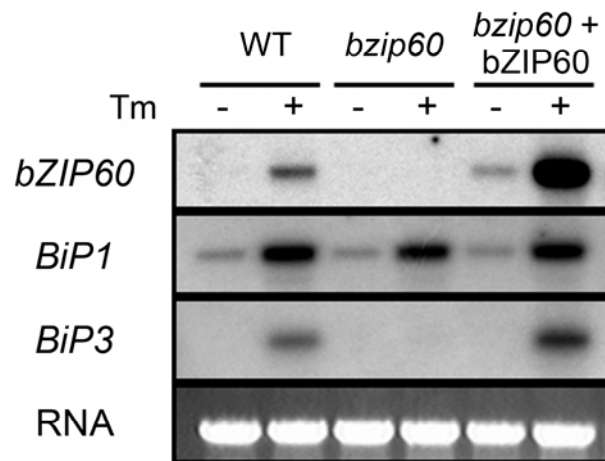


Supplemental Data. Iwata et al. (2008) *Arabidopsis* bZIP60 is a proteolysis-activated transcription factor involved in the endoplasmic reticulum stress response.



**Supplemental Figure 1. Complementation of *bzip60*.**

Seedlings of wild type (WT), *bzip60* (*bzip60*) and *bzip60* harboring the genomic fragment of the *bZIP60* gene, including 2.0 kb upstream from the start codon and 0.6 kb downstream from the stop codon (*bzip60* + bZIP60), were treated with 5 µg/mL tunicamycin for 5 h, and total RNA was extracted. Five µg of total RNA per lane was fractionated on agarose gel electrophoresis, transferred to nylon membrane and probed with *bZIP60*, *BiP1* and *BiP3* specific fragments.

```

*           20           *           40           *           60
Arabidopsis : -----M A E E F G S I D L L G D E D F F F D F D P S I V I D S L P A E D F L Q S S : 38
Soybean    : -----M D E L E E T L L T Q I D W E S F L D D I P E L N V D D E L Q D D N A V P V V T D N H S S P N : 47
Capsicum   : -----M V D N I D D I V A H I N W D D V D H I F H N V L H -----D D L F T V H D P D P : 37
Rice       : M D V E F F A D L D L D A L L A S F S S S A A A A G S G V S G L F A P S P P ---H D A E A G S P E S V S R R R P S P S : 57

*           80           *           100          *           120
Arabidopsis : P D S W I G S I E N Q L M N D E N H Q E E S F V E L D Q Q S V S D E I A D L L V D Y P T S D S G S V D L A A D K V L T V : 98
Soybean    : D D P V L S E I E N M L M T Q -----A E N D A V V L P E T P S S E A G Y Y K L F E I L V E E : 91
Capsicum   : S A P N F Q D I E Q L L M N D D D V E D Q A -----D T Q F A A E F L S D V L V D S E A Q S H Q S P S A B E E A F G F P : 93
Rice       : R E A A L S E I B R F L M E -----E G P A A E E G V G A E D F D A L L V D G G E E E E E E G K G S E A G G S T : 111

*           140          *           160          *           180
Arabidopsis : D S P A A A D D S G K E N S D L V V E K K S N D S G S E I H D D D D E E G D D A V A K K R R R V R N R D A A V R S R : 158
Soybean    : P K E G P V S P P S K I E -----S E E G S D K D K T D A A S D E E M S K K L K R O L R N R D A A V R S R : 141
Capsicum   : D S K V S S G S E D D K -----D K V S H S P S D A E L N N D D P I D K K R K R O L R N R D A A V R S R : 142
Rice       : D G D S G K ---E N E V A T -----P A E K E D V E A E V D --G D D E M S K K K R R O M R N R D S A M K S R : 159

*           200          *           220          *           240
Arabidopsis : E R K K E Y V Q L E K K S K Y L E R E C L R L E R M L E C F V A E N Q S L R Y C L O K G N G N N T T M S K O E S A V : 218
Soybean    : E R K K L Y V K N L E M K S R Y L E G E C R R L G H L L Q C Y A E N N A L R L C L Q -L R G T Y G A S M T M O E S A V : 200
Capsicum   : E R R K L Y V R L E L K S K Y F E S E C K R L C F V L O C C L A E N Q A L R F S L O N S S A N -G V S M T K O E S A V : 201
Rice       : E R K K Y V K O L E T K S K Y L E A E C R R L S Y A L Q C C A E N M A L R Q S L L K D R P V G A A T A M Q E S --A : 217

bZIP

*           260          *           280          *           300
Arabidopsis : L L L E S L L L G S L L W L L G V N F I C L F P Y M S H T K C C L L R P E P E -----K L V L N G L G ----- : 265
Soybean    : L L L E P L L L G S L L W C M G I I C H I S L P L M L W A A V L P -R E N I E Q K G L R R V T Q K G S ----- : 251
Capsicum   : L L L E S L L L G S L L W F L G I S C L L I L P S Q T W S I P E E N Q G S R N -----P G L L V P I K ----- : 248
Rice       : V L T E T L P L V S L L W L V S I V C L L P V E G L P N R N P V A R S S A G R -----D L A T V T G K ----- : 264

TMD

*           320          *           340
Arabidopsis : -S S S K P S -----Y T G V S R R C K G S R P R M K Y Q I L T L A A ----- : 295
Soybean    : -E S K -I S E C F Q M Q S F L K S R K S R A S R T K M K E N F I V E ----- : 284
Capsicum   : -R G K K T S R S L A F L S F M M G K R C K A S R S R M K E N P H S L G I V M --- : 286
Rice       : --K T S S E Q Q L E E T L L L H G R R C K G S R A R T K L D T G P F R L A A A A C : 304

```

