

Supplementary Materials for

The trithorax group factor ULTRAPETALA1 regulates

developmental as well as biotic and abiotic stress response genes in

Arabidopsis

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Table S1

Figures S1-S8

Supplemental Tables S2 through S8 are provided separately as Excel files.

Table S1. Pearson correlation coefficients (R^2) for each genotype at each stage sampled.

Vegetative	<i>Ler</i>	<i>ult1-3</i>	<i>35S:ULT1</i>	<i>clf-2</i>
$R^2 =$	0.9702	0.9700	N/A	N/A
Reproductive	<i>Ler</i>	<i>ult1-3</i>	<i>35S:ULT1</i>	<i>clf-2</i>
$R^2 =$	0.9905	0.9918	0.9917	0.9870

N/A, not applicable.

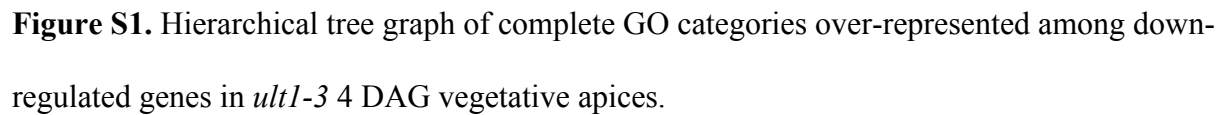


Figure S1. Hierarchical tree graph of complete GO categories over-represented among down-regulated genes in *ult1-3* 4 DAG vegetative apices.

