

Supplemental Figure S1. Multiple sequence alignments of ELF3 orthologs (**A**) and percentage of identical amino acid sequences (**B**). Protein sequences of AtELF3 (AT2G25930.1), BdELF3 (Bradi2g14290.1), SvELF3a (Sevir.5G206400.1) and SvELF3b (Sevir.3G123200.1) were used for multiple sequence alignments and for generating percentage of identical amino acids by Clustal Omega alignment with default parameters.

Supplemental Figure S2. Diel and circadian expression of *BdELF3* from the DIURNAL database. GCRMA (GeneChip Robust Multiarray Averaging) values from the DIURNAL database (Mockler et al., 2007) were plotted to show time-course expression profiles of *Bradi2g14290* (*BdELF3*) under either diel (**A**) or circadian conditions (**B**). Diel expression of *AtELF3* from DIURNAL database was used for comparison in (**A**). Shade boxes indicate dark periods. In (**B**), Circadian expression data was obtained by entraining plants with either photo- (LDHH) or thermo- (LLHC) conditions followed by sampling under the Free-Running condition (F) with constant light and temperature.

Supplemental Figure S3. Example of the Diel Explorer interface. The search interface (left) and plotting interface of Diel Explorer are shown (right). Users can search by gene or ortholog id, or by gene ontology term. Alternately, users can filter data by period, phase (lag) or significance cut offs. Data can be plotted in a line graph or heatmap.

Supplemental Figure S4. Summary of circadian regulated genes in *S. viridis*. Distribution of circadian regulated genes in *S. viridis* was plotted by their phases, with the y axis showing the number of genes considered significantly (Bonferroni Adjusted P-Value < 0.001) cycling under photo- (LDHH) or thermo- (LLHC) entrainment in *S. viridis* followed by free-running condition (F).

Supplemental Figure S5. Circadian expression of selected *A. thaliana* clock genes from the DIURNAL database. GCRMA (GeneChip Robust Multiarray Averaging) values were plotted to show time-course expression profiles of selected *A. thaliana* clock genes under

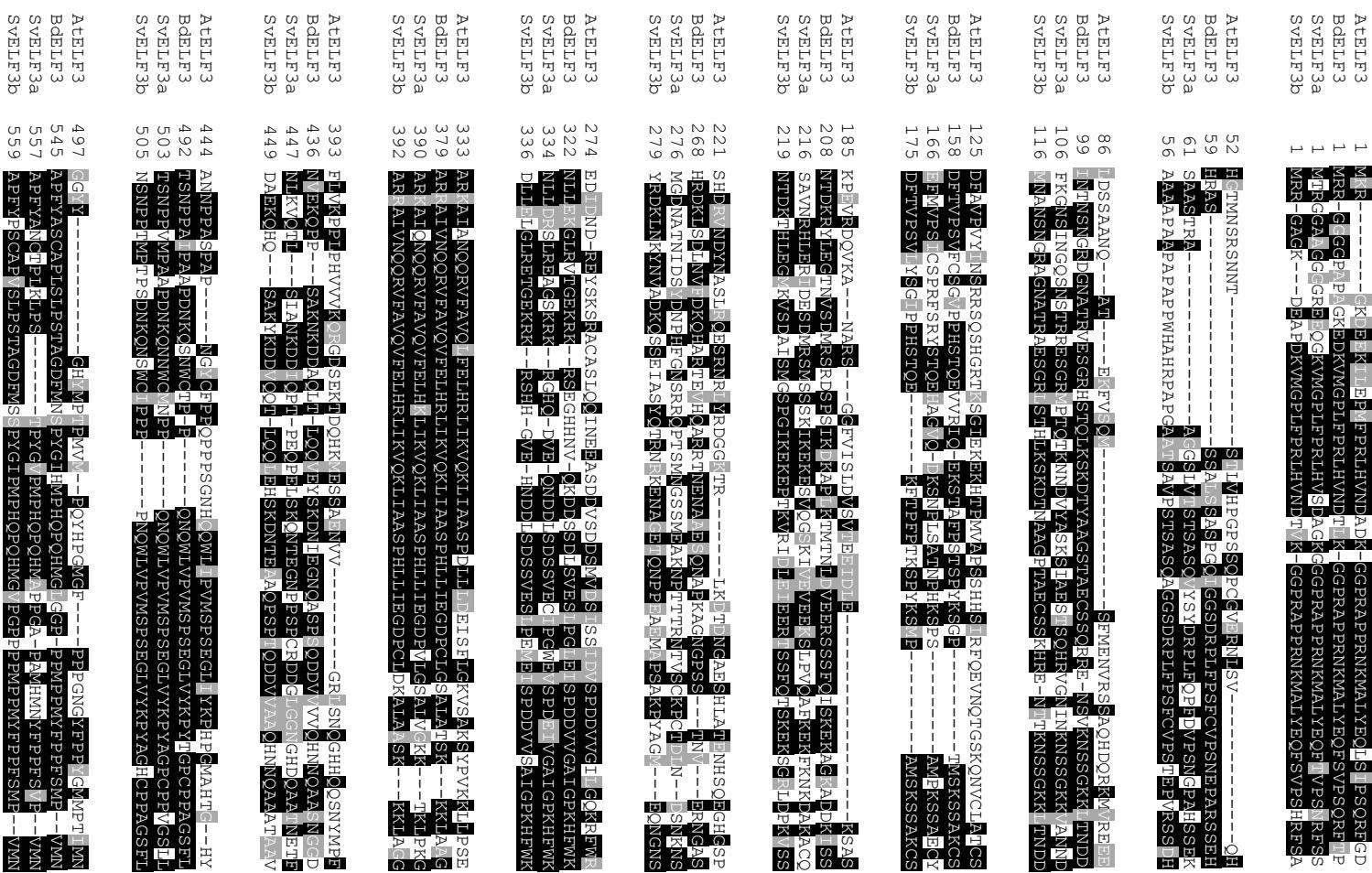
either photo- (LL23_LDHH) or thermo-entrainment (LL_LLHC) from the DIURNAL database (Mockler et al., 2007). Each gene cycles with a correlation of > 0.9 when compared to a best fit model (24-hour rhythm).

