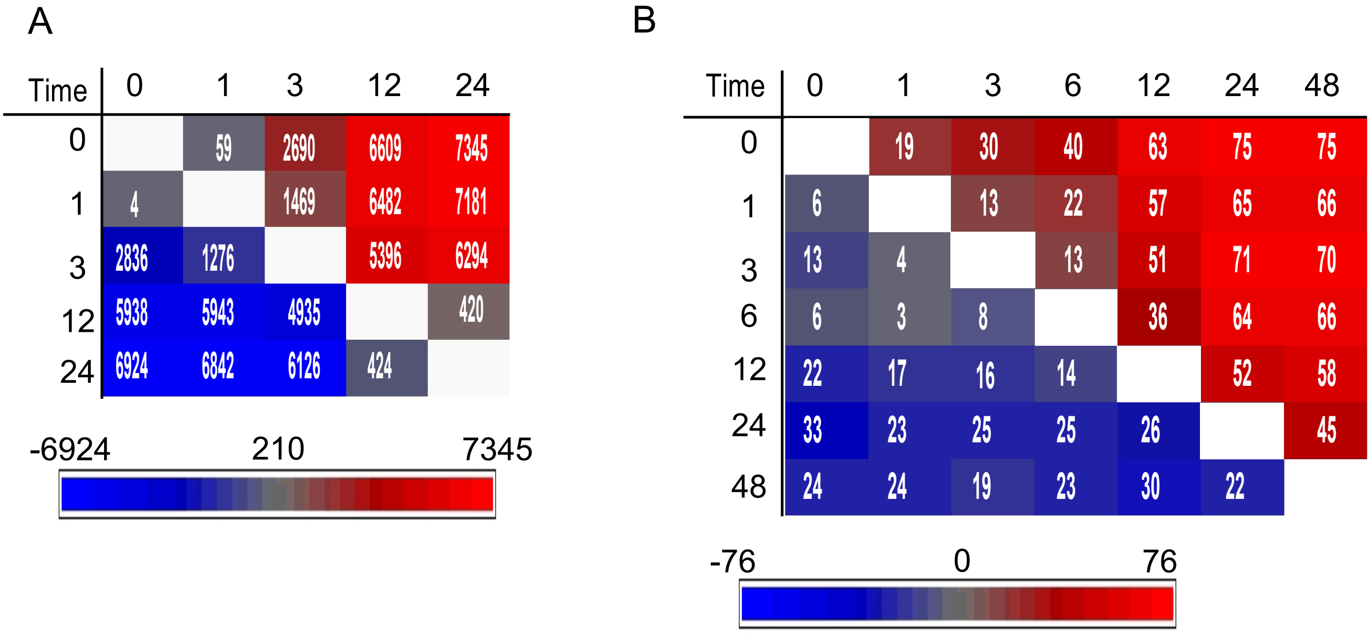


A

Time	0	1	3	12	24
0		59	2690	6609	7345
1	4		1469	6482	7181
3	2836	1276		5396	6294
12	5938	5943	4935		420
24	6924	6842	6126	424	