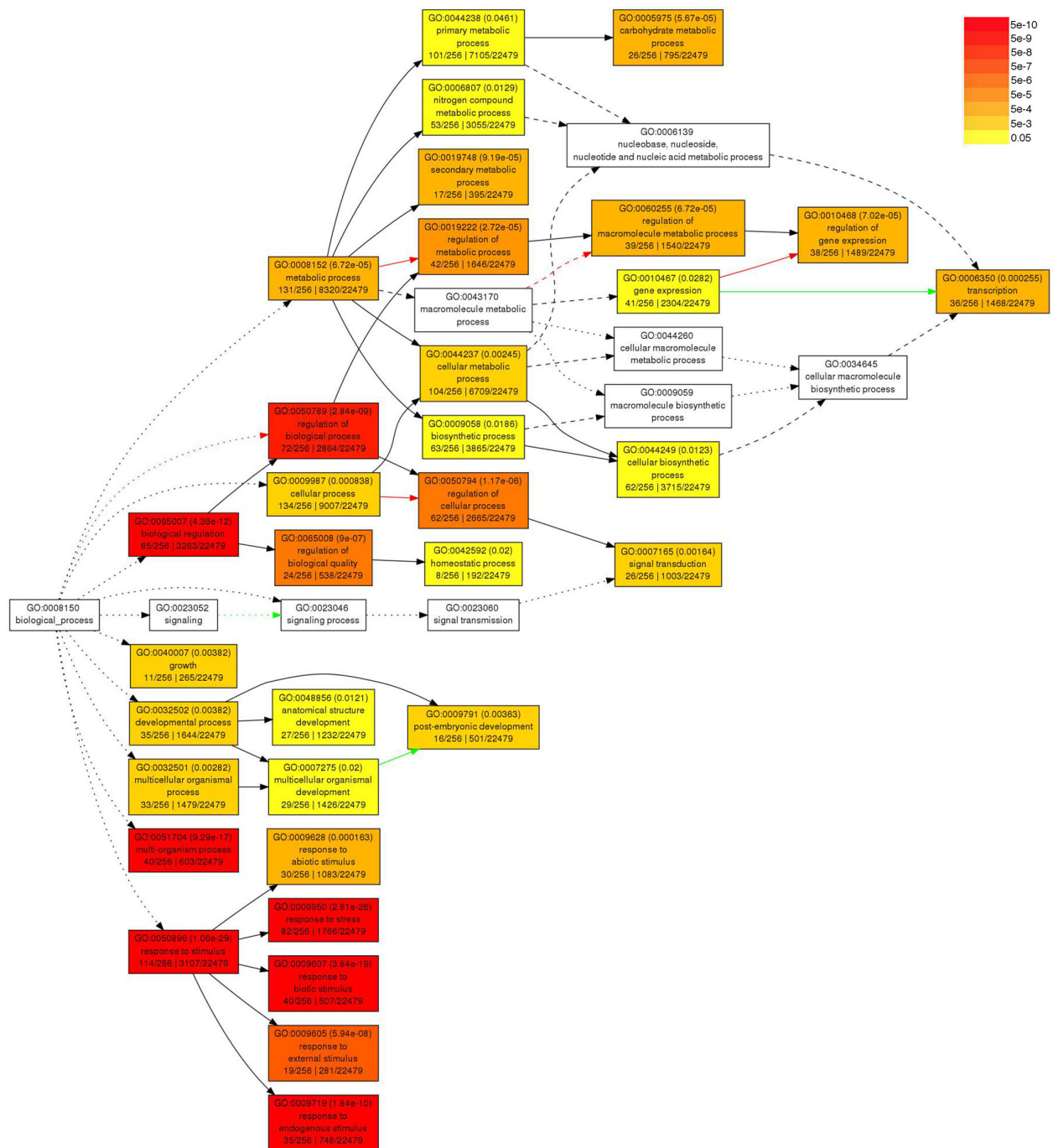


Figure S2. Hierarchical tree graph of GO slim categories over-represented among up-regulated genes in *ult1-3* 4 DAG vegetative apices.