## Supplemental Figure 2. Amino acid alignment of bZIP60 homologs.

Amino acid sequences of *Arabidopsis* bZIP60 and homologs from *Oryza sativa* (BAF20014), *Capsicum annuum* (AAX20030) and *Glycine max* (ABI34650) were aligned using ClustalW. Identical amino acid residues among all species are shaded in black, and conserved residues in at least two species are highlighted with gray boxes. bZIP domains (bZIP) and transmembrane domains (TMD) are indicated.

### Supplemental Table 1. Genes induced more than 3-fold by tunicamycin treatment.

FI, fold induction; Genes whose induction is significantly lower in the *bzip60* mutant seedlings than in wild-type seedlings are shown in boldface type with *P*-values.

| AGI code                     | Description  | WT         |              |              | <i>bzip60</i> |             |             | <i>cis</i> -element  | <i>P</i> -value |
|------------------------------|--|------------|--------------|--------------|---------------|-------------|-------------|----------------------|-----------------|
|                              |  | -Tm        | +Tm          | FI           | -Tm           | +Tm         | FI          |                      |                 |
| Protein folding (25 genes)   |  |            |              |              |               |             |             |                      |                 |
| <b>AT1G09080</b>             | <b>BiP3</b>  | <b>1.3</b> | <b>151.8</b> | <b>119.5</b> | <b>0.7</b>    | <b>17.5</b> | <b>25.8</b> | ERSEx2               | <b>0.0083</b>   |
| <b>AT3G08970</b>             | <b>ERdj3A</b>  | <b>1.0</b> | <b>24.0</b>  | <b>24.0</b>  | <b>1.0</b>    | <b>15.8</b> | <b>15.9</b> |                      | <b>0.0038</b>   |
| <b>AT1G72280</b>             | <b>ER oxidoreductin (ERO1)</b>                               | <b>1.0</b> | <b>13.7</b>  | <b>13.5</b>  | <b>1.0</b>    | <b>6.2</b>  | <b>6.4</b>  |                      | <b>0.0010</b>   |
| <b>AT1G77510</b>             | <b>PDI</b>   | <b>1.1</b> | <b>13.8</b>  | <b>12.1</b>  | <b>0.8</b>    | <b>6.9</b>  | <b>8.2</b>  | ERSE                 | <b>0.0074</b>   |
| <b>AT4G24190</b>             | <b>GRP94</b>   | <b>1.1</b> | <b>12.3</b>  | <b>11.4</b>  | <b>0.9</b>    | <b>6.8</b>  | <b>7.5</b>  | ERSE, ERSE-L, UPRE   | <b>0.0021</b>   |
| AT2G02810                    | UDP-galactose/UDP-glucose transporter                        | 1.0        | 10.7         | 10.4         | 1.0           | 9.5         | 9.9         | ERSE-L               |                 |
| AT5G42020                    | BiP2   | 1.1        | 10.3         | 9.5          | 0.9           | 7.2         | 8.1         | ERSE-II, XBP1BS      |                 |
| AT1G04980                    | PDI-related  | 1.1        | 9.9          | 9.0          | 0.9           | 7.2         | 8.3         | ERSE                 |                 |
| AT5G28540                    | BiP1   | 1.1        | 9.8          | 8.9          | 0.9           | 7.1         | 8.0         | ERSE-II, XBP1BS      |                 |
| <b>AT2G32920</b>             | <b>PDI, putative</b>   | <b>1.1</b> | <b>9.5</b>   | <b>8.7</b>   | <b>0.9</b>    | <b>3.6</b>  | <b>4.0</b>  | ERSE-L               | <b>0.0178</b>   |
| <b>AT3G51980</b>             | <b>SIL1, putative</b>  | <b>1.0</b> | <b>8.2</b>   | <b>8.3</b>   | <b>1.0</b>    | <b>5.1</b>  | <b>5.1</b>  | ERSE                 | <b>0.0351</b>   |
| AT3G55700                    | UDP-glucuronosyl/UDP-glucosyl transferase family protein     | 1.1        | 8.1          | 7.6          | 0.9           | 2.1         | 2.2         |                      |                 |
| AT3G62600                    | ERdj3B   | 1.1        | 8.0          | 7.5          | 0.9           | 5.5         | 5.9         | ERSE                 |                 |
