

## **Supplemental Material to:**

**Eduardo González-Grandío and Pilar Cubas\***

**Identification of gene functions associated to active and  
dormant buds in Arabidopsis**

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## **Supplemental Table I**

Expression data from Tatematsu et al. 2005 and Reddy et al. 2013 were retrieved from Gene Omnibus database (<http://www.ncbi.nlm.nih.gov/geo/>) and sorted by FDR. The 1000 most statistically significant up- and down-regulated genes with fold change  $<-1.1$  or  $>1.1$  were used for the analysis (Sheet 1: Gene lists). Activation and dormancy genes of the three experiments were compared pair-wise to obtain common elements lists (Sheet 2: Pairwise comparisons). Genes common for the three experiments were further analyzed using ATTED-II<sup>9</sup>, Mapman<sup>17</sup>, Genevestigator [ENREF\\_12](#)<sup>11</sup> and TAIR (<http://www.arabidopsis.org/>) gene description database (Sheets 3 and 4: Bud activation and bud dormancy genes). Genes in bold are *BRC1*-dependent genes according to Gonzalez-Grandío et al. (2013).

**Supplemental Figure 1. *Bud activation genes co-regulation networks.*** Networks of *bud activation* co-regulated genes from Supplemental Table I were represented using Network Drawer (ATTED-II<sup>9</sup>). Additional co-regulated genes were included. From left to right, cell cycle-related, flavonoid synthesis-related and cytokinin signaling networks. The same applies to the next supplemental figures.

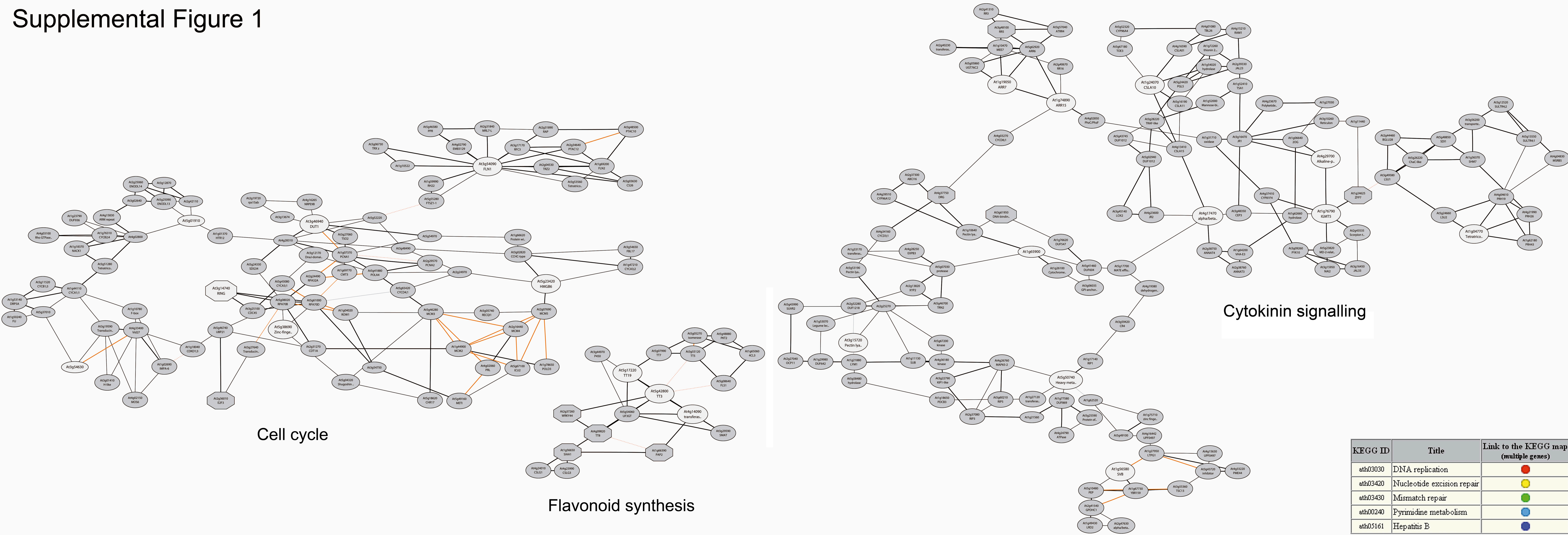
**Supplemental Figure 2. *Bud dormancy genes: ABA signaling co-regulation networks.***

