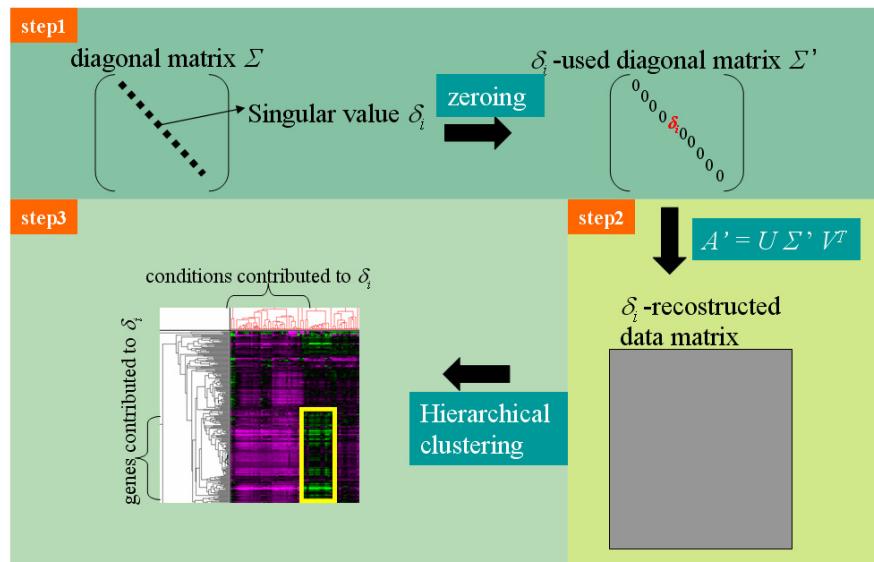
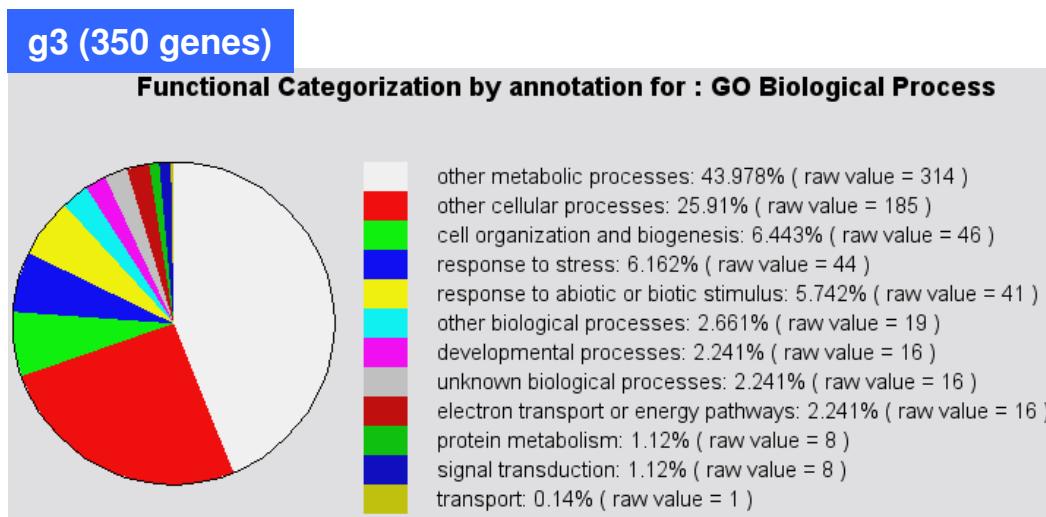
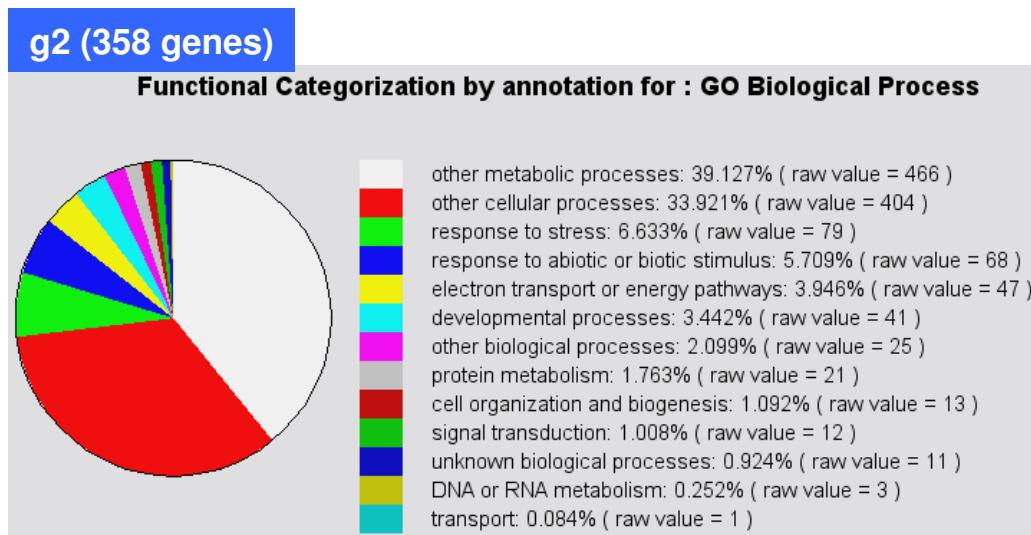