| <b>AT1G09210</b>             | <b>CRT2</b>  | <b>1.1</b> | <b>7.8</b>   | <b>7.1</b>   | <b>0.9</b>    | <b>5.2</b>  | <b>5.7</b>  | ERSE, ERSE-L         | <b>0.0056</b>   |
| AT5G61790                    | CNX1   | 1.1        | 7.5          | 7.0          | 0.9           | 6.3         | 6.8         | ERSE, UPRE           |                 |
| AT1G14360                    | UDP-galactose/UDP-glucose transporter                        | 1.0        | 7.3          | 6.9          | 1.0           | 6.6         | 7.0         | ERSE                 |                 |
| AT1G56300                    | DnaJ protein, putative                                       | 1.0        | 5.9          | 6.2          | 1.0           | 5.2         | 5.0         |                      |                 |
| <b>AT4G16660</b>             | <b>HSP like protein (containing HDEL)</b>                    | <b>1.1</b> | <b>6.4</b>   | <b>6.1</b>   | <b>0.9</b>    | <b>4.0</b>  | <b>4.3</b>  | ERSE, UPRE           | <b>0.0389</b>   |
| <b>AT1G21750</b>             | <b>putative PDI</b>  | <b>1.1</b> | <b>6.4</b>   | <b>6.0</b>   | <b>0.9</b>    | <b>4.1</b>  | <b>4.4</b>  | ERSEx2, UPRE         | <b>0.0209</b>   |
| <b>AT5G07340</b>             | <b>CNX2</b>  | <b>1.1</b> | <b>4.8</b>   | <b>4.5</b>   | <b>0.9</b>    | <b>3.7</b>  | <b>4.0</b>  |                      | <b>0.0322</b>   |
| <b>AT2G47470</b>             | <b>putative PDI precursor</b>                                | <b>1.1</b> | <b>4.6</b>   | <b>4.3</b>   | <b>0.9</b>    | <b>3.2</b>  | <b>3.5</b>  | UPRE                 | <b>0.0215</b>   |
| <b>AT1G56340</b>             | <b>CRT1</b>  | <b>1.1</b> | <b>4.4</b>   | <b>4.1</b>   | <b>0.9</b>    | <b>2.7</b>  | <b>2.9</b>  | ERSE, ERSE-L, UPREx2 | <b>0.0366</b>   |
| <b>AT3G54960</b>             | <b>PDI-like</b>  | <b>1.1</b> | <b>4.4</b>   | <b>3.9</b>   | <b>0.8</b>    | <b>1.9</b>  | <b>2.2</b>  | ERSE-L               | <b>0.0123</b>   |
| <b>AT4G21180</b>             | <b>ERdj2B</b>  | <b>1.0</b> | <b>4.0</b>   | <b>3.9</b>   | <b>1.0</b>    | <b>2.5</b>  | <b>2.6</b>  | ERSE-L               | <b>0.0239</b>   |
| AT5G58710                    | ROC7   | 1.0        | 3.4          | 3.4          | 1.0           | 2.5         | 2.5         | ERSE, ERSE-L, UPRE   |                 |
| Secretory pathway (21 genes) |  |            |              |              |               |             |             |                      |                 |
| <b>AT1G09180</b>             | <b>SAR1B</b>   | <b>1.1</b> | <b>10.5</b>  | <b>9.7</b>   | <b>0.9</b>    | <b>1.9</b>  | <b>2.2</b>  | ERSE-Lx2             | <b>0.0019</b>   |
| <b>AT1G70490</b>             | <b>putative ADP-ribosylation factor 1 (Arf)</b>              | <b>1.0</b> | <b>9.0</b>   | <b>8.9</b>   | <b>1.0</b>    | <b>1.8</b>  | <b>1.8</b>  | ERSE                 | <b>0.0103</b>   |
| AT1G29310                    | Sec61 alpha  | 1.1        | 8.0          | 7.2          | 0.9           | 4.6         | 5.2         | ERSE                 |                 |
| <b>AT3G15980</b>             | <b>putative coatomer complex subunit (COPI-vesicle coat)</b> | <b>1.0</b> | <b>6.9</b>   | <b>6.7</b>   | <b>1.0</b>    | <b>1.2</b>  | <b>1.2</b>  |                      | <b>0.0035</b>   |
| <b>AT5G14670</b>             | <b>ADP-ribosylation factor (Arf)- like</b>                   | <b>0.9</b> | <b>5.9</b>   | <b>6.3</b>   | <b>1.1</b>    | <b>1.5</b>  | <b>1.5</b>  |                      | <b>0.0234</b>   |
| AT3G60540                    | Sec61 beta   | 1.1        | 6.1          | 5.8          | 0.9           | 4.5         | 4.8         | ERSEx2               |                 |
| AT3G05230                    | signal peptidase   | 1.0        | 5.1          | 5.1          | 1.0           | 3.5         | 3.5         |                      |                 |
| AT1G27350                    | RAMP4-like   | 1.0        | 5.1          | 5.0          | 1.0           | 4.3         | 4.4         | ERSE                 |                 |