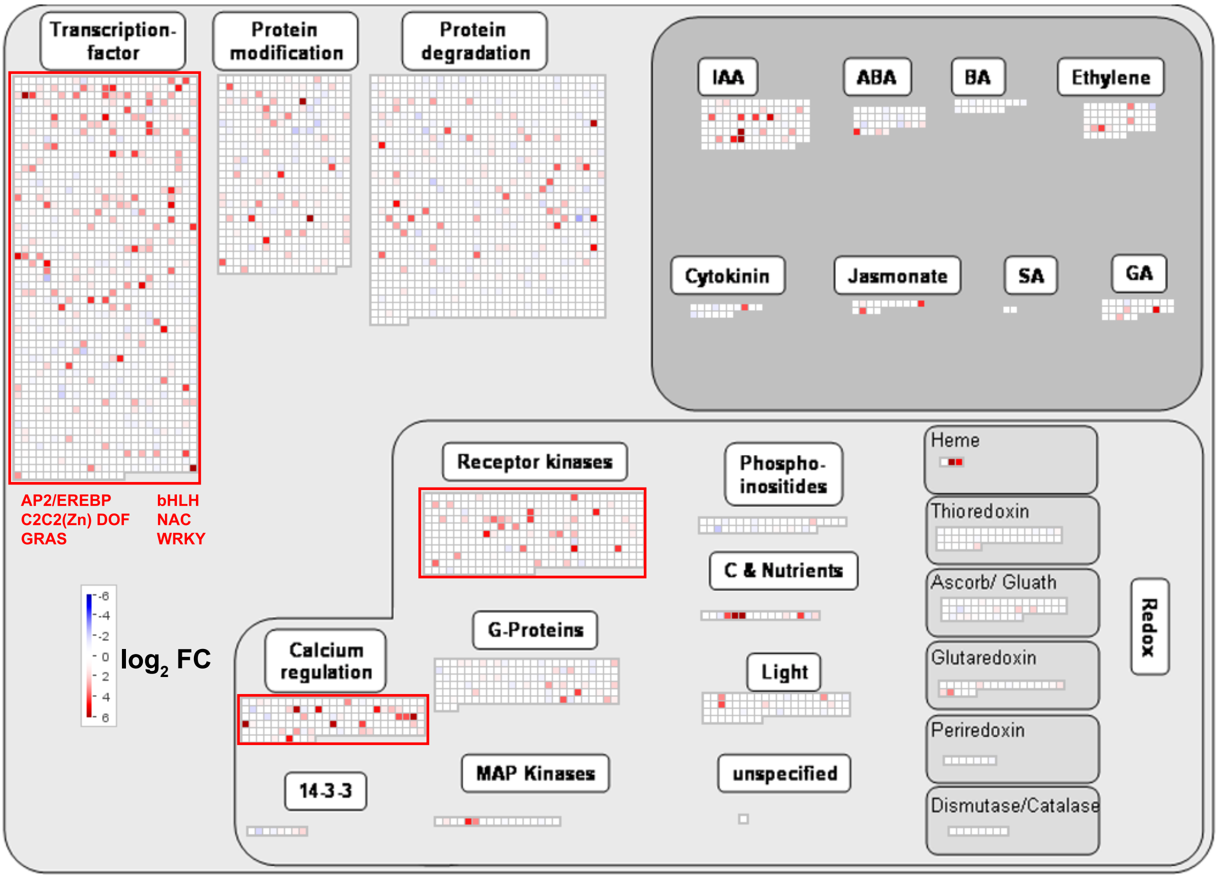
B

Time	0	1	3	6	12	24	48
0		19	30	40	63	75	75
1	6		13	22	57	65	66
3	13	4		13	51	71	70
6	6	3	8		36	64	66
12	22	17	16	14		52	58
24	33	23	25	25	26		45
48	24	24	19	23	30	22	