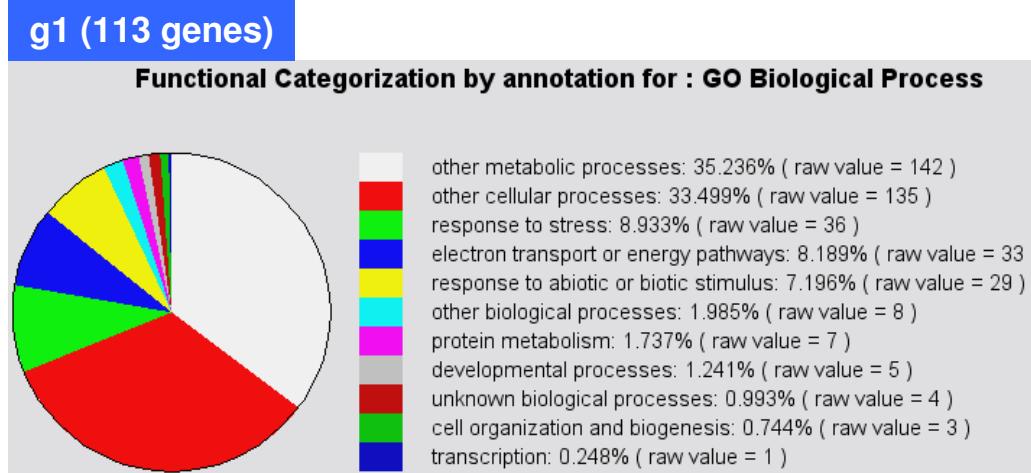
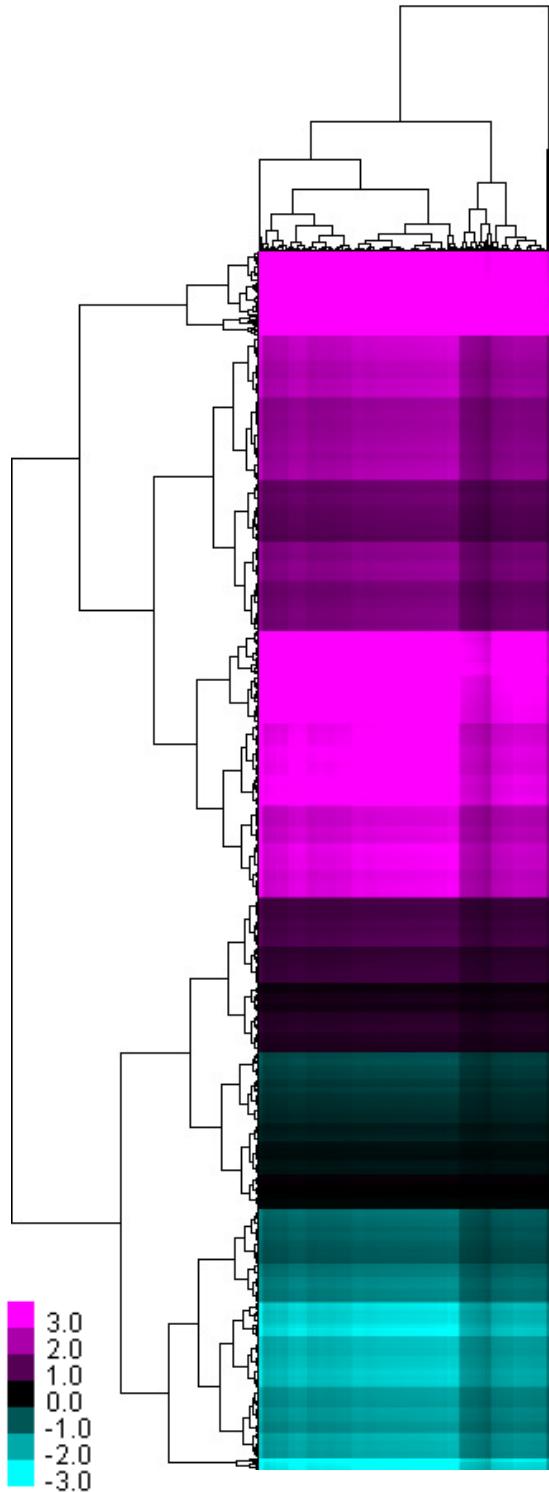