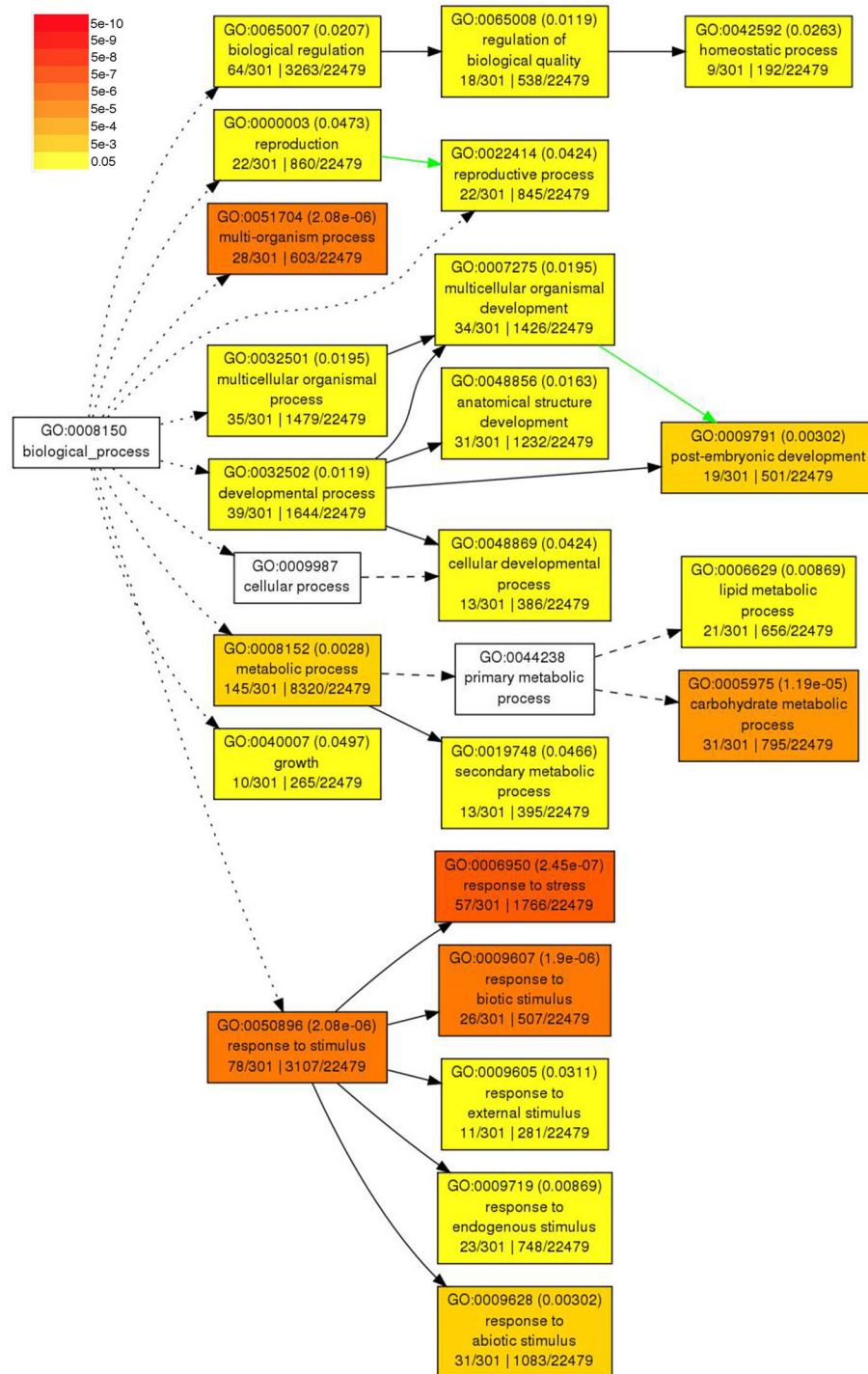


Figure S4. Hierarchical tree graph of GO slim categories over-represented among up-regulated genes in *ult1-3* inflorescence apices.

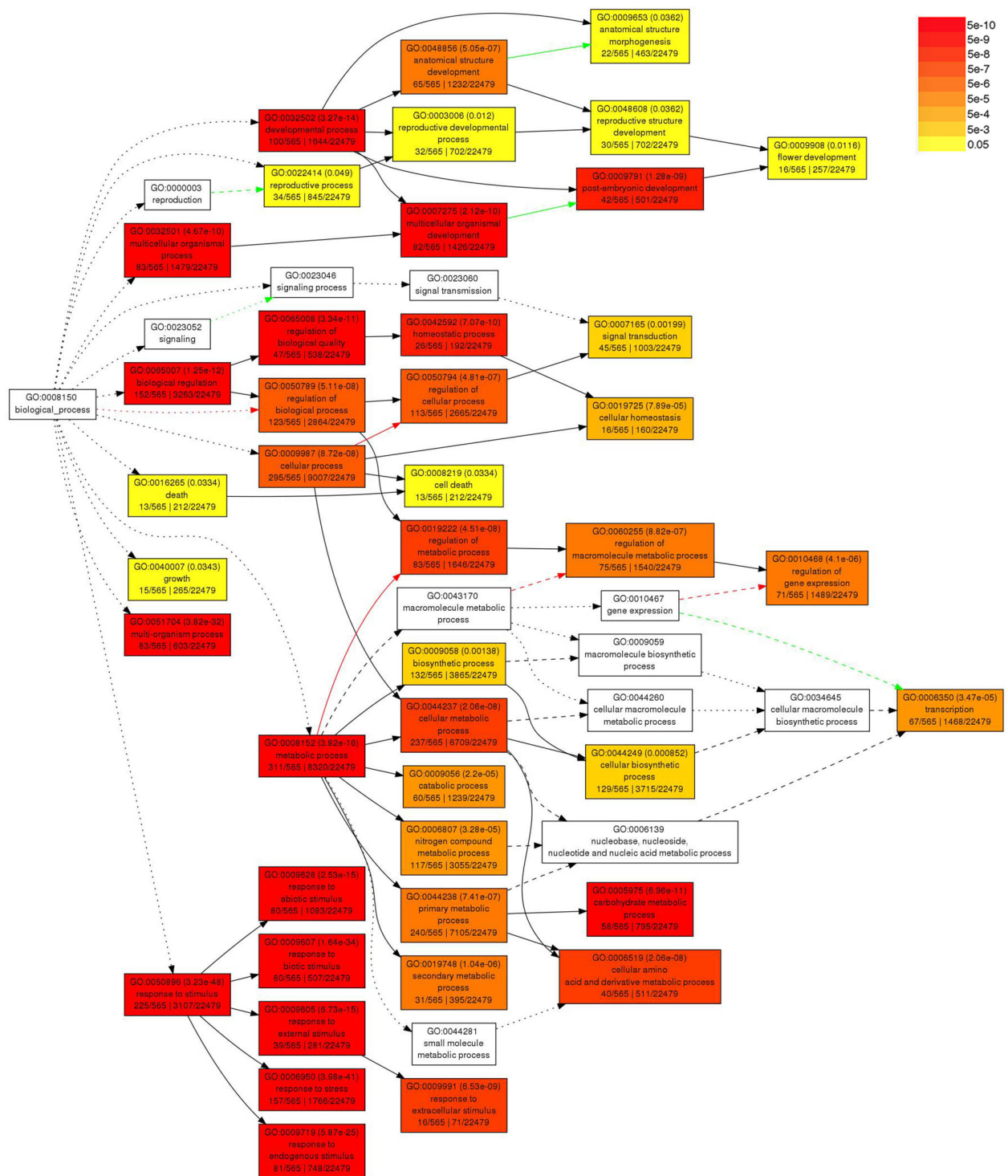


Figure S6. Hierarchical tree graph of GO slim categories over-represented among up-regulated genes in 35S:ULT1 inflorescence apices.