| AT1G27330                    | RAMP4-like   | 1.0        | 5.2          | 5.0          | 1.0           | 4.4         | 4.6         | ERSE, ERSE-L         |                 |
| AT5G50460                    | Sec61 gamma  | 1.0        | 4.7          | 4.5          | 1.0           | 4.0         | 4.2         |                      |                 |
| AT4G24920                    | SEC61 Gamma -like  | 1.1        | 4.4          | 4.2          | 0.9           | 3.3         | 3.4         |                      |                 |
| AT2G45070                    | putative SEC61 beta  | 1.0        | 4.0          | 4.0          | 1.0           | 3.2         | 3.2         | ERSE-L               |                 |
| <b>AT1G10630</b>             | <b>ADP-ribosylation factor (Arf), putative</b>               | <b>1.0</b> | <b>3.9</b>   | <b>3.9</b>   | <b>1.0</b>    | <b>1.4</b>  | <b>1.4</b>  |                      | <b>0.0034</b>   |
| <b>AT3G44340</b>             | <b>Sec24 like</b>  | <b>1.0</b> | <b>3.9</b>   | <b>3.8</b>   | <b>1.0</b>    | <b>1.7</b>  | <b>1.7</b>  |                      | <b>0.0131</b>   |
| <b>AT2G03120</b>             | <b>signal peptide peptidase</b>                              | <b>1.0</b> | <b>3.8</b>   | <b>3.8</b>   | <b>1.0</b>    | <b>3.0</b>  | <b>3.0</b>  |                      | <b>0.0318</b>   |

|                                 |  |            |             |            |            |            |            |                    |               |
|---------------------------------|--|------------|-------------|------------|------------|------------|------------|--------------------|---------------|
| AT1G21900                       | emp24/gp25L/p24 family protein, similar to Transmembrane protein Tmp21 | 1.0        | 3.5         | 3.5        | 1.0        | 3.6        | 3.7        |                    |               |
| <b>AT3G07680</b>                | <b>putative coated vesicle membrane protein</b>                        | <b>1.0</b> | <b>3.4</b>  | <b>3.4</b> | <b>1.0</b> | <b>2.4</b> | <b>2.4</b> | ERSE, ERSE-L, UPRE | <b>0.0056</b> |
| <b>AT1G62020</b>                | <b>coatomer alpha subunit, putative</b>                                | <b>1.0</b> | <b>3.3</b>  | <b>3.2</b> | <b>1.0</b> | <b>1.2</b> | <b>1.2</b> |                    | <b>0.0219</b> |
| AT1G52600                       | signal peptidase subunit, putative                                     | 1.0        | 3.2         | 3.2        | 1.0        | 2.8        | 2.7        | XBP1BS, UPREx2     |               |
| AT2G34250                       | SEC61 alpha  | 1.0        | 3.1         | 3.1        | 1.0        | 2.9        | 2.9        | ERSE-L             |               |
| <b>AT1G78920</b>                | <b>AVP2, Golgi-localized proton-translocating pyrophosphatase</b>      | <b>1.0</b> | <b>2.9</b>  | <b>3.0</b> | <b>1.0</b> | <b>1.4</b> | <b>1.4</b> |                    | <b>0.0025</b> |
| Protein degradation (11 genes)  |  |            |             |            |            |            |            |                    |               |
| AT5G40010                       | AAA-type ATPase  | 1.0        | 7.5         | 7.6        | 1.0        | 4.0        | 3.9        |                    |               |
| AT2G02230                       | phloem-specific lectin, F-box family                                   | 1.0        | 5.6         | 5.6        | 1.0        | 6.1        | 6.1        |                    |               |
| <b>AT4G05010</b>                | <b>F-box family protein</b>  | <b>0.9</b> | <b>4.7</b>  | <b>5.1</b> | <b>1.1</b> | <b>1.8</b> | <b>1.7</b> | ERSE, ERSE-L       | <b>0.0063</b> |
| AT5G17760                       | AAA-type ATPase  | 1.0        | 4.6         | 4.5        | 1.0        | 3.9        | 4.0        |                    |               |