Supplemental Figure S6. Anti-FLAG western of ELF3 transgenic lines used for complementation analysis. Representative blot of protein extracts from day 12 seedlings taken at Zeitgeber time 12 grown under 12-hour light :12-hour dark growth conditions at 22 °C that were probed with FLAG antibody to detect the 3xFLAG epitope. RPT5 is used as a loading control.

Supplemental Figure S7. Relative Amplitude Error vs period plots. The periods and relative amplitude error (RAE) of 8 AtELF3 *elf3*-2 (**A**), BdELF3 *elf3*-2 (**B**), and SvELF3 *elf3*-2 (**C**) seedlings were plotted along with wild type and *elf3*-2 mutants (Note, only 3 of 8 *elf3* seedlings has measurable rhythms). RAE=0.5 was used as a cutoff (dotted line), above which a seedling is not considered rhythmic (Plautz et al., 1997). Note that wild type and *elf3* mutant data were reproduced on all plots for comparison purposes.

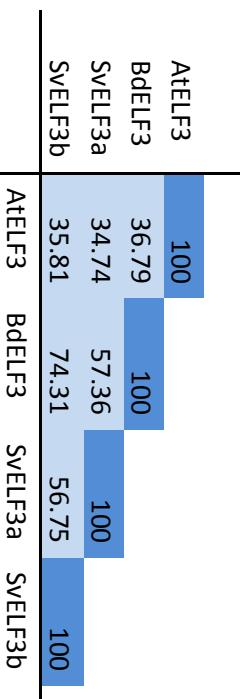
Supplemental Figure 1

A



B

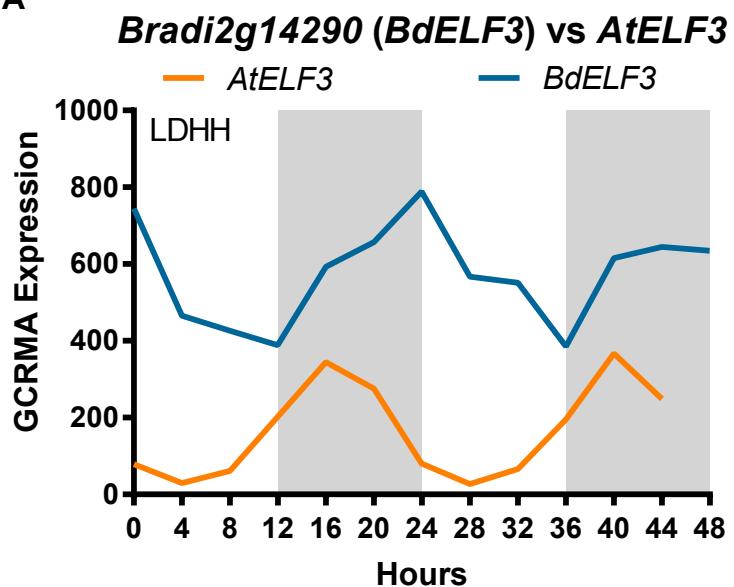
| | AtELF3 | BdELF3 | SveLF3a | SveLF3b |
|---------|--------|--------|------------------|------------------|
| AtELF3 | 100 | | | |
| BdELF3 | | 100 | | |
| SveLF3a | | | Sevir.5G206400.1 | |
| SveLF3b | | | | Sevir.3G123200.1 |