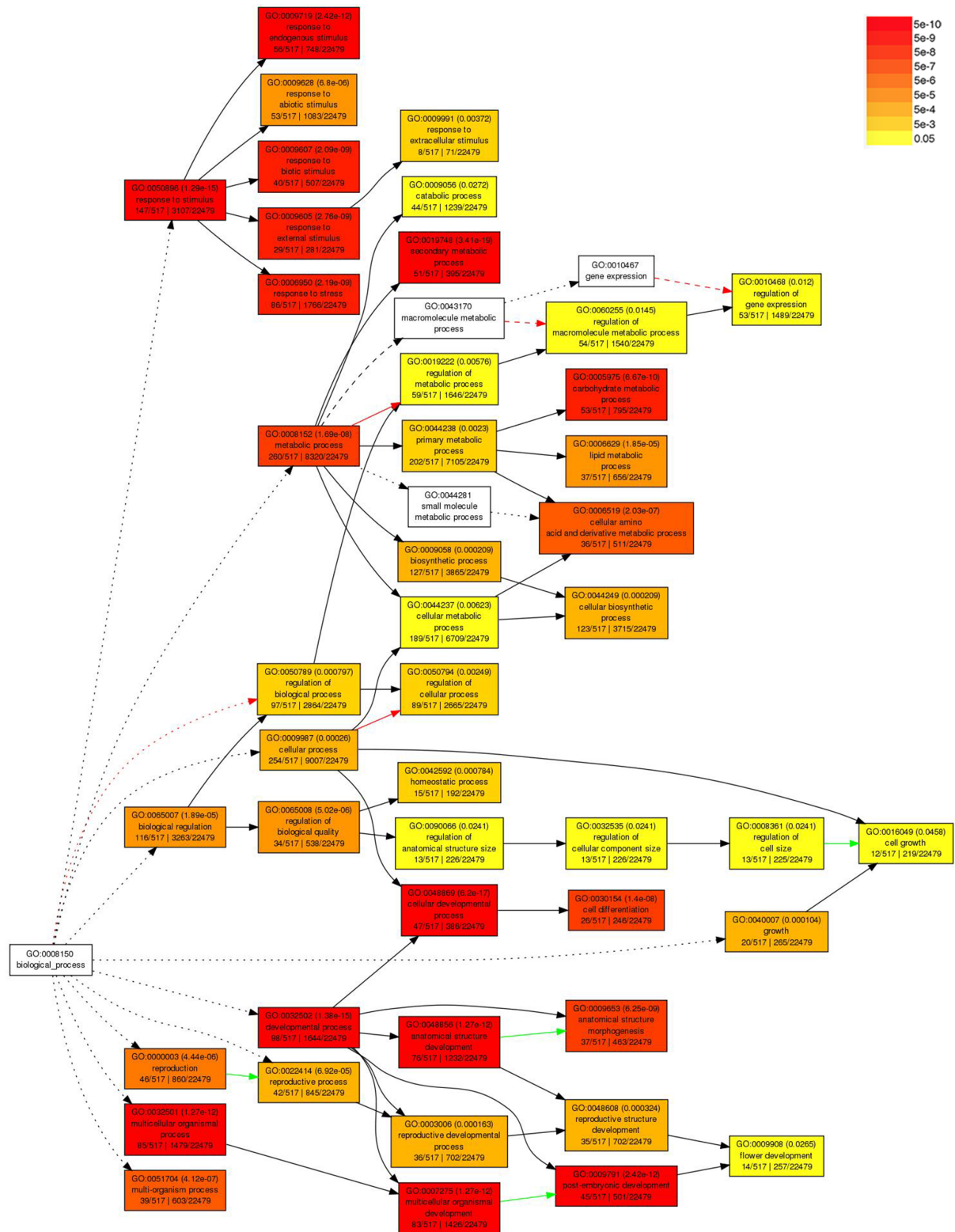


Figure S7. Hierarchical tree graph of GO slim categories over-represented among down-regulated genes in *clf-2* inflorescence apices.

