021	0.018	0.020	0.020	0.019	0.020
PE(22:0/18:2)	C18H31O2	[M-H]-	0.029	0.032	0.036	0.041	0.046	0.029	0.033	0.027	0.032	0.031	0.033	0.030	0.033	0.029	0.030	0.030
PE(24:0/18:3)	C18H29O2	[M-H]-	0.036	0.035	0.034	0.038	0.042	0.048	0.047	0.050	0.050	0.046	0.033	0.034	0.035	0.032	0.036	0.035
PE(24:1/18:2)	C18H31O2	[M-H]-	0.050	0.047	0.051	0.053	0.055	0.041	0.042	0.044	0.043	0.043	0.045	0.042	0.043	0.042	0.044	0.042
PE(24:0/18:2)	C18H31O2	[M-H]-	0.048	0.047	0.054	0.055	0.061	0.044	0.045	0.041	0.052	0.046	0.044	0.041	0.042	0.043	0.043	0.043
PE(23:0/23:0)	C23H45O2	[M-H]-	0.000	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
PG(12:0/12:0)	C12H23O2	[M-H]-	0.000	0.000	0.001	0.000	0.000	0.000	0.001	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
PG(14:0/14:0)	C14H27O2	[M-H]-	0.034	0.027	0.050	0.026	0.015	0.034	0.034	0.023	0.023	0.029	0.023	0.020	0.007	0.027	0.014	0.010
PG(16:0/16:1)	C16H31O2	[M-H]-	0.266	0.215	0.208	0.201	0.221	0.382	0.416	0.489	0.459	0.395	0.368	0.350	0.325	0.342	0.379	0.344
PG(16:0/16:0)	C16H31O2	[M-H]-	0.326	0.308	0.321	0.374	0.340	0.250	0.253	0.260	0.309	0.268	0.410	0.437	0.438	0.456	0.419	0.441
PG(18:3/16:1)	C18H29O2	[M-H]-	3.692	3.486	3.281	3.128	3.576	4.512	4.549	4.834	4.371	4.392	3.219	2.760	2.741	2.829	3.096	2.802
PG(18:3/16:0)	C16H31O2	[M-H]-	2.196	2.316	2.672	2.771	2.866	1.262	1.102	0.978	1.137	1.342	1.739	1.723	1.842	1.809	1.581	1.768
PG(18:2/16:1)	C18H31O2	[M-H]-	0.455	0.402	0.378	0.350	0.384	0.265	0.288	0.284	0.314	0.383	0.311	0.233	0.210	0.236	0.258	0.224
PG(18:2/16:0)	C16H31O2	[M-H]-	1.035	1.018	1.173	1.205	1.116	0.604	0.564	0.499	0.594	0.563	0.737	0.651	0.657	0.651	0.661	0.648
PG(18:1/16:0)	C16H31O2	[M-H]-	1.093	0.960	1.204	1.190	0.961	0.633	0.605	0.534	0.692	0.624	0.699	0.532	0.547	0.469	0.558	0.524
PG(18:4-O/16:1)	C18H27O3	[M-H]-	0.004	0.003	0.003	0.003	0.003	0.007	0.008	0.007	0.015	0.004	0.003	0.004	0.003	0.006	0.004	0.003
PG(18:4-O/16:0)	C18H27O3	[M-H]-	0.002	0.001	0.002	0.002	0.001	0.001	0.002	0.001	0.003	0.001	0.001	0.002	0.001	0.001	0.001	0.001
PG(18:3-O/16:1)	C18H29O3	[M-H]-	0.018	0.015	0.014	0.013	0.008	0.021	0.022	0.022	0.023	0.012	0.005	0.007	0.005	0.005	0.005	0.005
PG(18:3-O/16:0)	C18H29O3	[M-H]-	0.007	0.007	0.008	0.008	0.005	0.006	0.005	0.005	0.006	0.003	0.005	0.004	0.003	0.004	0.004	0.004
PG(18:2-O/16:1)	C18H31O3	[M-H]-	0.003	0.003	0.002	0.002	0.001	0.002	0.003	0.002	0.003	0.002	0.002	0.002	0.001	0.001	0.001	0.001