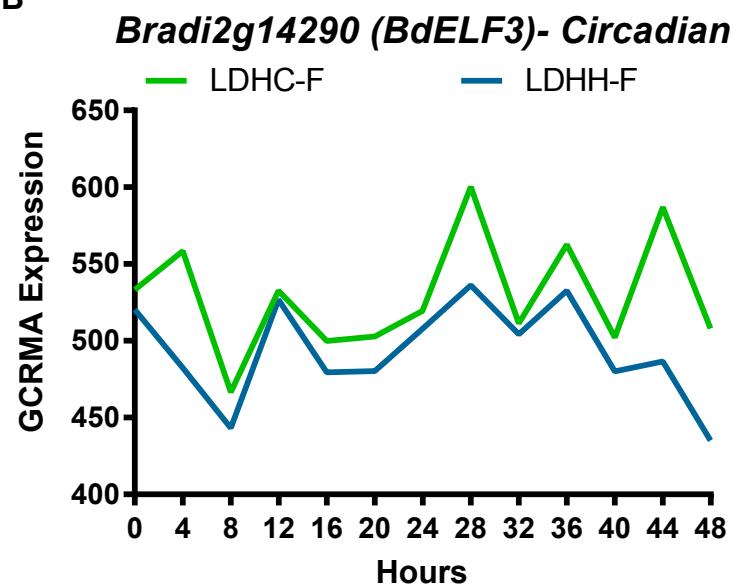
| | | | | | | |
|---------|------|----------------|----------|---------|--------------|-----------|
| AtELF3 | 53.9 | PYCSSQQQQQ | QPNEQM | GHPG-NI | NTQQQQRSDNEP | QQQQQPTKS |
| BdELF3 | 60.2 | PWVSSAVEQSR | RAPARN | HEH | SRNSCNM | -RNEASAGI |
| SveLF3a | 60.7 | PGAPASAVEEQSGH | AVOFGH | RAEQS | TSNCMSH | -PSGI |
| SveLF3b | 61.7 | TIVSASAVEQSVH | MAFPRNGH | IEHRS | SCNSMS | -IRSEAL |

Supplemental Figure 2

A



B



Supplemental Figure 3

Diel Explorer

Welcome
Sample Info
Search and Browse Data
Plot Data
Adding Your Own Data
Contact Us

Search Data with GENEID or GO

Search using small sets of GENEIDs
GENEIDs, Orthologs, or GO separated by a comma are allowed