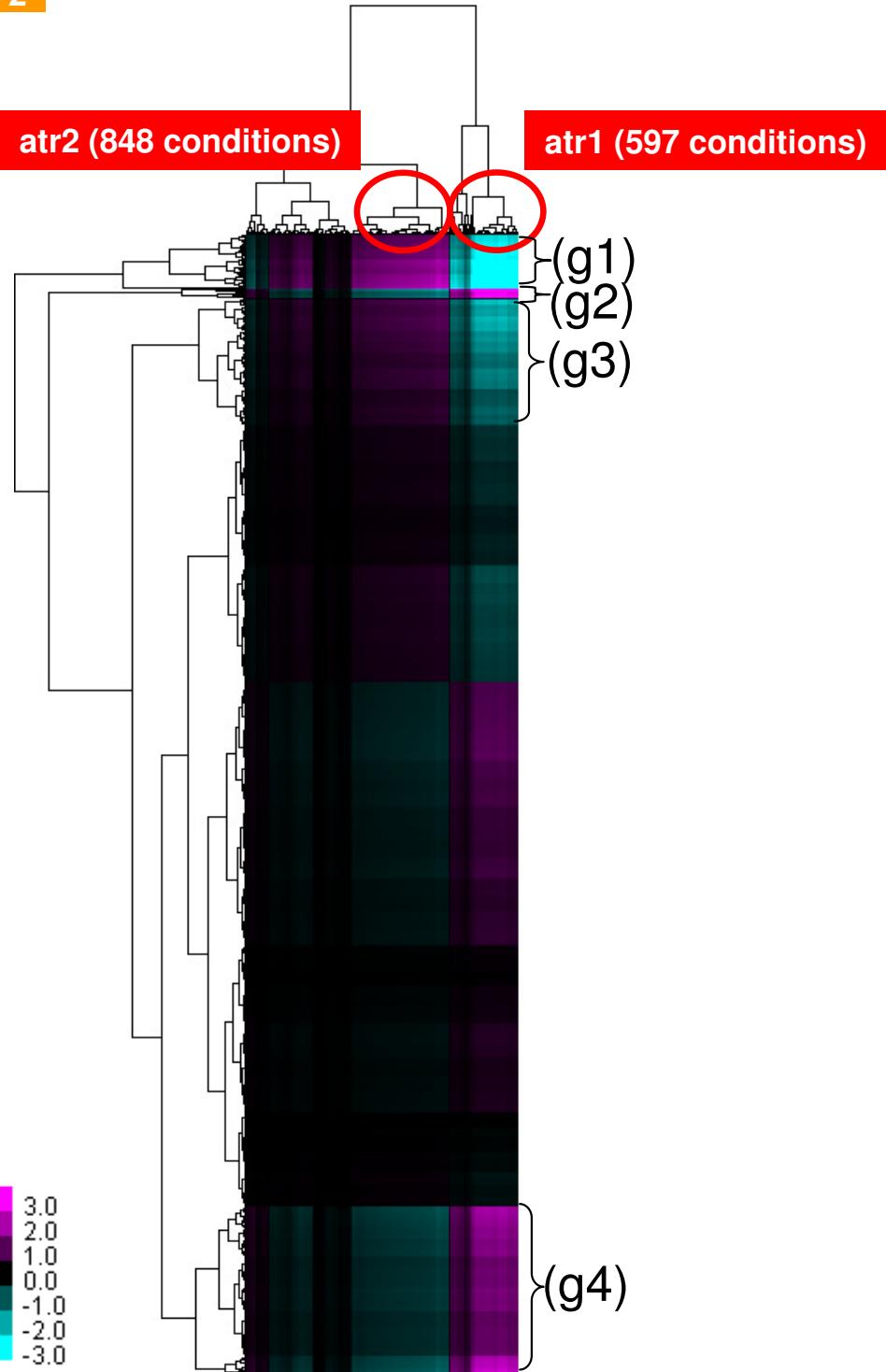
## SUPPLEMENTARY DATA

Supplementary Figure S1.

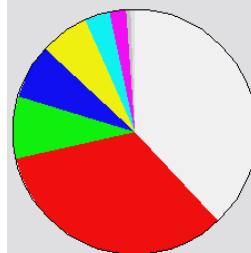


$\delta_1$



$\delta_2$ **g1 (78 genes)**

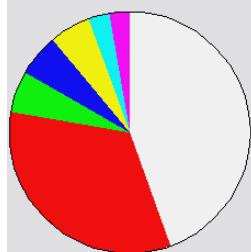
Functional Categorization by annotation for : GO Biological Process



other metabolic processes:	38.127%	( raw value = 114 )
other cellular processes:	33.445%	( raw value = 100 )
electron transport or energy pathways:	8.361%	( raw value = 25 )
response to abiotic or biotic stimulus:	7.358%	( raw value = 22 )
response to stress:	6.355%	( raw value = 19 )
other biological processes:	3.344%	( raw value = 10 )
protein metabolism:	2.341%	( raw value = 7 )
unknown biological processes:	0.669%	( raw value = 2 )

**g2 (14 genes)**

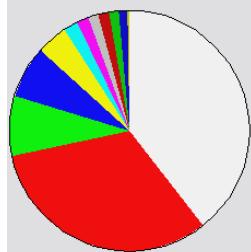
Functional Categorization by annotation for : GO Biological Process



other metabolic processes:	44.444%	( raw value = 16 )
other cellular processes:	33.333%	( raw value = 12 )
response to stress:	5.556%	( raw value = 2 )
electron transport or energy pathways:	5.556%	( raw value = 2 )
response to abiotic or biotic stimulus:	5.556%	( raw value = 2 )
other biological processes:	2.778%	( raw value = 1 )
cell organization and biogenesis:	2.778%	( raw value = 1 )

**g3 (182 genes)**

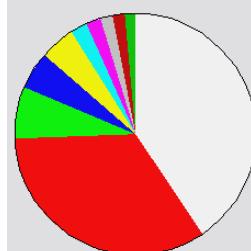
Functional Categorization by annotation for : GO Biological Process