PG(18:2/16:0-O)	C16H31O3	[M-H]-	0.009	0.008	0.008	0.008	0.007	0.006	0.007	0.007	0.007	0.008	0.006	0.005	0.004	0.005	0.005	0.004
PG(18:3/18:3)	C18H29O2	[M-H]-	0.054	0.059	0.068	0.064	0.064	0.043	0.040	0.037	0.040	0.038	0.044	0.045	0.043	0.043	0.041	0.044
PG(18:3/18:2)	C18H29O2	[M-H]-	0.067	0.059	0.093	0.059	0.039	0.076	0.122	0.072	0.082	0.023	0.028	0.027	0.020	0.024	0.022	0.023
PG(18:3/18:1)	C18H33O2	[M-H]-	0.009	0.011	0.017	0.014	0.011	0.007	0.009	0.005	0.007	0.010	0.010	0.009	0.007	0.009	0.008	0.010
PG(18:2/18:2)	C18H31O2	[M-H]-	0.041	0.042	0.056	0.050	0.036	0.027	0.028	0.019	0.025	0.026	0.037	0.040	0.031	0.033	0.033	0.029
PG(18:3/18:0)	C18H29O2	[M-H]-	0.031	0.037	0.041	0.038	0.035	0.035	0.037	0.025	0.032	0.028	0.024	0.019	0.020	0.020	0.018	0.019
PG(18:2/18:0)	C18H31O2	[M-H]-	0.034	0.037	0.044	0.049	0.040	0.034	0.034	0.023	0.029	0.026	0.024	0.019	0.019	0.024	0.018	0.020
PG(18:4-O/18:3)	C18H27O3	[M-H]-	0.003	0.003	0.002	0.002	0.002	0.003	0.003	0.003	0.003	0.002	0.001	0.001	0.001	0.001	0.001	0.001
PG(18:4-O/18:2)	C18H27O3	[M-H]-	0.001	0.001	0.001	0.000	0.000	0.001	0.001	0.001	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000
PG(20:0/20:0)	C20H39O2	[M-H]-	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
PI(34:3)	C6H10O8P	[M-H]-	2.779	2.634	2.599	2.319	2.257	3.536	3.912	3.887	4.129	3.252	2.369	2.116	1.810	2.513	1.967	1.894
PI(16:0/18:3)	C16H31O2	[M-H]-	2.084	1.890	1.889	1.846	1.706	2.710	2.852	2.950	2.878	2.473	1.824	1.495	1.349	1.951	1.461	1.405
PI(16:0/18:2)	C16H31O2	[M-H]-	1.878	1.895	1.982	1.998	1.698	1.585	1.601	1.438	1.534	1.520	1.495	1.254	1.026	1.581	1.201	1.073
PI(34:1)	C6H10O8P	[M-H]-	0.371	0.391	0.427	0.387	0.345	0.319	0.340	0.281	0.377	0.329	0.399	0.272	0.203	0.338	0.252	0.235
PI(16:0/18:1)	C16H31O2	[M-H]-	0.107	0.098	0.102	0.134	0.090	0.125	0.122	0.100	0.120	0.111	0.152	0.095	0.075	0.116	0.077	0.080
PI(34:0)	C6H10O8P	[M-H]-	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.001	0.000	0.000	0.000	0.000
PI(16:0/18:0)	C16H31O2	[M-H]-	0.012	0.000	0.025	0.000	0.000	0.002	0.002	0.001	0.000	0.000	0.012	0.000	0.000	0.000	0.000	0.001
PI(36:0)	C6H10O8P	[M-H]-	0.016	0.011	0.009	0.012	0.002	0.015	0.003	0.018	0.000	0.001	0.015	0.000	0.001	0.015	0.006	0.001
PI(18:0/18:0)	C18H35O2	[M-H]-	0.000	0.007	0.000	0.007	0.001	0.000	0.000	0.000	0.003	0.002	0.000	0.001	0.002	0.002	0.004	0.000
