

## **SUPPLEMENTAL DATA**

**Supplemental Table S1** A list of upregulated genes in *LEC1*-OXi plants

**Supplemental Table S2** A list of downregulated genes in *LEC1*-OXi plants

**Supplemental Table S3** Upregulated fatty acid synthetic genes in *LEC1*-OXi plants

Classification of the fatty acid synthetic genes is according to (Beisson et al., 2003).

**Supplemental Table S4** Primers used in this study

**Supplemental Figure S1** Correlation analysis of differentially expressed genes in two biological repeats of the microarray experiment

**Supplemental Figure S2** Biological process ontology map of differentially expressed genes between wild type and *LEC1*-OXi plants

Ontology categories that are significantly enriched among differentially expressed genes are displayed as boxes in the map, the saturation degree of yellow color represents the significance of enrichment. Within each box, the number of genes in the differentially expressed gene list and the number of genes of the whole genome that belong to the selected category are shown as numerator and denominator, respectively. The *p*-value of hypergeometric test for differentially expressed genes within the selected category is shown in parenthesis. Unenriched categories are shown as black dots. Connections between two unenriched categories are shown as dashed black arrows, connections between enriched and unenriched categories are shown as solid black arrows, and connections between two enriched categories are shown as solid red arrows.

**Supplemental Figure S3** Amino acid sequence alignment of AtLEC1, AtL1L, BnLEC1 and BnL1L proteins

The BnLEC1 and BnL1L sequences have been deposited in GenBank under the accession numbers EU371726 and EU371727, respectively. Shaded residues are

conserved among different proteins.

**Beisson F, Koo AJK, Ruuska S, Schwender J, Pollard M, Thelen JJ, Paddock T, Salas JJ, Savage L, Milcamps A, Mhaske VB, Cho Y, Ohlrogge JB** (2003) *Arabidopsis* Genes Involved in Acyl Lipid Metabolism. A 2003 Census of the Candidates, a Study of the Distribution of Expressed Sequence Tags in Organs, and a Web-Based Database. *Plant Physiol.* **132**: 681-697