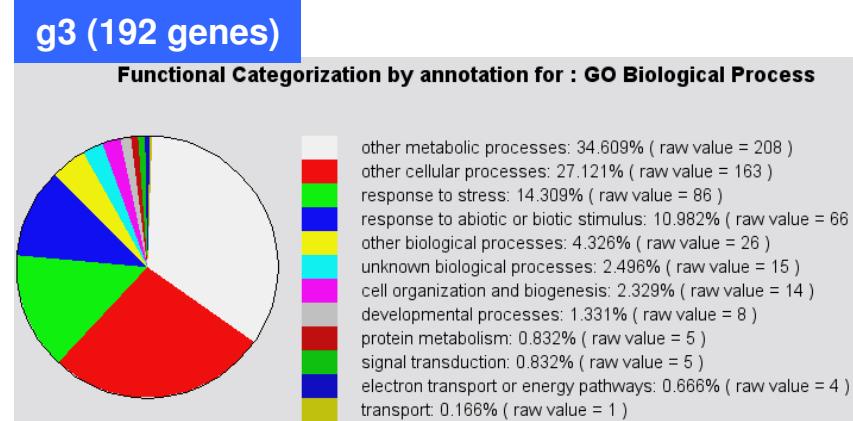
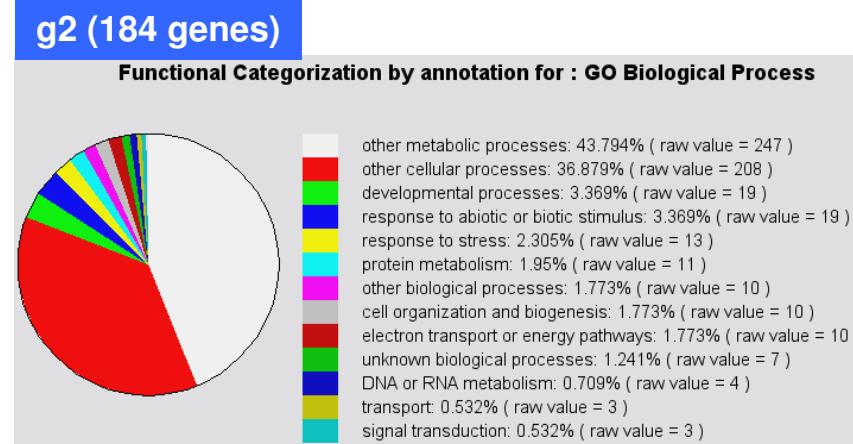
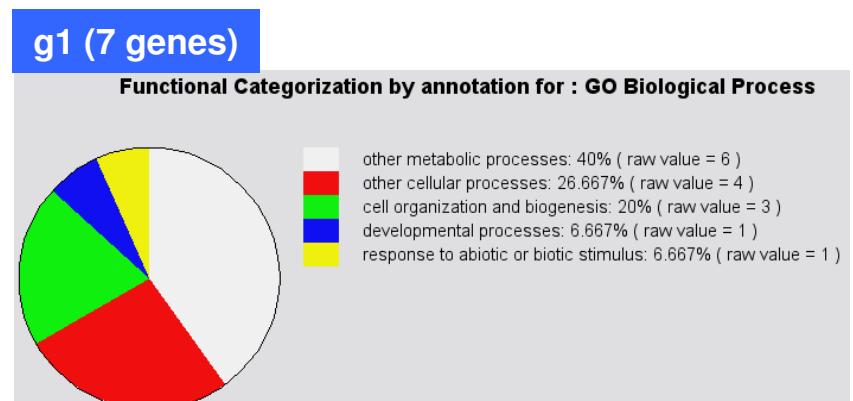
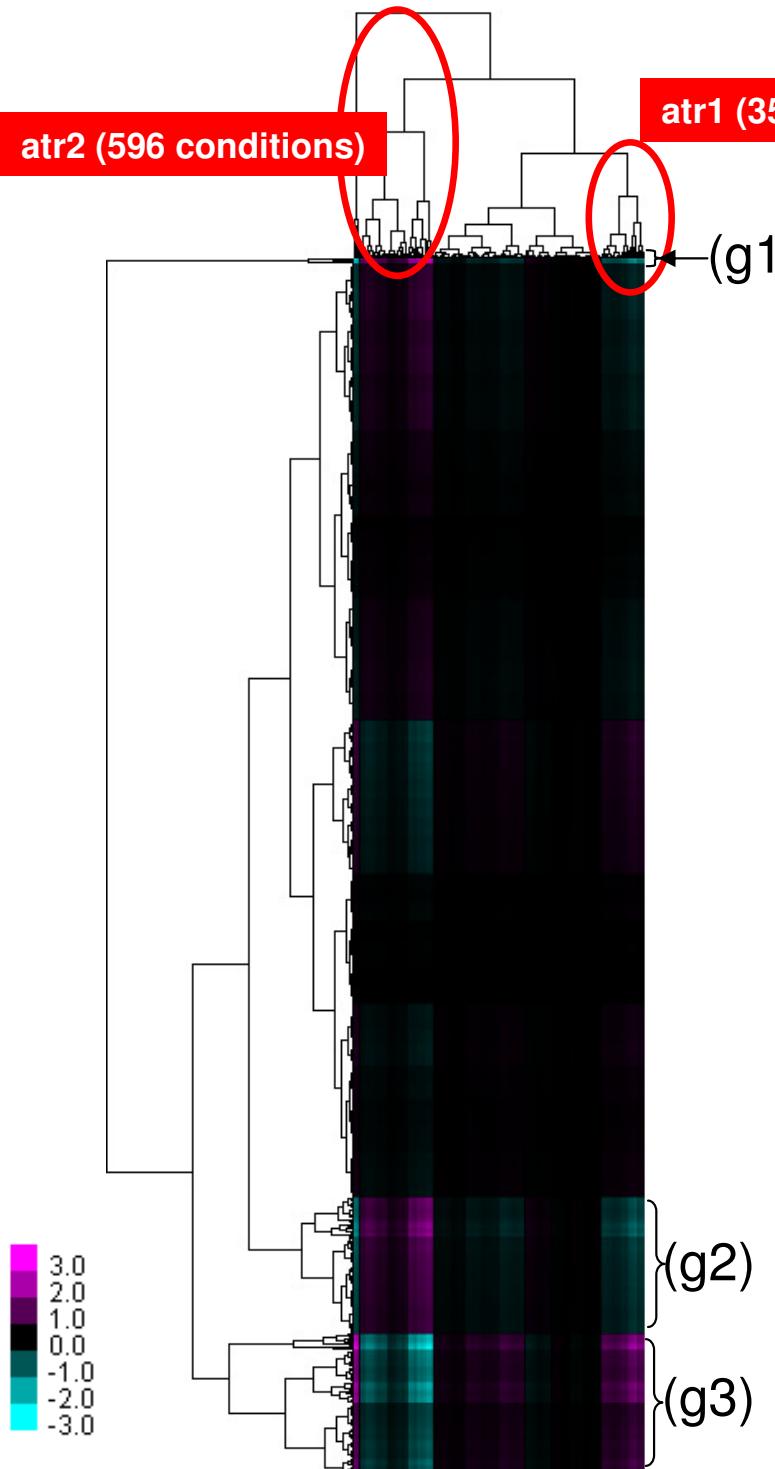
other metabolic processes:	39.444%	( raw value = 213 )
other cellular processes:	32.222%	( raw value = 174 )
response to stress:	8.148%	( raw value = 44 )
response to abiotic or biotic stimulus:	7.037%	( raw value = 38 )
electron transport or energy pathways:	4.074%	( raw value = 22 )
other biological processes:	1.952%	( raw value = 10 )
protein metabolism:	1.667%	( raw value = 9 )
developmental processes:	1.481%	( raw value = 8 )
cell organization and biogenesis:	1.481%	( raw value = 8 )
unknown biological processes:	1.296%	( raw value = 7 )
signal transduction:	1.111%	( raw value = 6 )
transport:	0.185%	( raw value = 1 )