| <b>AT4G05380</b>                | <b>AAA-type ATPase</b>   | <b>0.9</b> | <b>3.9</b>  | <b>4.5</b> | <b>1.1</b> | <b>1.1</b> | <b>1.0</b> |                    | <b>0.0070</b> |
| <b>AT1G18260</b>                | <b>SEL-1 protein-related</b>   | <b>1.0</b> | <b>4.2</b>  | <b>4.0</b> | <b>1.0</b> | <b>2.9</b> | <b>2.9</b> | ERSE               | <b>0.0154</b> |
| AT1G64470                       | ubiquitin, putative  | 1.0        | 4.1         | 4.0        | 0.9        | 2.4        | 2.5        | ERSE-L             |               |
| <b>AT3G17000</b>                | <b>E2, ubiquitin-conjugating enzyme, putative</b>                      | <b>0.9</b> | <b>3.8</b>  | <b>4.0</b> | <b>1.0</b> | <b>2.1</b> | <b>2.0</b> | UPREx2             | <b>0.0460</b> |
| <b>AT4G21810</b>                | <b>Derlin-like</b>   | <b>0.9</b> | <b>3.1</b>  | <b>3.3</b> | <b>1.1</b> | <b>2.3</b> | <b>2.2</b> | ERSE-L             | <b>0.0124</b> |
| <b>AT1G80110</b>                | <b>expressed protein, similar to SKP1 interacting partner 3</b>        | <b>1.0</b> | <b>3.2</b>  | <b>3.3</b> | <b>1.0</b> | <b>3.1</b> | <b>3.0</b> | ERSE-L             | <b>0.0425</b> |
| AT3G23280                       | zinc finger (C3HC4-type RING finger) family protein                    | 1.0        | 3.2         | 3.2        | 1.0        | 2.9        | 2.9        |                    |               |
| Transcription factor (13 genes) |  |            |             |            |            |            |            |                    |               |
| <b>AT1G01380</b>                | <b>myb family TF (CPC, ETC1)</b>                                       | <b>1.0</b> | <b>8.4</b>  | <b>8.5</b> | <b>1.0</b> | <b>1.0</b> | <b>1.0</b> |                    | <b>0.0237</b> |
| AT2G40340                       | AP2 domain TF (DREB subfamily)   | 0.9        | 7.3         | 8.4        | 1.1        | 6.5        | 6.0        | XBP1BS             |               |
| <b>AT1G42990</b>                | <b>bZIP60</b>  | <b>1.6</b> | <b>13.6</b> | <b>8.3</b> | <b>0.4</b> | <b>0.4</b> | <b>1.1</b> | ERSE-L             | <b>0.0001</b> |
| <b>AT5G22290</b>                | <b>NAM (no apical meristem)-like protein</b>                           | <b>1.0</b> | <b>6.5</b>  | <b>6.7</b> | <b>1.0</b> | <b>3.6</b> | <b>3.5</b> | ERSE-L, UPRE       | <b>0.0253</b> |
| <b>AT5G64060</b>                | <b>NAC1-like</b>   | <b>1.2</b> | <b>7.8</b>  | <b>6.6</b> | <b>0.8</b> | <b>1.1</b> | <b>1.4</b> |                    | <b>0.0142</b> |
| <b>AT3G28210</b>                | <b>zinc finger protein (PMZ), putative</b>                             | <b>0.9</b> | <b>3.8</b>  | <b>4.3</b> | <b>1.1</b> | <b>2.1</b> | <b>1.9</b> |                    | <b>0.0123</b> |
| <b>AT3G49530</b>                | <b>NAC2-like protein</b>   | <b>0.9</b> | <b>3.5</b>  | <b>3.8</b> | <b>1.1</b> | <b>1.8</b> | <b>1.7</b> | ERSE-L             | <b>0.0037</b> |
| AT1G67970                       | putative heat shock transcription factor                               | 1.0        | 3.5         | 3.7        | 1.0        | 2.8        | 2.7        |                    |               |
| AT3G48360                       | speckle-type POZ protein-related                                       | 0.8        | 2.8         | 3.6        | 1.2        | 3.8        | 3.3        |                    |               |
| AT3G46080                       | zinc finger (C2H2-type)-like protein                                   | 0.8        | 2.9         | 3.5        | 1.2        | 3.4        | 2.9        |                    |               |
| AT5G03720                       | heat shock transcription factor -like protein                          | 1.0        | 3.6         | 3.5        | 1.0        | 3.7        | 3.8        | XBP1BS             |               |