**Supplemental Figure 3. *Bud dormancy genes: auxin and ethylene signaling gene network.***

**Supplemental Figure 4. *Bud dormancy genes: dark-induced, sugar repressed gene network.***

**Supplemental Figure 5. *Bud dormancy genes: autophagy and protein degradation gene network.***

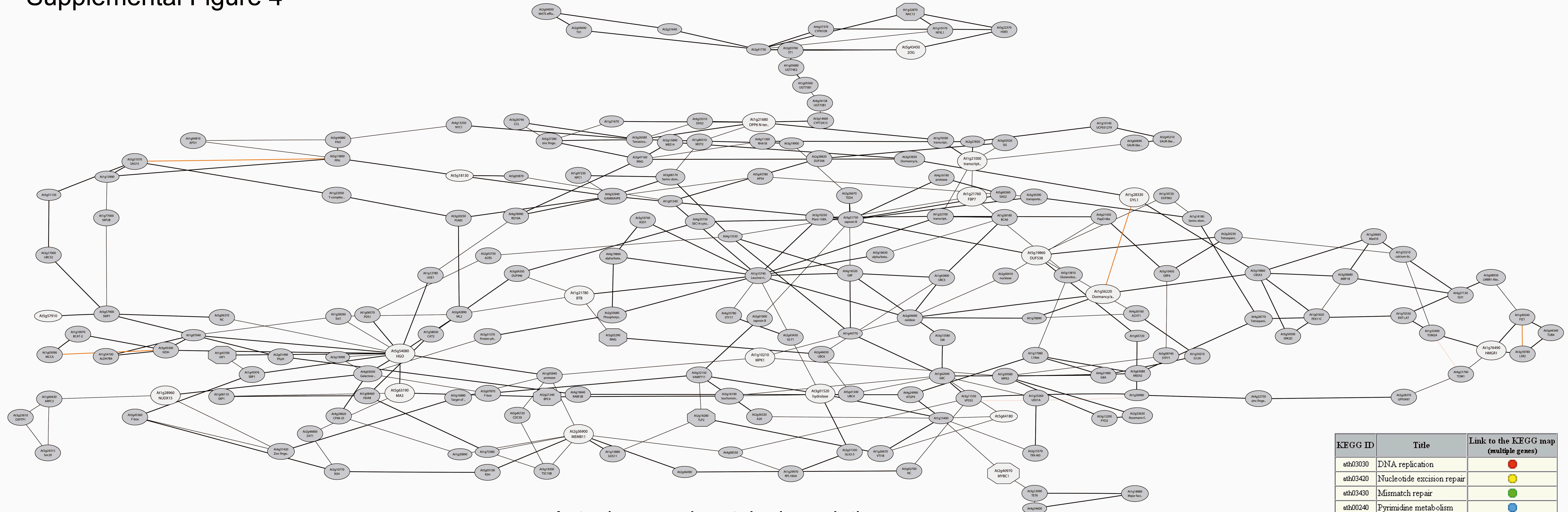
# Supplemental Figure 1







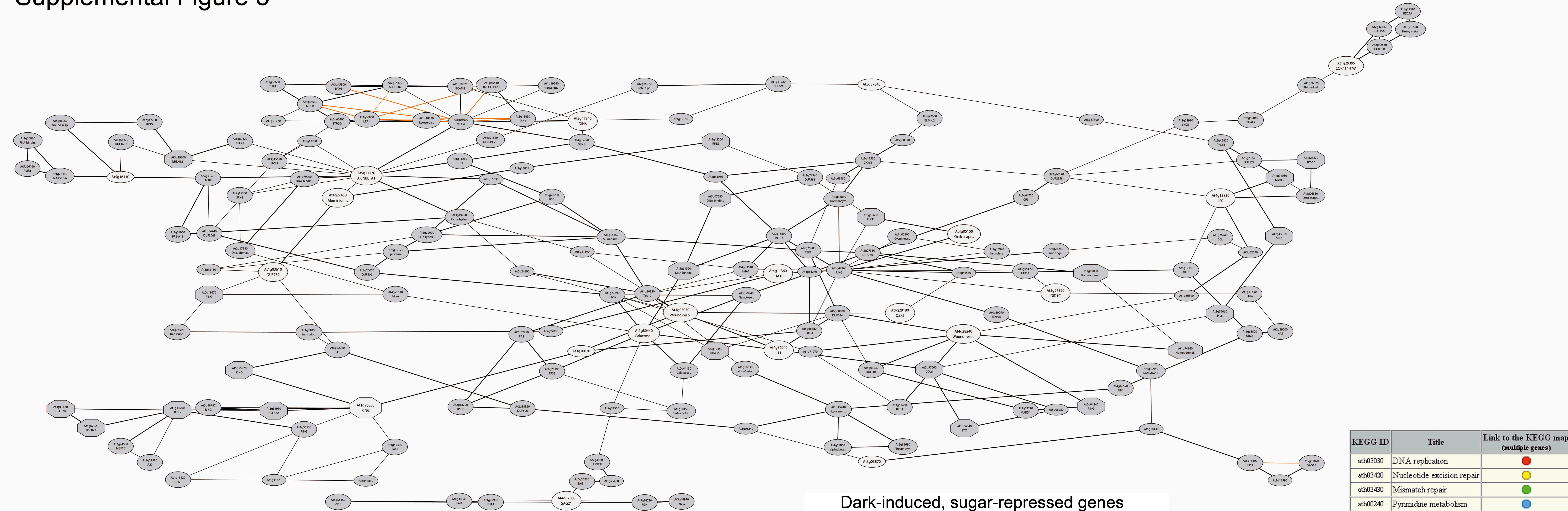
# Supplemental Figure 4



## Autophagy and protein degradation

KEGG ID	Title	Link to the KEGG map (multiple genes)
ath03030	DNA replication	
ath03420	Nucleotide excision repair	
ath03430	Mismatch repair	
ath00240	Pyrimidine metabolism	
ath05161	Hepatitis B	

# Supplemental Figure 5



Dark-induced, sugar-repressed genes

KEGG ID	Title	Link to the KEGG map (multiple genes)
ath03030	DNA replication	
ath03420	Nucleotide excision repair	
ath03430	Mismatch repair	
ath00240	Pyrimidine metabolism	
ath05161	Hepatitis B	