example: Sevir.2G310200.1, Sevir.1G000100.1

refresh page to clear search

Search Data with File

Genes, Orthologs, or GO Selected with Search

Browse and Filter Data

Normalize Data: Yes No

Species: All

Entrainment: ldhhf

Benjamini-Hochberg Q-Value: 1e-06

Lag (Phase): 2

Adjusted P-value: 1e-06

Show: 25 entries

Color Line Graph By

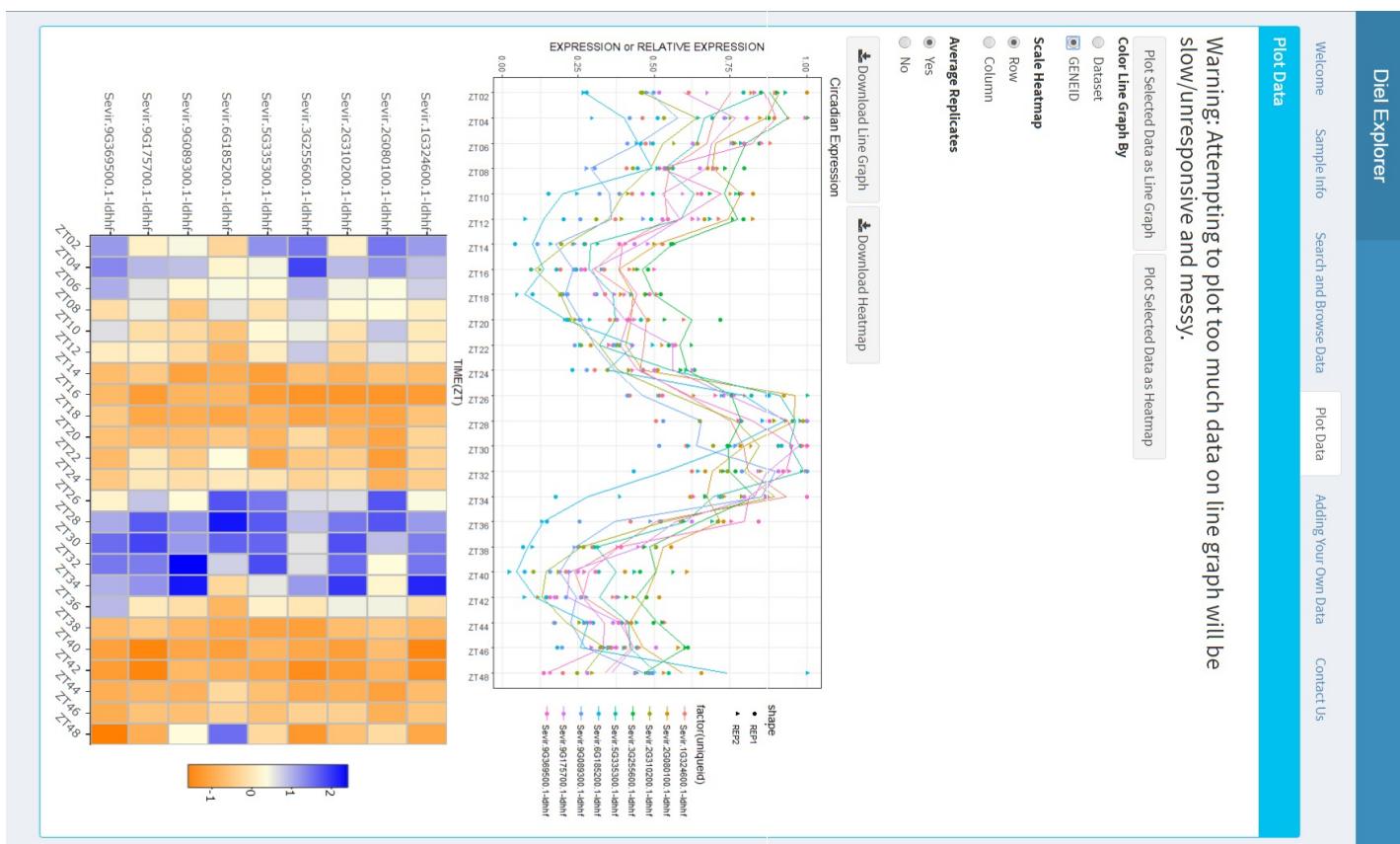
- Dataset
- GENEID
- Row
- Column
- Yes
- No