| <b>AT1G56170</b>                | <b>Hap5b</b>   | <b>1.0</b> | <b>3.0</b>  | <b>3.0</b> | <b>1.0</b> | <b>1.2</b> | <b>1.1</b> | ERSE-L             | <b>0.0082</b> |
| AT5G63160                       | speckle-type POZ protein-related                                       | 1.0        | 2.9         | 3.0        | 1.0        | 2.7        | 2.8        |                    |               |
| Others (25 genes)               |  |            |             |            |            |            |            |                    |               |
| AT1G07050                       | expressed protein (CONSTANS-like-related)                              | 1.0        | 13.8        | 14.1       | 1.0        | 14.8       | 14.5       | ERSE-L             |               |
| AT3G24090                       | glutamine:fructose-6-phosphate amidotransferase, putative              | 1.0        | 7.1         | 7.1        | 1.0        | 6.4        | 6.4        | ERSE, UPRE         |               |
| AT4G21820                       | putative protein, calmodulin binding                                   | 1.1        | 7.1         | 6.7        | 0.9        | 2.9        | 3.0        |                    |               |
| AT1G78340                       | glutathione transferase, putative (GST7-like)                          | 0.9        | 6.0         | 6.6        | 1.1        | 6.2        | 5.9        |                    |               |
| <b>AT2G34430</b>                | <b>photosystem II type I chlorophyll a /b binding protein</b>          | <b>1.0</b> | <b>6.5</b>  | <b>6.4</b> | <b>1.0</b> | <b>3.7</b> | <b>3.8</b> |                    | <b>0.0238</b> |
| AT2G25110                       | MIR domain-containing protein  | 1.0        | 6.2         | 6.0        | 1.0        | 5.2        | 5.4        | ERSE-Lx2           |               |
| AT4G14420                       | elicitor like protein, lesion inducing protein                         | 1.0        | 5.6         | 5.5        | 1.0        | 4.0        | 4.2        |                    |               |
| AT1G64460                       | phosphatidylinositol 3- and 4-kinase family protein                    | 1.0        | 5.6         | 5.4        | 1.0        | 3.4        | 3.6        |                    |               |

|                    |   |            |             |             |            |             |             |                       |
|--------------------|---|------------|-------------|-------------|------------|-------------|-------------|-----------------------|
| AT2G42530          | cold-regulated protein cor15b precursor                           | 0.9        | 4.1         | 4.8         | 1.1        | 3.6         | 3.4         |                       |
| <b>AT3G03640</b>   | <b>glycosyl hydrolase family 1 (beta-glucosidase)</b>             | <b>0.9</b> | <b>4.4</b>  | <b>4.7</b>  | <b>1.1</b> | <b>3.5</b>  | <b>3.3</b>  | <b>0.0341</b>         |
| <b>AT5G47120</b>   | <b>Bax inhibitor-1 (BI-1)</b>                                     | <b>1.0</b> | <b>4.5</b>  | <b>4.6</b>  | <b>1.0</b> | <b>2.8</b>  | <b>2.8</b>  | <b>ERSE</b>           |
| AT2G28630          | beta-ketoacyl-CoA synthase family                                 | 1.0        | 4.3         | 4.5         | 1.0        | 4.6         | 4.6         |                       |
| AT1G17960          | threonyl-tRNA synthetase, putative                                | 1.1        | 4.6         | 4.3         | 0.9        | 0.5         | 0.6         |                       |
| AT1G78290          | serine-threonine protein kinase, putative                         | 1.0        | 4.1         | 4.0         | 1.0        | 5.1         | 5.2         |                       |
| AT5G43860          | CLH2 (chlorophyllase)   | 1.0        | 3.9         | 4.0         | 1.0        | 4.4         | 4.3         |                       |