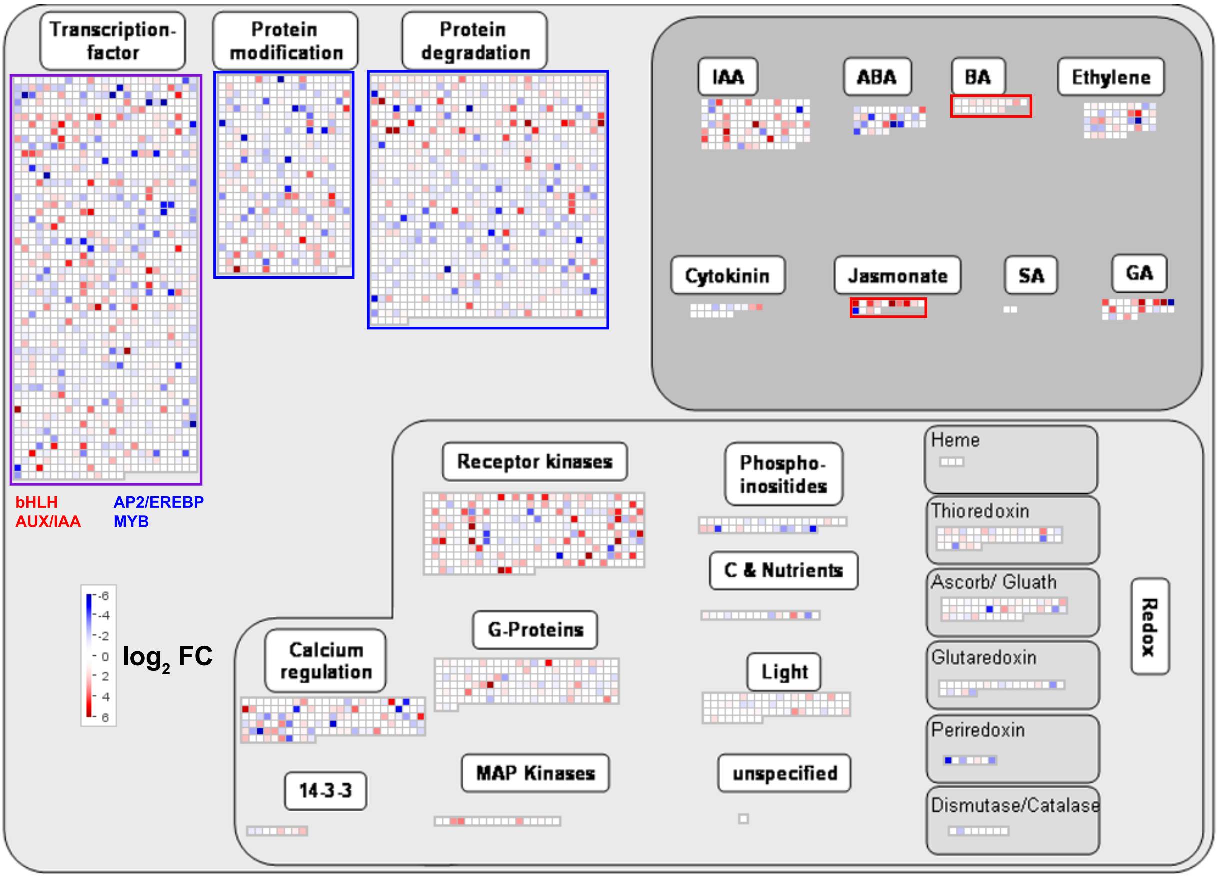
Supplemental Figure 1. Overview of the changes in transcripts and metabolites during germination in rice. A) The number of genes whose transcripts were significantly different in abundance between all combinations of time points. **B)** The number of metabolites that were significantly different in abundance between all combinations of time points. Red = up-regulated, Blue = down-regulated.

Supplemental Figure 2. Two-way comparison of 0 versus 3 HAI and 3 versus 12 HAI using MapMan to visualise an overview of regulation.