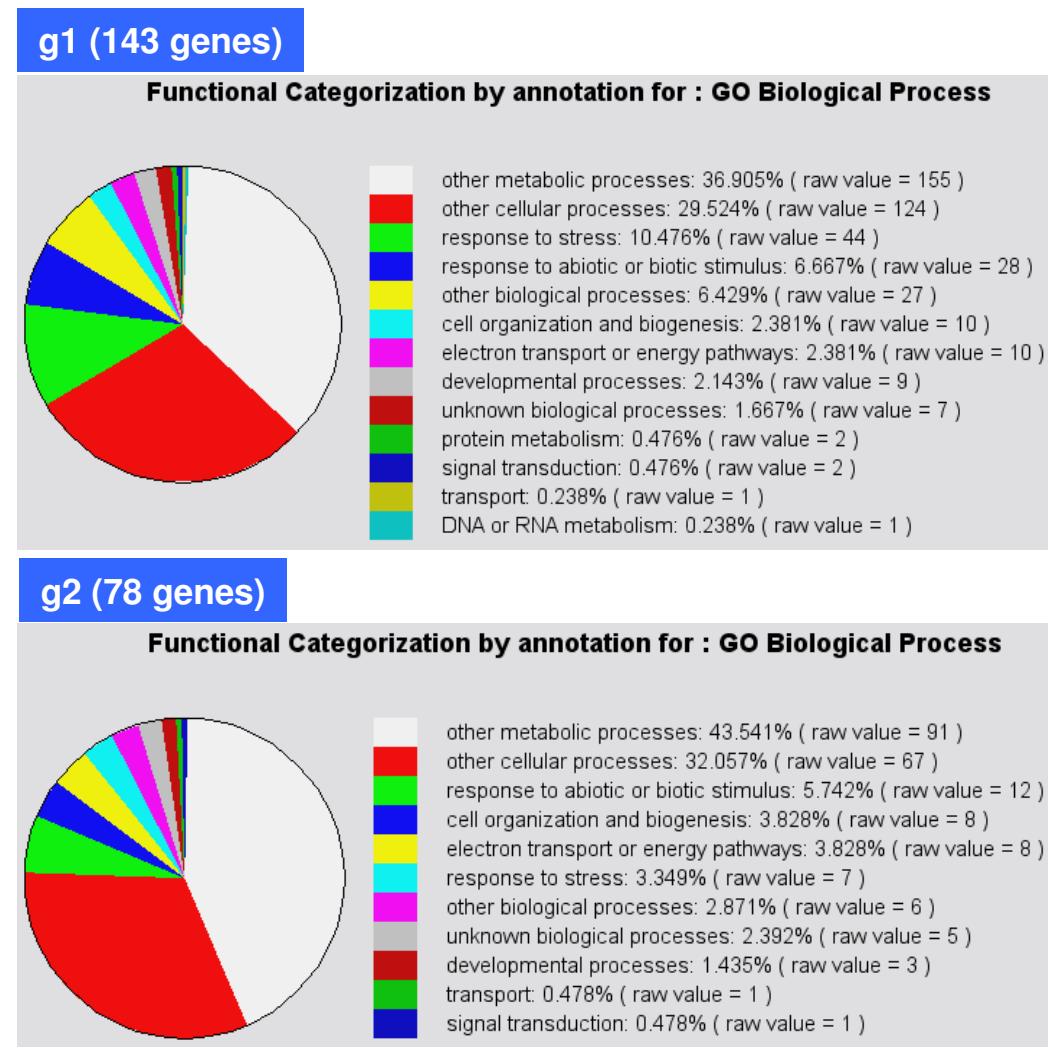
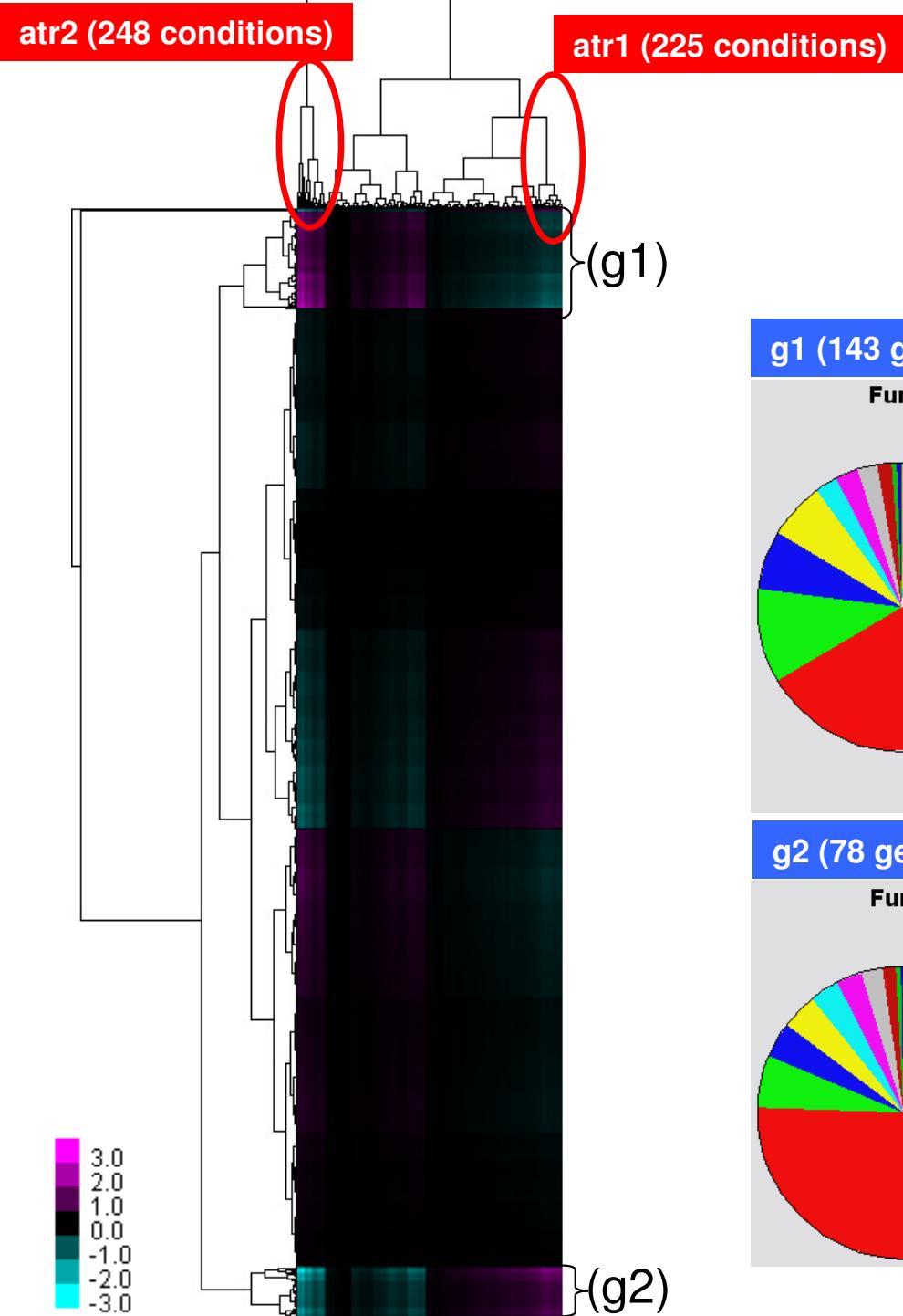
**g4 (239 genes)**