| AT2G27690          | cytochrome p450, putative   | 0.8        | 3.3         | 4.0         | 1.1        | 4.5         | 3.9         |                       |
| AT2G40880          | putative cysteine proteinase inhibitor B (cystatin B)             | 1.0        | 3.7         | 3.9         | 1.0        | 3.3         | 3.2         |                       |
| AT2G30750          | cytochrome p450 family (CYP71A12)                                 | 1.1        | 4.1         | 3.8         | 0.8        | 2.4         | 3.0         |                       |
| AT5G60100          | pseudo-response regulator 3 (APRR3)                               | 1.0        | 3.6         | 3.7         | 1.0        | 4.0         | 4.0         | ERSE-L                |
| AT2G45790          | putative phosphomannomutase                                       | 1.0        | 3.5         | 3.6         | 1.0        | 2.5         | 2.4         |                       |
| <b>AT3G18750</b>   | <b>mitogen activated protein kinase kinase, putative</b>          | <b>1.1</b> | <b>3.6</b>  | <b>3.4</b>  | <b>0.9</b> | <b>1.2</b>  | <b>1.2</b>  | <b>0.0153</b>         |
| AT5G43440          | l-aminocyclopropane-1-carboxylate oxidase                         | 0.9        | 3.1         | 3.3         | 1.0        | 3.2         | 3.1         |                       |
| <b>AT2G40670</b>   | <b>ARR16, two-component response regulator protein</b>            | <b>1.0</b> | <b>3.3</b>  | <b>3.2</b>  | <b>1.0</b> | <b>2.4</b>  | <b>2.5</b>  | <b>0.0171</b>         |
| AT2G38240          | oxidoreductase, similar to flavonol synthase                      | 0.6        | 1.8         | 3.1         | 1.3        | 3.8         | 2.9         |                       |
| AT3G44870          | S-adenosyl-L-methionine:carboxyl methyltransferase family protein | 0.9        | 2.5         | 3.0         | 0.9        | 2.5         | 2.8         |                       |
| -----              |   |            |             |             |            |             |             |                       |
| Unknown (34 genes) |   |            |             |             |            |             |             |                       |
| <b>AT5G64510</b>   | <b>putative protein</b>   | <b>1.0</b> | <b>26.7</b> | <b>26.8</b> | <b>1.0</b> | <b>10.7</b> | <b>10.7</b> | <b>XBP1BS, UPREx2</b> |
| <b>AT5G23575</b>   | <b>transmembrane protein, putative</b>                            | <b>1.1</b> | <b>10.1</b> | <b>9.4</b>  | <b>0.9</b> | <b>2.6</b>  | <b>2.8</b>  | <b>0.0239</b>         |
| <b>AT1G56580</b>   | <b>expressed protein</b>  | <b>1.0</b> | <b>9.0</b>  | <b>8.8</b>  | <b>1.0</b> | <b>1.5</b>  | <b>1.5</b>  | <b>0.0248</b>         |
| <b>AT2G25460</b>   | <b>expressed protein</b>  | <b>0.9</b> | <b>8.1</b>  | <b>8.6</b>  | <b>1.1</b> | <b>2.0</b>  | <b>1.9</b>  | <b>ERSE</b>           |
| AT4G34630          | putative protein  | 1.0        | 7.7         | 7.4         | 1.0        | 6.9         | 7.2         | ERSE-L                |
| AT4G29520          | putative protein  | 1.1        | 7.3         | 6.8         | 0.9        | 6.2         | 6.7         | ERSE-L                |
| <b>AT5G42050</b>   | <b>unknown protein</b>  | <b>1.0</b> | <b>5.9</b>  | <b>6.1</b>  | <b>1.0</b> | <b>2.6</b>  | <b>2.5</b>  | <b>UPRE</b>           |
| <b>AT5G02220</b>   | <b>Expressed protein</b>  | <b>1.0</b> | <b>5.6</b>  | <b>5.9</b>  | <b>1.0</b> | <b>2.9</b>  | <b>2.8</b>  | <b>ERSE-L, UPRE</b>   |
| <b>AT5G35080</b>   | <b>putative protein</b>   | <b>1.0</b> | <b>5.7</b>  | <b>5.6</b>  | <b>1.0</b> | <b>3.8</b>  | <b>3.9</b>  | <b>ERSE</b>           |
| AT5G15190          | putative protein  | 1.0        | 5.1         | 5.3         | 1.0        | 3.7         | 3.5         | ERSE-L                |
| AT3G51400          | putative protein  | 1.0        | 5.1         | 5.3         | 1.0        | 6.5         | 6.4         |                       |