0 v 3 HAI

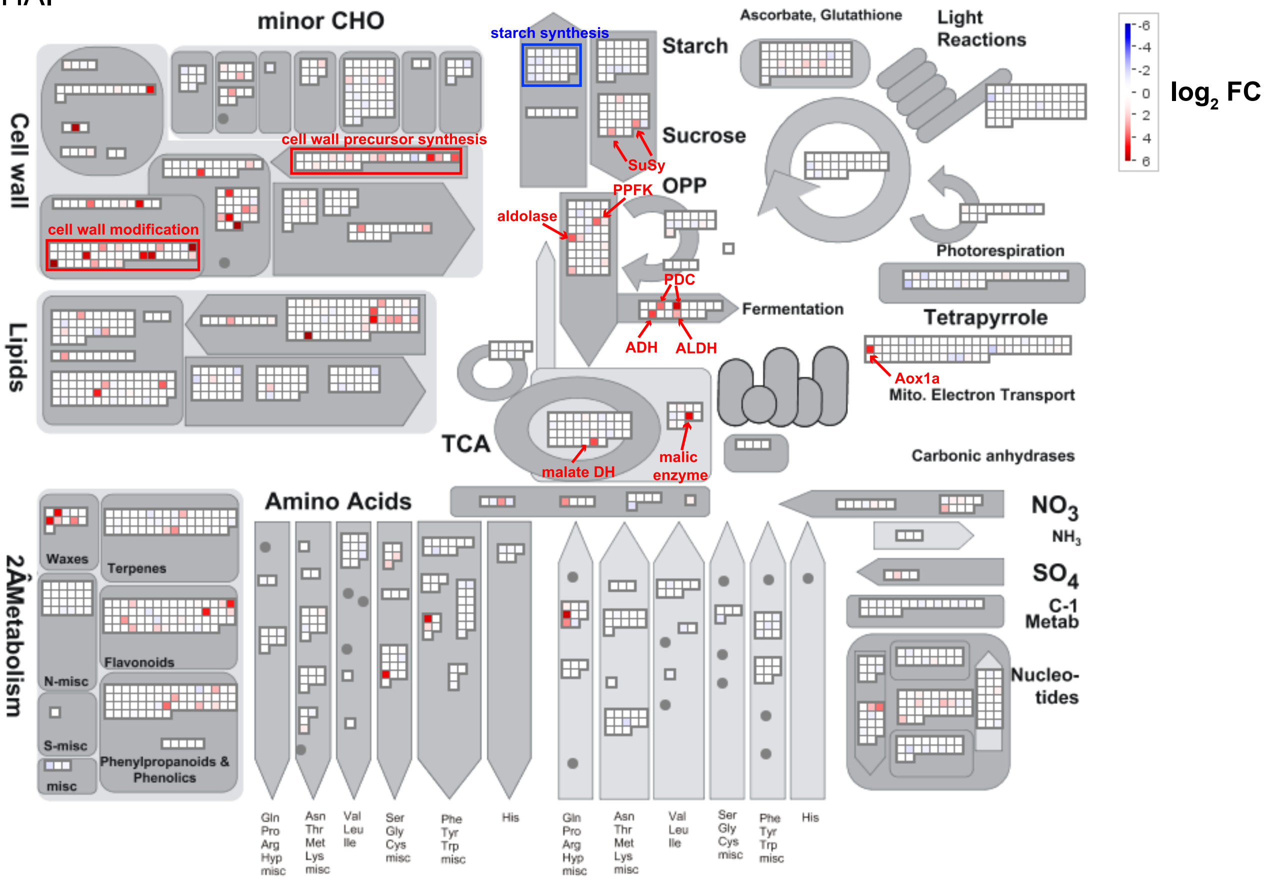


3 v 12 HAI

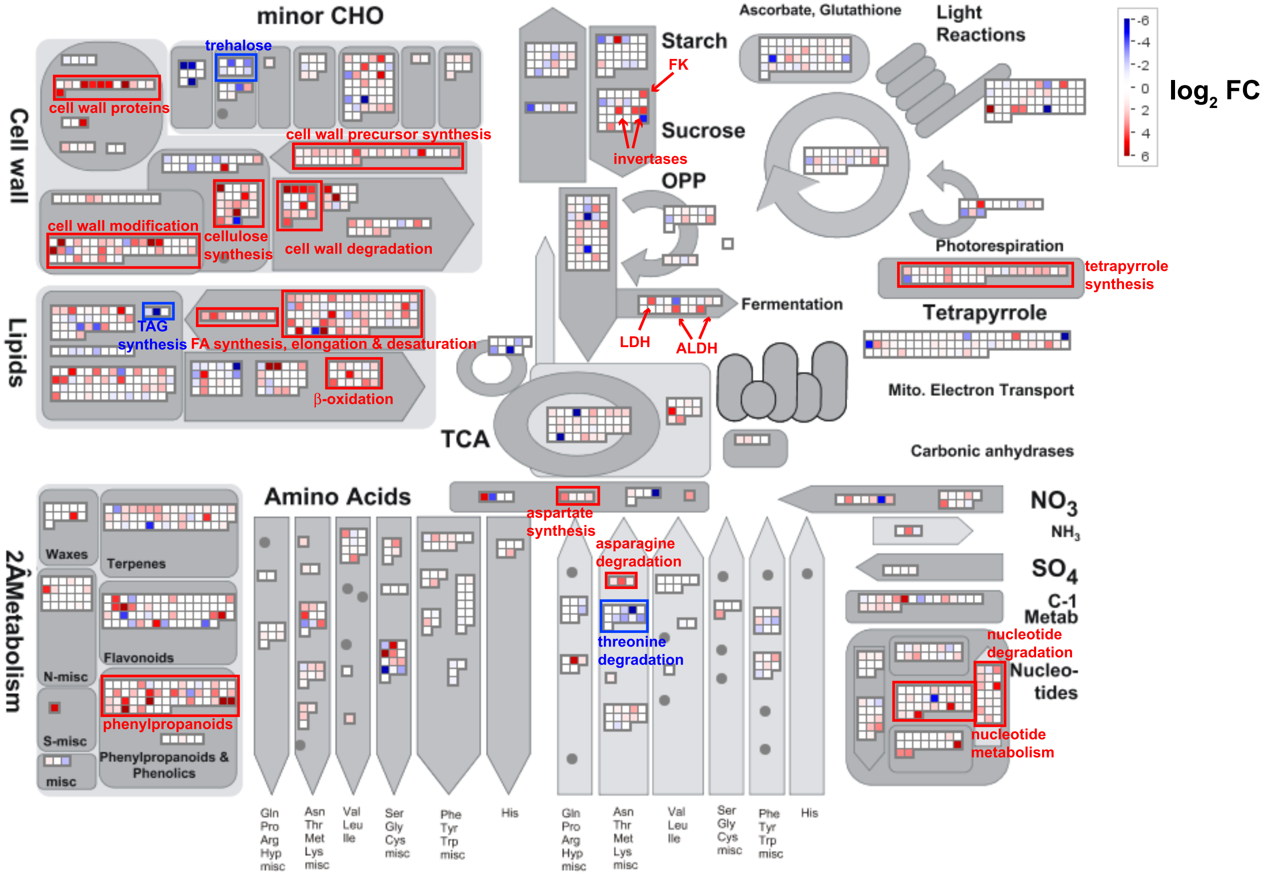