Functional Categorization by annotation for : GO Biological Process



other metabolic processes:	40.551%	( raw value = 309 )
other cellular processes:	33.99%	( raw value = 259 )
response to stress:	6.824%	( raw value = 52 )
electron transport or energy pathways:	4.987%	( raw value = 38 )
response to abiotic or biotic stimulus:	4.856%	( raw value = 37 )
developmental processes:	2.1%	( raw value = 16 )
unknown biological processes:	1.837%	( raw value = 14 )
other biological processes:	1.706%	( raw value = 13 )
cell organization and biogenesis:	1.575%	( raw value = 12 )
protein metabolism:	1.312%	( raw value = 10 )
transcription:	0.131%	( raw value = 1 )
signal transduction:	0.131%	( raw value = 1 )

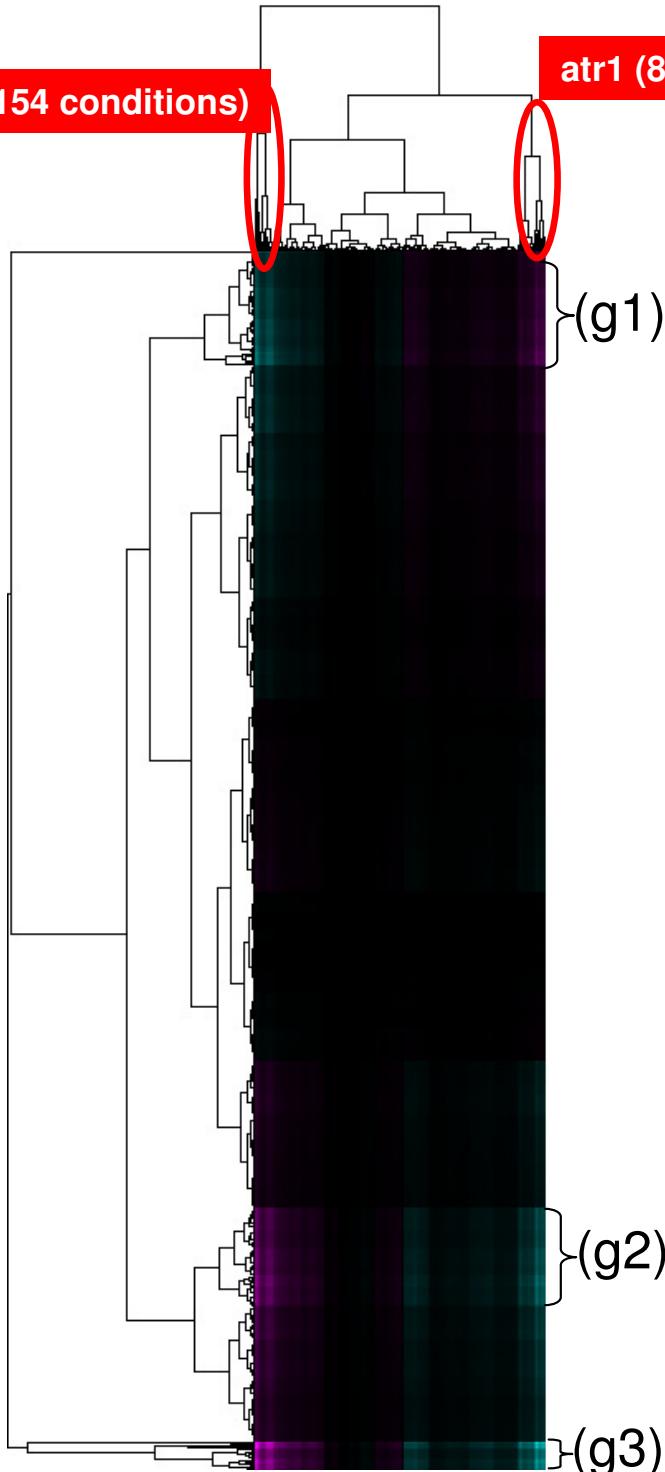
$\delta_3$ 

$\delta_4$ 

$\delta_5$ 

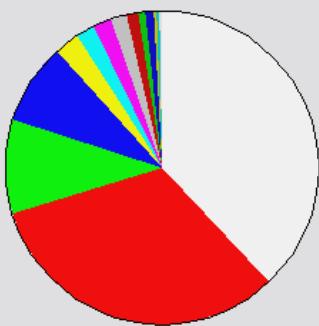
atr2 (154 conditions)

atr1 (87 conditions)



g1 (152 genes)

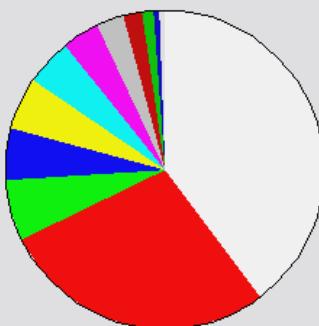
Functional Categorization by annotation for : GO Biological Process



other metabolic processes:	38% ( raw value = 190 )
other cellular processes:	32.2% ( raw value = 161 )
response to stress:	9.8% ( raw value = 49 )
response to abiotic or biotic stimulus:	8.4% ( raw value = 42 )
protein metabolism:	2.6% ( raw value = 13 )
developmental processes:	2% ( raw value = 10 )
other biological processes:	2% ( raw value = 10 )
electron transport or energy pathways:	1.8% ( raw value = 9 )
cell organization and biogenesis:	1% ( raw value = 5 )
signal transduction:	0.8% ( raw value = 4 )
unknown biological processes:	0.8% ( raw value = 4 )
DNA or RNA metabolism:	0.4% ( raw value = 2 )
transport:	0.2% ( raw value = 1 )

g2 (132 genes)