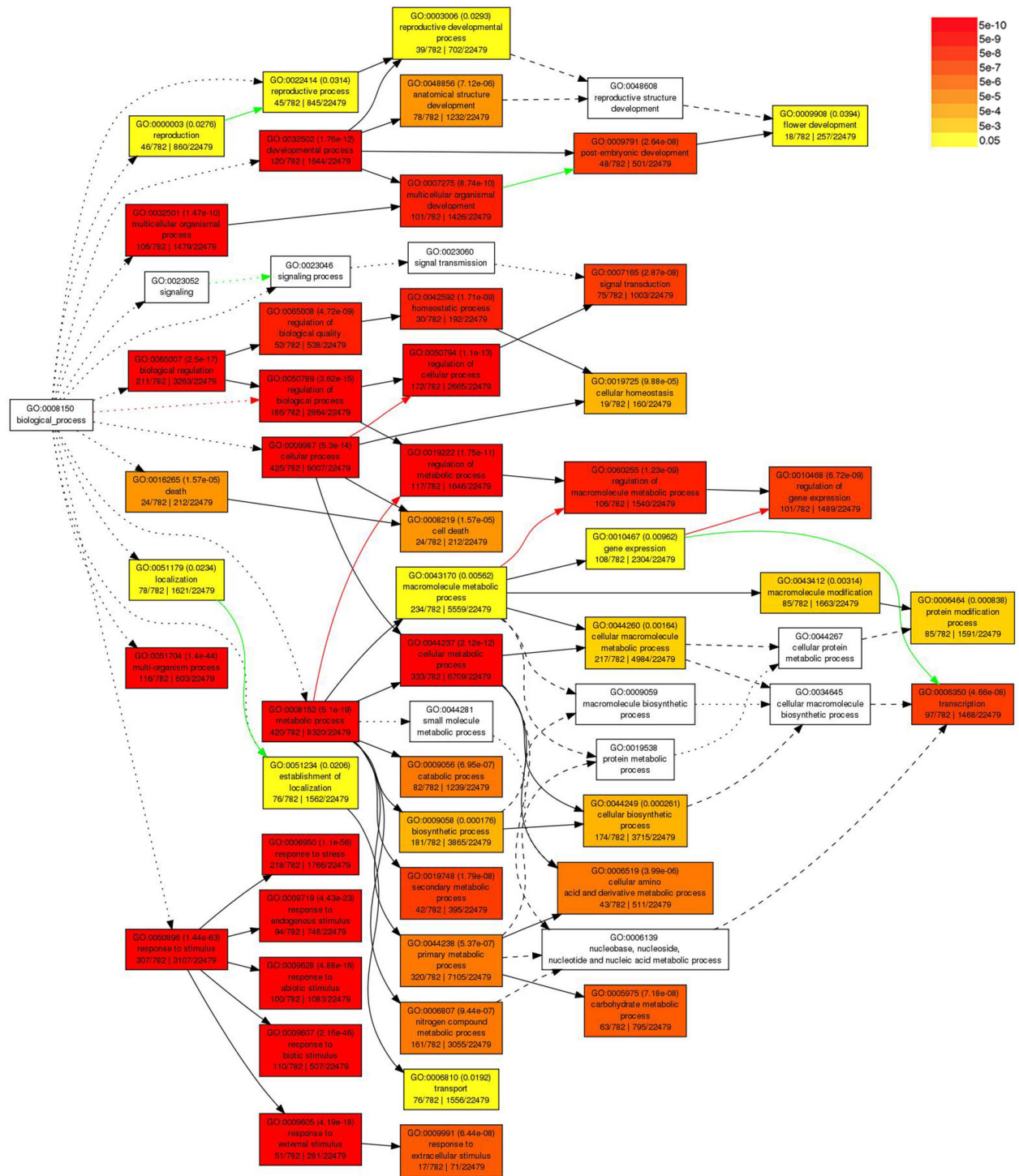


Figure S8. Hierarchical tree graph of GO slim categories over-represented among up-regulated genes in *clf-2* inflorescence apices.