Scale Heatmap

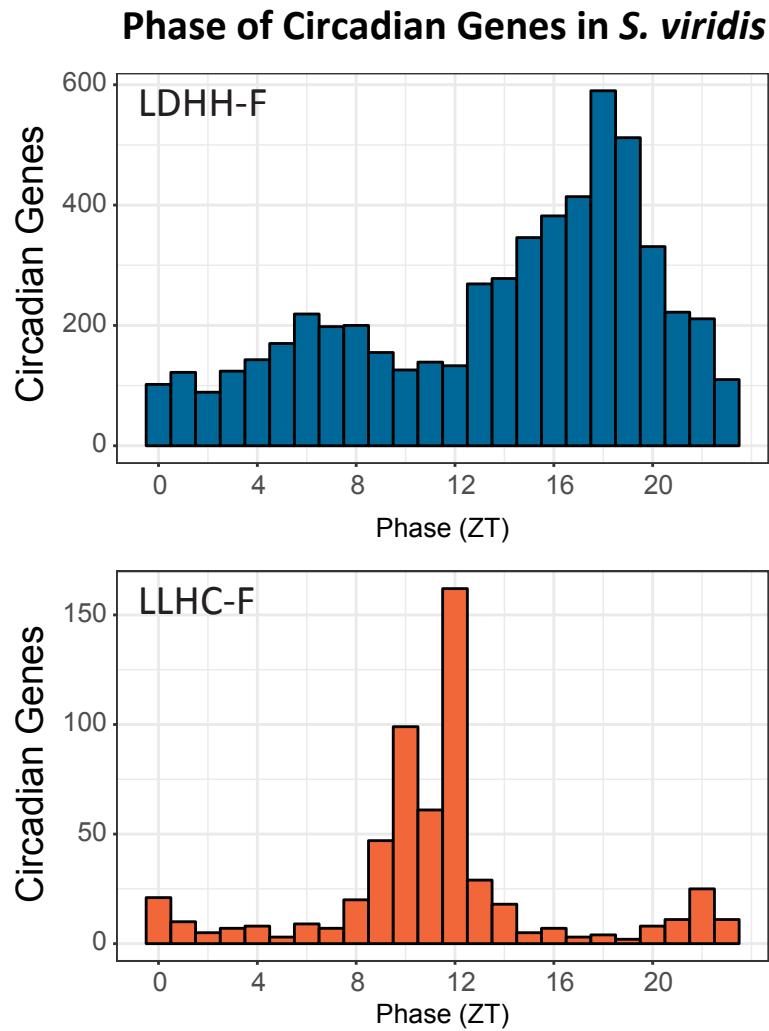
Average Replicates

Plot Data

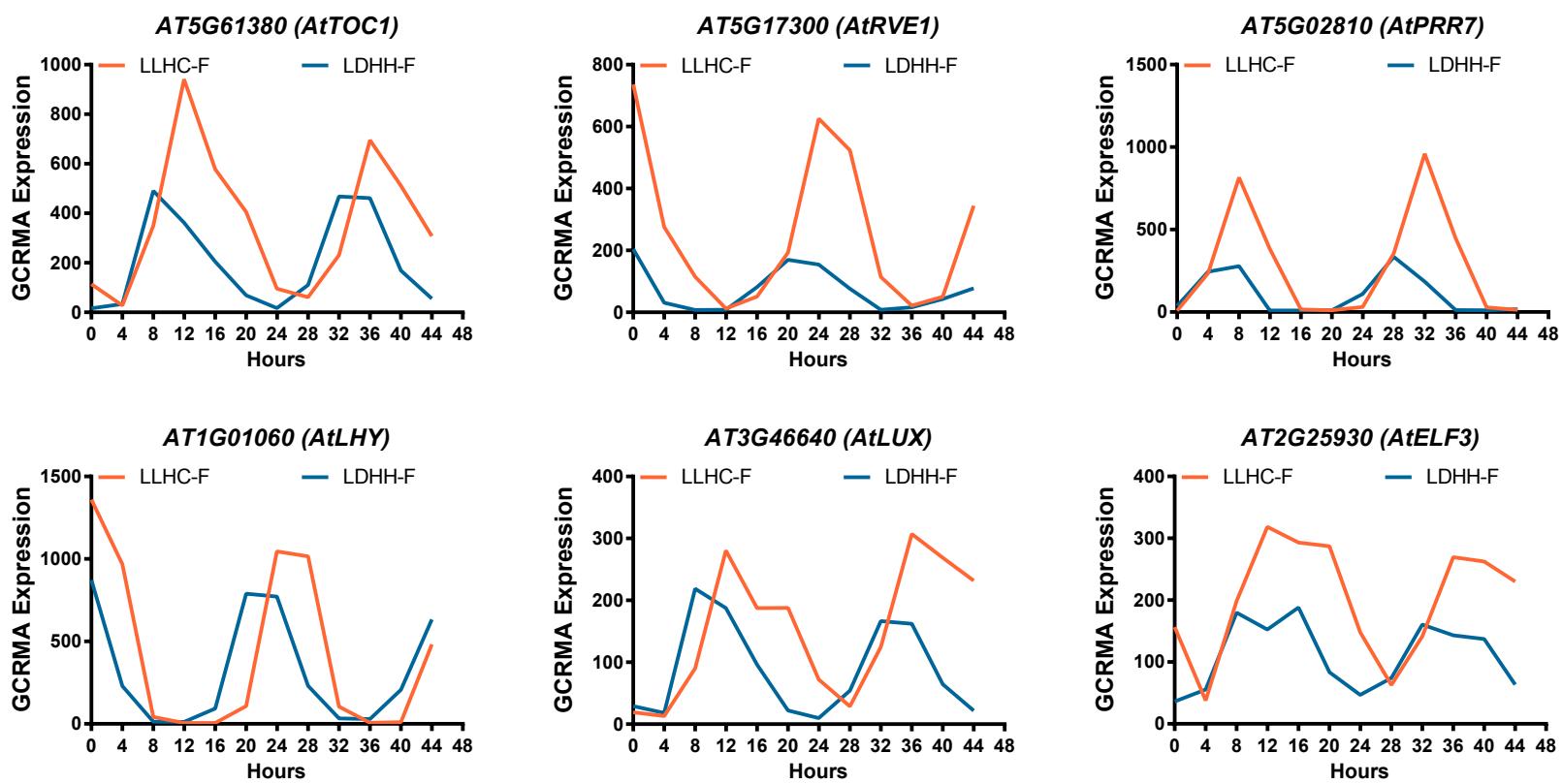
Plot Selected Data as Line Graph Plot Selected Data as Heatmap