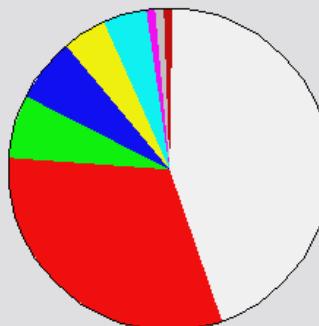
Functional Categorization by annotation for : GO Biological Process



other metabolic processes:	39.763% ( raw value = 134 )
other cellular processes:	28.19% ( raw value = 95 )
response to abiotic or biotic stimulus:	6.231% ( raw value = 21 )
response to stress:	5.341% ( raw value = 18 )
cell organization and biogenesis:	5.341% ( raw value = 18 )
electron transport or energy pathways:	4.748% ( raw value = 16 )
other biological processes:	3.858% ( raw value = 13 )
unknown biological processes:	2.671% ( raw value = 9 )
protein metabolism:	2.077% ( raw value = 7 )
developmental processes:	1.187% ( raw value = 4 )
signal transduction:	0.593% ( raw value = 2 )

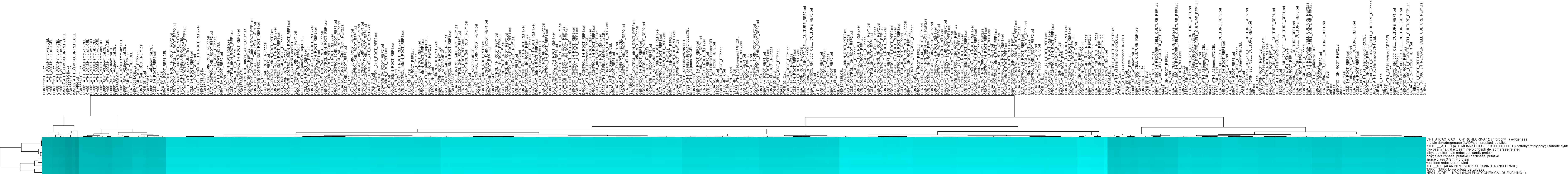
g3 (37 genes)

Functional Categorization by annotation for : GO Biological Process

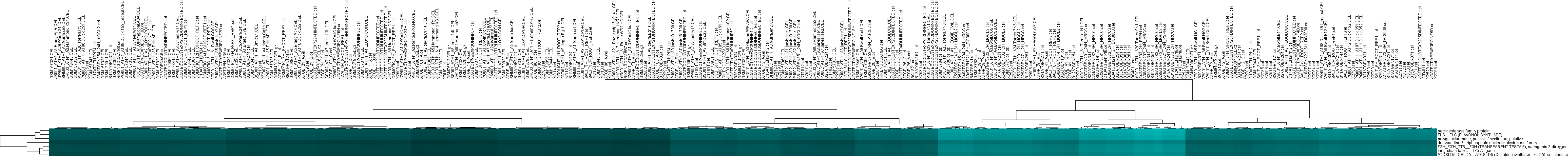


other metabolic processes:	44.643% ( raw value = 50 )
other cellular processes:	31.25% ( raw value = 35 )
response to stress:	6.25% ( raw value = 7 )
response to abiotic or biotic stimulus:	6.25% ( raw value = 7 )
other biological processes:	4.464% ( raw value = 5 )
cell organization and biogenesis:	4.464% ( raw value = 5 )
transport:	0.893% ( raw value = 1 )
unknown biological processes:	0.893% ( raw value = 1 )
electron transport or energy pathways:	0.893% ( raw value = 1 )