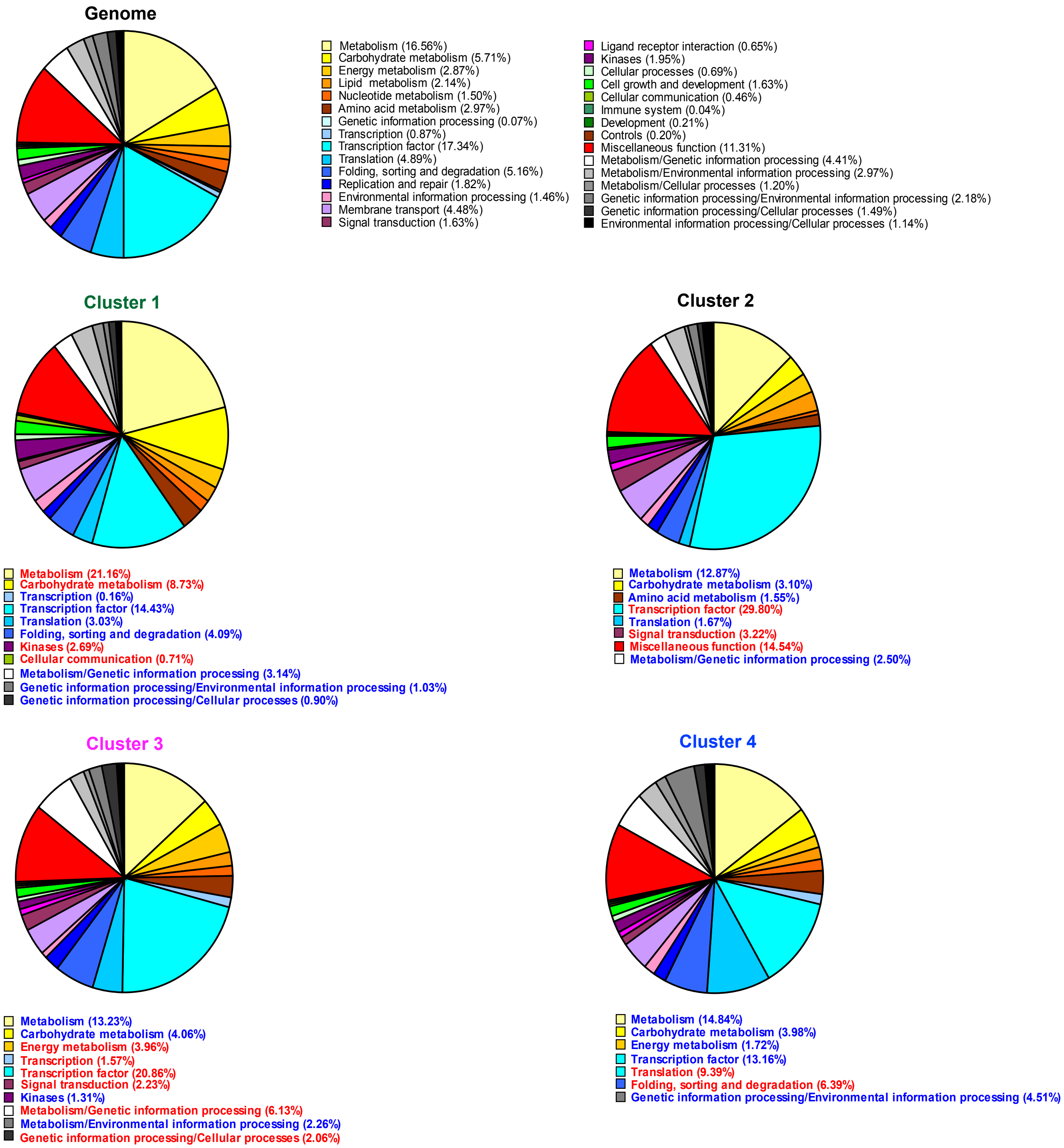
Supplemental Figure 3. Two-way comparison of 0 versus 3 HAI and 3 versus 12 HAI using MapMan to visualise an overview of metabolism.