| AT1G11210          | expressed protein   | 0.9        | 4.5         | 5.0         | 1.1        | 5.9         | 5.5         |                       |
| <b>AT4G32670</b>   | <b>putative protein</b>   | <b>1.1</b> | <b>5.3</b>  | <b>5.0</b>  | <b>0.9</b> | <b>1.2</b>  | <b>1.3</b>  | <b>0.0009</b>         |
| AT5G42900          | putative protein  | 0.8        | 3.9         | 4.6         | 1.1        | 4.4         | 3.9         | XBP1BS                |
| AT1G29060          | expressed protein   | 0.8        | 3.7         | 4.5         | 1.1        | 1.6         | 1.5         | ERSE                  |
| AT4G08230          | glycine rich protein  | 1.0        | 4.5         | 4.4         | 1.0        | 4.1         | 4.2         | ERSE, ERSE-L          |
| AT4G04330          | expressed protein   | 0.9        | 3.9         | 4.3         | 1.0        | 4.9         | 4.7         |                       |
| AT4G32340          | putative protein  | 0.9        | 3.7         | 4.3         | 1.1        | 3.9         | 3.6         |                       |
| AT5G47420          | putative protein  | 1.0        | 4.3         | 4.3         | 1.0        | 4.0         | 4.0         | ERSE                  |
| AT2G19460          | expressed protein   | 1.0        | 3.9         | 4.0         | 1.0        | 3.6         | 3.5         |                       |
| AT4G33980          | putative protein  | 0.8        | 3.3         | 3.9         | 1.1        | 3.6         | 3.2         | XBP1BS                |
| AT1G13340          | hypothetical protein  | 0.8        | 3.2         | 3.8         | 1.1        | 3.6         | 3.2         |                       |
| <b>AT4G30500</b>   | <b>putative protein</b>   | <b>1.0</b> | <b>3.5</b>  | <b>3.7</b>  | <b>1.0</b> | <b>3.0</b>  | <b>2.9</b>  | <b>ERSE-L</b>         |
| AT1G52590          | expressed protein   | 0.8        | 3.1         | 3.7         | 1.2        | 2.3         | 2.0         | XBP1BS, UPREx2        |
| <b>AT1G67960</b>   | <b>unknown protein</b>  | <b>1.0</b> | <b>3.7</b>  | <b>3.6</b>  | <b>1.0</b> | <b>2.2</b>  | <b>2.2</b>  | <b>ERSE</b>           |
| AT3G15630          | expressed protein   | 0.7        | 2.6         | 3.6         | 1.3        | 3.6         | 2.9         |                       |
| AT4G29960          | expressed protein   | 1.0        | 3.5         | 3.5         | 1.0        | 3.0         | 3.1         | ERSE                  |
| AT1G42480          | expressed protein   | 1.0        | 3.6         | 3.5         | 1.0        | 2.6         | 2.8         | XBP1BS, UPRE          |

|                  |                                   |            |            |            |            |            |            |             |               |
|------------------|-----------------------------------|------------|------------|------------|------------|------------|------------|-------------|---------------|
| AT3G53670        | putative protein                  | 1.0        | 3.5        | 3.4        | 1.0        | 3.2        | 3.2        | ERSE-L      |               |
| AT5G24470        | putative protein                  | 1.0        | 3.4        | 3.5        | 1.0        | 3.9        | 3.9        |             |               |
| AT3G26740        | light regulated protein, putative | 0.8        | 2.8        | 3.4        | 1.1        | 4.4        | 3.8        |             |               |
| AT4G14270        | Expressed protein                 | 0.8        | 2.6        | 3.2        | 1.2        | 2.6        | 2.2        |             |               |
| <b>AT5G10695</b> | <b>Expressed protein</b>          | <b>0.8</b> | <b>2.3</b> | <b>3.0</b> | <b>1.2</b> | <b>2.3</b> | <b>1.9</b> | <b>UPRE</b> | <b>0.0214</b> |
| AT3G44860        | methyltransferase-related         | 0.5        | 1.5        | 3.0        | 1.3        | 3.2        | 2.5        | ERSE-Lx2    |               |