PS(14:0/14:0)	C14H27O2	[M-H]-	0.049	0.055	0.055	0.061	0.029	0.040	0.041	0.032	0.026	0.032	0.053	0.041	0.045	0.037	0.041	0.028
PS(16:0/18:3)	C16H31O2	[M-H]-	0.094	0.096	0.087	0.094	0.115	0.132	0.120	0.140	0.115	0.129	0.067	0.056	0.059	0.083	0.065	0.064
PS(20:0/20:0)	C20H39O2	[M-H]-	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
PS(24:0/18:3)	C24H47O2	[M-H]-	0.045	0.053	0.044	0.047	0.052	0.089	0.091	0.110	0.101	0.106	0.046	0.046	0.049	0.056	0.055	0.053
PS(24:0/18:2)	C18H31O2	[M-H]-	0.063	0.071	0.073	0.081	0.063	0.071	0.078	0.069	0.077	0.073	0.054	0.053	0.050	0.065	0.049	0.055
SQDG(32:0)	C6H9O7S	[M-H]-	0.028	0.021	0.027	0.031	0.023	0.027	0.040	0.037	0.038	0.027	0.050	0.031	0.029	0.049	0.030	0.031
SQDG(16:0/16:0)	C16H31O2	[M-H]-	0.033	0.020	0.091	0.027	0.009	0.035	0.062	0.034	0.030	0.022	0.025	0.006	0.005	0.014	0.003	0.003
SQDG(34:3)	C6H9O7S	[M-H]-	0.916	0.847	0.895	0.832	0.896	0.895	0.956	0.930	0.872	0.881	0.937	0.617	0.549	0.772	0.654	0.596
SQDG(16:0/18:3)	C18H29O2	[M-H]-	1.102	0.919	1.816	0.926	0.815	1.237	1.525	1.234	1.139	1.216	0.864	0.691	0.715	0.852	0.812	0.766
SQDG(16:0/18:4-O)	C18H27O3	[M-H]-	0.002	0.001	0.003	0.001	0.001	0.002	0.003	0.002	0.002	0.001	0.001	0.001	0.001	0.003	0.001	0.001
SQDG(36:6)	C6H9O7S	[M-H]-	0.184	0.176	0.203	0.180	0.211	0.242	0.255	0.246	0.232	0.261	0.207	0.158	0.151	0.177	0.153	0.156
SQDG(18:3/18:3) AND MGDG(18:1/18:3)	C18H29O2	[M-H]-	0.081	0.082	0.000	0.012	0.000	0.000	0.007	0.000	0.036	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TrGDG(18:3/16:3)	C18H29O2	[M+OAc]-	0.009	0.009	0.015	0.009	0.006	0.010	0.012	0.013	0.011	0.009	0.014	0.007	0.007	0.011	0.009	0.009

Table S-5.5 Oxylipin lipidomics analysis of wild type, *lpa66* mutants, and *dot4* mutants.

	chemical formula	**adduct**	**WT1**	**WT2**	**WT3**	**WT4**	**WT5**	***lpa66 1***	***lpa66 2***	***lpa66 3***	***lpa66 4***	***lpa66 5***	***dot4 1***	***dot4 2***	***dot4 3***	***dot4 4***	***dot4 5***	***dot4 6***
TrGDG(18:3/18:3)	C18H29O2	[M+OAc]-	0.007	0.006	0.009	0.006	0.005	0.007	0.009	0.008	0.007	0.007	0.011	0.005	0.005	0.013	0.006	0.005
Total Signal Detected			**190.991**	**182.712**	**180.274**	**178.919**	**167.266**	**192.602**	**197.318**	**200.793**	**192.911**	**179.515**	**165.013**	**143.968**	**137.023**	**150.926**	**146.238**	**143.514**

Tables S-5.5 Lipids here are reported as nmol per mg dry weight. Some compound identification produces ambiguities in which case, several compound ID names are listed.