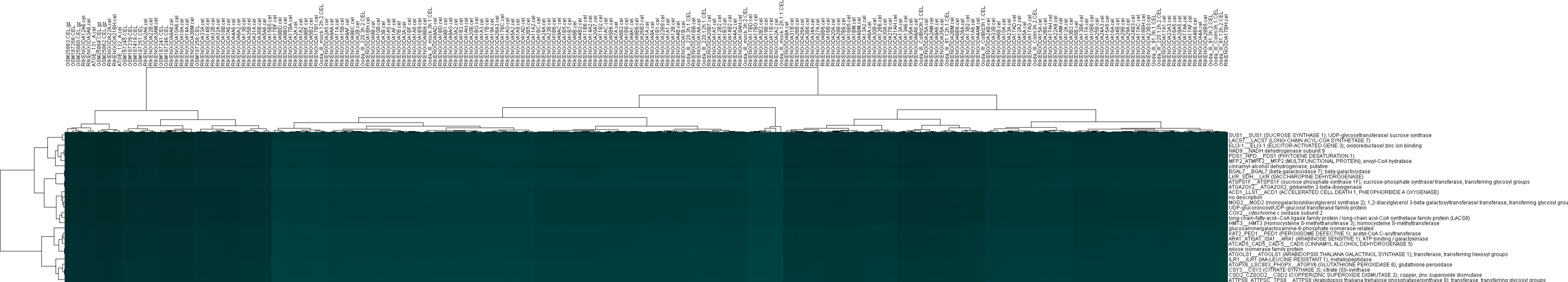


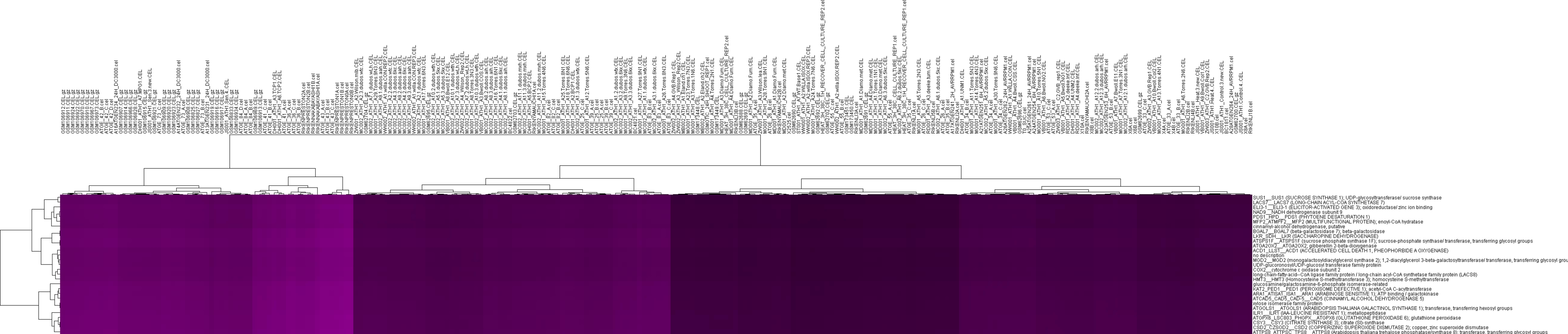


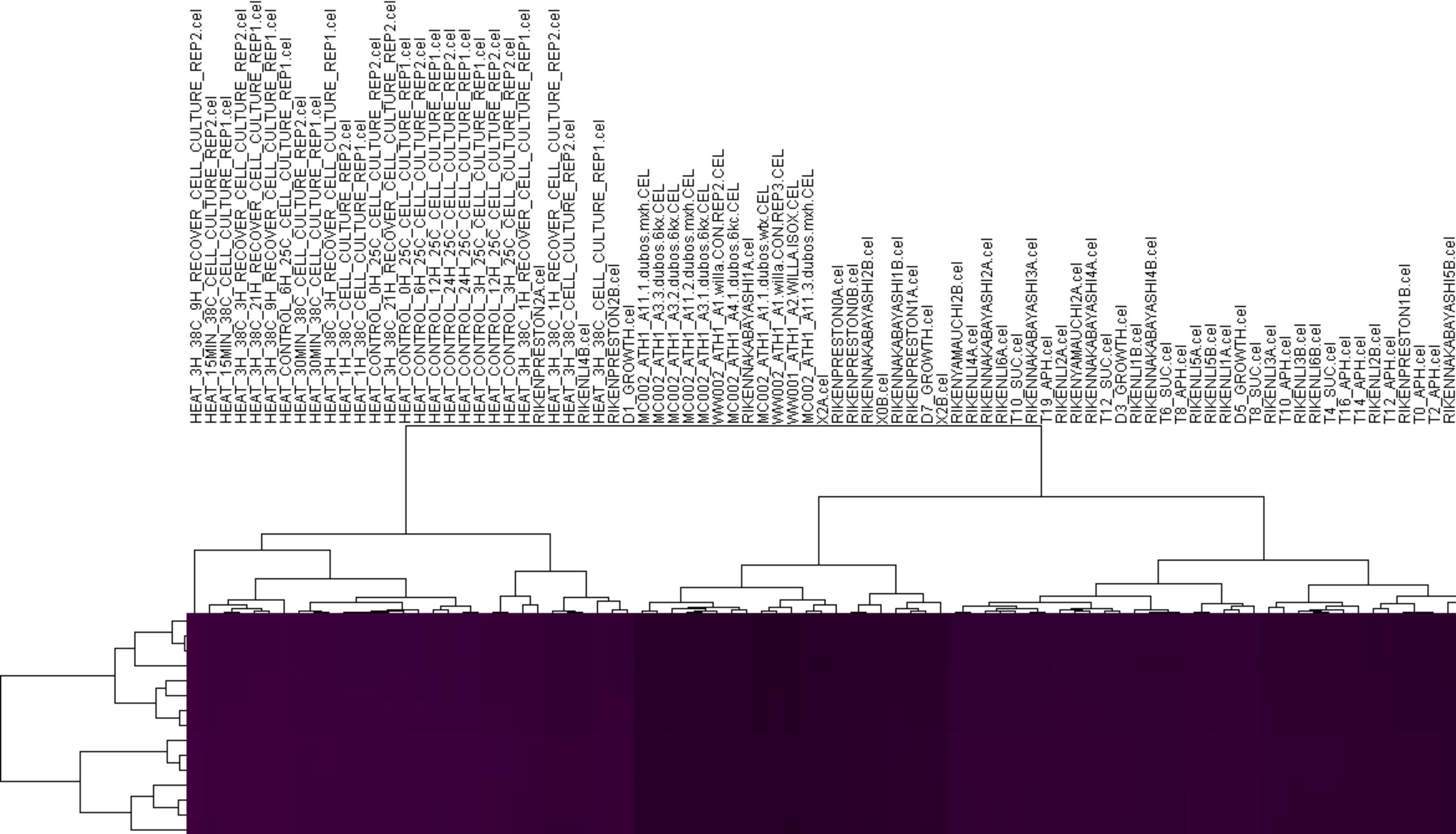




pectinesterase family protein  
FLS\_FLS (FLAVONOL SYNTHASE)  
polygalacturonase, putative / pectinase, putative  
deoxyuridine 5'-triphosphate nucleotidohydrolase family  
F3H\_F3'H\_TT6\_F3H (TRANSPARENT TESTA 6); naringenin 3-dioxygenase  
long-chain-fatty-acid-CoA ligase  
ATCSLD5 CSLD5 ATCSLD5 (Cellulose synthase-like D5); cellulose







cholinephosphate cytidylyltransferase, putative / phosphorylcholine transferase, putative / CTP:phosphocholine cytidylyltransferase, putative  
 glutamate-tRNA ligase, putative / glutamyl-tRNA synthetase, putative / GluRS, putative  
 FSD3\_FSD3 (FE SUPEROXIDE DISMUTASE 3); iron superoxide dismutase  
 APS1\_AP51 (ATP sulfurylase 3)  
 prephenate dehydratase family protein  
 CS26\_CS26 (cysteine synthase 26); cysteine synthase  
 EMB2742\_EMB2742 (EMBRYO DEFECTIVE 2742); CTP synthase  
 IPMS1\_MAML-4\_IPMS1/MAML-4 (METHYLTHIOALKYLALATE SYNTHASE-LIKE 4); 2-isopropylmalate synthase  
 GDH1\_GDH1 (GLUTAMATE DEHYDROGENASE 1); oxidoreductase  
 isocitrate dehydrogenase, putative / NADP+ isocitrate dehydrogenase, putative  
 THA2\_THA2 (THREONINE ALDOLASE 2); threonine aldolase  
 ASP2\_AAT2\_AP52 (ASPARTATE AMINOTRANSFERASE 2)  
 hexokinase, putative  
 ribose-5-phosphate isomerase  
 6-phosphogluconate dehydrogenase NAD-binding domain-containing protein

