

Molecular dissection of pea shoot apical meristem

Chui E Wong, Dacheng Liang, Mohan B Singh, Christine Beveridge, Belinda Phipson, Gordon Smyth, and Prem L Bhalla

Supplementary Material

Supplementary Table S1 & Figure S1

(Supplementary Tables S2-S4 – see separate files)

Supplementary Table S1. Functional classification of unigenes according to GO biological processes using BLAST2GO (Conesa et al., 2005). Representative GO categories (at Level 4 or 5) with number of sequences annotated at a child GO term greater than 50 and annotation density of greater than 20 is presented to give a general overview of the annotated transcripts.

GO ID	Term
GO:0007166	cell surface receptor linked signal transduction
GO:0007010	cytoskeleton organization and biogenesis
GO:0044262	cellular carbohydrate metabolic process
GO:0051276	chromosome organization and biogenesis
GO:0042254	ribosome biogenesis and assembly
GO:0030154	cell differentiation
GO:0009651	response to salt stress
GO:0009416	response to light stimulus
GO:0006886	intracellular protein transport
GO:0006259	DNA metabolic process
GO:0031497	chromatin assembly
GO:0065004	protein-DNA complex assembly
GO:0007242	intracellular signaling cascade
GO:0006796	phosphate metabolic process
GO:0016070	RNA metabolic process
GO:0019219	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
GO:0006350	transcription
GO:0006412	translation
GO:0044267	cellular protein metabolic process

Supplementary Figure S1. Phylogenetic analysis of (A) *PsWUS* and (B) *PsANT*-LIKE genes. Phylogenetic trees are constructed using CLUSTAL W (version 1.83) and the results displayed as NJ-tree with branch length. Nucleotide sequences of various genes other than pea were retrieved from public databases (www.arabidopsis.org; www.phytozome.net; www.ncbi.nlm.nih.gov/). WOX: WUSCHEL-related homeobox; AIN: AINTEGUMENTA; AIL:AINTEGUMENTA-LIKE).