Table S-5.6. Cardiolipin lipidomics analysis of wild type, lpa66 mutants, and dot4 mutants **WT**

Mass	**Compour**	**Compound Na**	**WT 1**	**WT 2**	**WT 3**	**WT 4**	**WT 5**	**ave**	**stdev**	**lpa66 1**	**lpa66 2**	**lpa66 3**	**lpa66 4**	**lpa66 5**	**ave**	**stdev**	**dot4 1**	**dot4 2**	**dot4 3**	**dot4 4**	**dot4 5**	**dot4 6**	**ave**	**stdev**
1417.9	C79H13€	**CL(70:9)**	0.059	0.035	0.040	0.018	0.050	0.040	0.015	0.041	0.065	0.043	0.000	0.067	0.043	0.027	0.051	0.050	0.041	0.046	0.015	0.025	0.038	0.015
1419.9	C79H13€	**CL(70:8)**	0.000	0.012	0.003	0.034	0.002	0.010	0.014	0.008	0.025	0.000	0.020	0.005	0.011	0.010	0.015	0.021	0.000	0.000	0.019	0.012	0.011	0.009
1422	C79H14(	**CL(70:7)**	0.000	0.015	0.010	0.013	0.022	0.012	0.008	0.015	0.000	0.018	0.000	0.005	0.008	0.008	0.003	0.003	0.016	0.013	0.000	0.010	0.007	0.006
1424	C79H14z	**CL(70:6)**	0.009	0.000	0.000	0.002	0.000	0.002	0.004	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.014	0.009	0.004	0.006
1426	C79H144	**CL(70:5)**	0.007	0.000	0.000	0.000	0.000	0.001	0.003	0.000	0.000	0.005	0.000	0.000	0.001	0.002	0.000	0.000	0.000	0.000	0.015	0.000	0.002	0.006
1439.9	C81H134	**CL(72:12)**	0.121	0.098	0.107	0.103	0.091	0.104	0.011	0.185	0.186	0.209	0.171	0.228	0.196	0.022	0.170	0.123	0.123	0.156	0.140	0.173	0.148	0.022
1441.9	C81H13€	**CL(72:11)**	0.393	0.329	0.404	0.431	0.384	0.388	0.037	0.482	0.520	0.470	0.480	0.528	0.496	0.026	0.366	0.345	0.330	0.404	0.348	0.411	0.367	0.033
1443.9	C81H13€	**CL(72:10)**	0.573	0.471	0.558	0.636	0.577	0.563	0.059	0.497	0.557	0.446	0.519	0.540	0.512	0.043	0.381	0.357	0.316	0.421	0.326	0.371	0.362	0.038
1446	C81H14(	**CL(72:9)**	0.342	0.299	0.349	0.434	0.314	0.348	0.052	0.248	0.223	0.233	0.291	0.271	0.253	0.028	0.239	0.203	0.154	0.249	0.227	0.192	0.211	0.035
1448	C81H14z	**CL(72:8)**	0.109	0.123	0.109	0.122	0.119	0.116	0.007	0.056	0.072	0.019	0.056	0.053	0.051	0.019	0.035	0.057	0.038	0.045	0.058	0.046	0.046	0.009
1450	C81H144	**CL(72:7)**	0.007	0.010	0.003	0.018	0.000	0.008	0.007	0.013	0.000	0.000	0.000	0.000	0.003	0.006	0.008	0.008	0.000	0.018	0.002	0.010	0.008	0.006
		Total Cardiolip	**1.621**	**1.392**	**1.582**	**1.811**	**1.560**	**1.593**	**0.150**	**1.545**	**1.647**	**1.443**	**1.536**	**1.696**	**1.573**	**0.100**	**1.268**	**1.166**	**1.017**	**1.352**	**1.163**	**1.261**	**1.205**	**0.116**

Table S-5.6. Lipids are represented as nmol per mg dry weight.