0 v 3 HAI

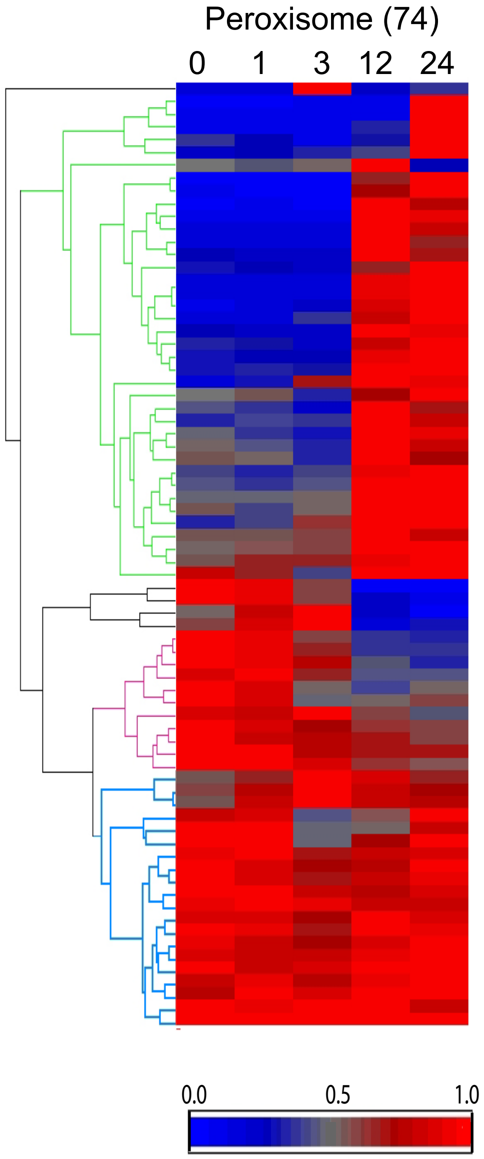


3 v 12 HAI

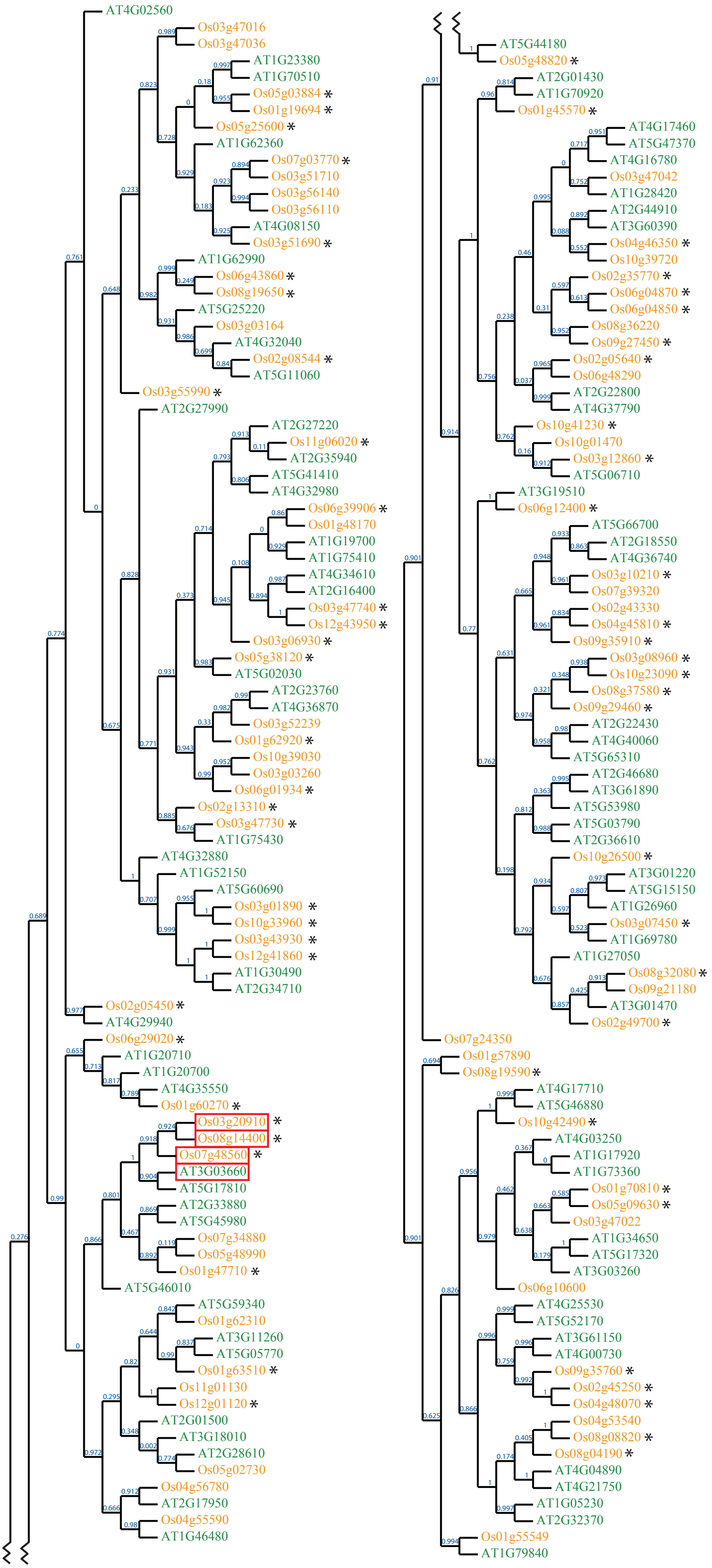




Supplemental Figure 4. Functional categorisation of the transcripts grouped into each cluster. Of the 24,150 transcripts that were present at any one time point a functional classification could be ascribed to over 10,000 as outlined in the material and methods. The breakdown of the genome as well as the four clusters defined in Figure 2B is shown. The frequency of transcripts in each FUNCAT and the respective percentage when a z-score statistic and associated p-value were calculated to be different from that of the genome. Functional groups that were found to be over-represented (shown in red) or under represented (shown in blue) are listed for each cluster, as determined by the z-score test with a confidence of p<0.01.

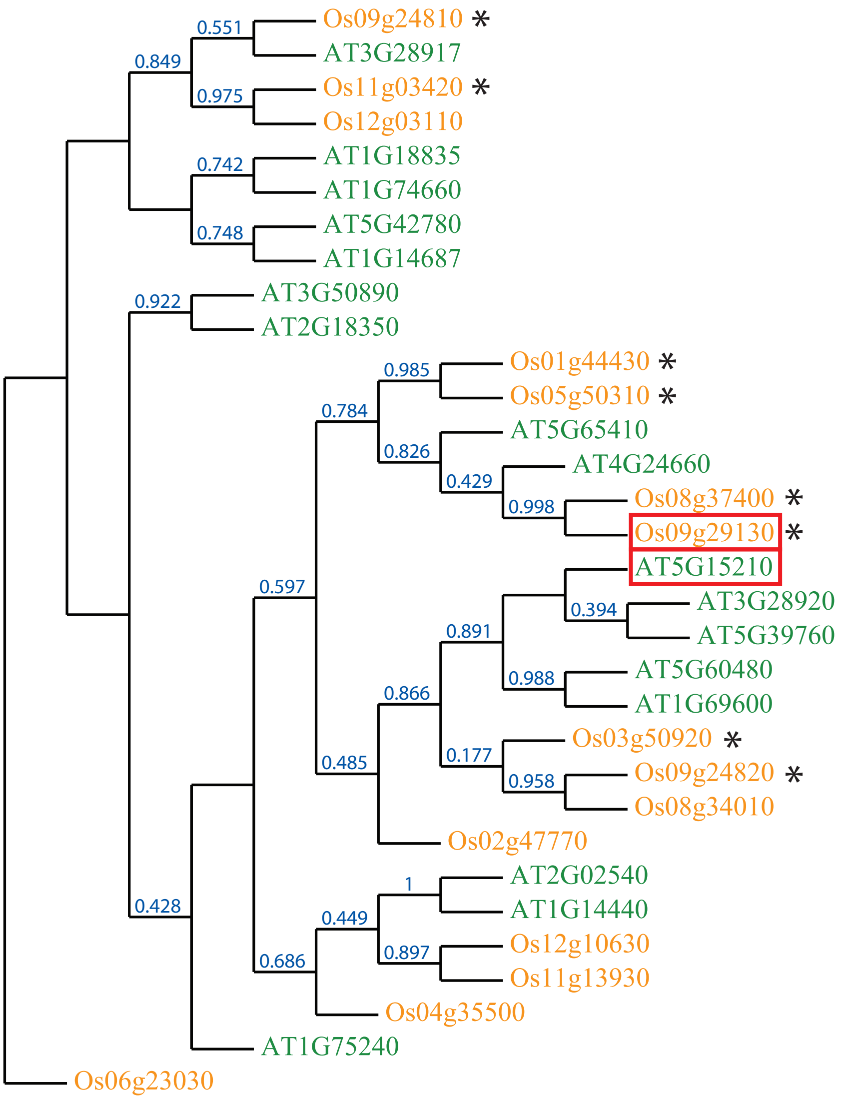


Supplemental Figure 5. All 74 transcripts encoding proteins predicted to be peroxisomal were hierarchically clustered.



Supplementary Figure 6A. Phylogenetic analysis of the homeobox (HB) transcription factor family in rice and Arabidopsis. Protein sequences for members of the HB TF family from rice (indicated in orange) and Arabidopsis (indicated in green) were downloaded from the Plant Transcription Factor Database (Riano-Pachon et al, 2007; http://plntfdb.bio.uni-potsdam.de/v2.0/) and used for building a phylogenetic tree. Multiple sequence alignment using MUSCLE, tree building using PhyML and tree drawing using TreeDyn were performed via the "One Click" mode (with the Gblocks program deselected) available from the Phylogeny.fr platform ([1]Dereeper et al, 2008; http://www.phylogeny.fr/). Branch support values determined by the approximate Likelihood-Ratio Test (aLRT) are indicated in blue. Rice HB TFs found to be expressed in the present study are indicated with an asterix. Expression profiles of Arabidopsis TFs were investigated using the Arabidopsis eFP browser (Winter et al, 2007) as shown in Figure 7. Rice and Arabidopsis TFs showing both germination-specific and transient expression at early stages of germination are boxed in red. Due to the large size of the HB TF family the phylogenetic tree has been split to allow the whole tree to be presented on a single page.

[1] **Dereeper A, Guignon V, Blanc G, Audic S, Buffet S, Chevenet F, Dufayard JF, Guindon S, Lefort V, Lescot M, Claverie JM, Gascuel O** (2008) Phylogeny.fr: robust phylogenetic analysis for the non-specialist. Nucleic Acids Res **36:** W465-469



Supplementary Figure 6B. Phylogenetic analysis of the Zn-finger homeodomain (zf-HD) transcription factor family in rice and Arabidopsis. Protein sequences for members of the zf-HD TF family from rice (indicated in orange) and Arabidopsis (indicated in green) were downloaded from the Plant Transcription Factor Database (Riano-Pachon et al, 2007; http://plntfdb.bio.uni-potsdam.de/v2.0/) and used for building a phylogenetic tree. Multiple sequence alignment using MUSCLE, tree building using PhyML and tree drawing using TreeDyn were performed via the "One Click" mode (with the Gblocks program deselected) available from the Phylogeny.fr platform ([1]Dereeper et al, 2008; http://www.phylogeny.fr/). Branch support values determined by the approximate Likelihood-Ratio Test (aLRT) are indicated in blue. Rice zf-HD TFs found to be expressed in the present study are indicated with an asterix. Expression profiles of Arabidopsis TFs were investigated using the Arabidopsis eFP browser (Winter et al, 2007) as shown in Figure 7. Rice and Arabidopsis TFs showing both germination-specific and transient expression at early stages of germination are boxed in red.

[1] **Dereeper A, Guignon V, Blanc G, Audic S, Buffet S, Chevenet F, Dufayard JF, Guindon S, Lefort V, Lescot M, Claverie JM, Gascuel O** (2008) Phylogeny.fr: robust phylogenetic analysis for the non-specialist. Nucleic Acids Res **36:** W465-469