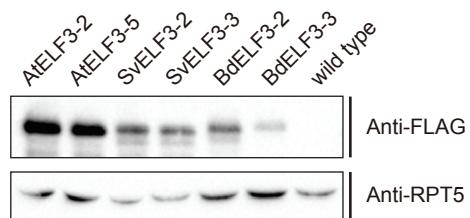
Supplemental Figure 4



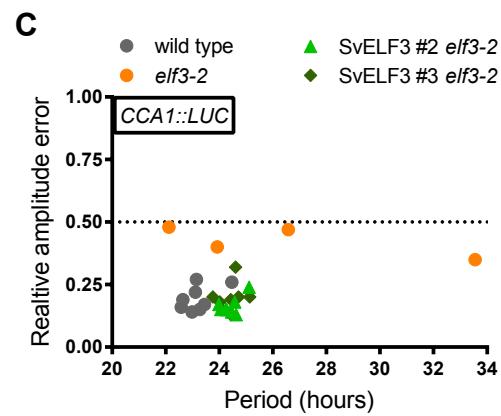
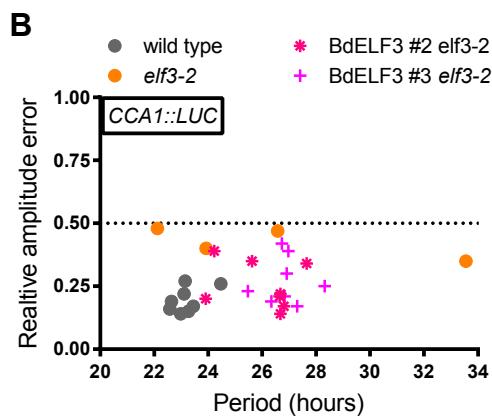
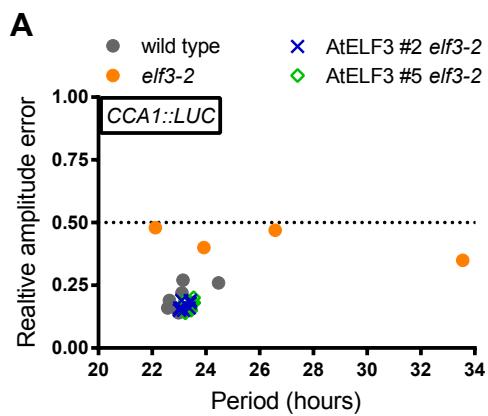
Supplemental Figure 5



Supplemental Figure 6



Supplemental Figure 7



Supplemental Table 1. List of all primers used.

| Primers used for cloning At/Bd/SvELF3 coding sequence (CDS) without any stop codon ^a | | |
|---|----------------------------------|-------------------------------|
| Amplified Fragments | Forward primer (5'->3') | Reverse primer (5'->3') |
| AtELF3 | <u>CACCATGAAGAGAGGGAAAGATGAG</u> | <i>AGGCTTAGAGGAGTCATAGCG</i> |
| SvELF3 | <u>CACCATGACGAGGGGAGGTG</u> | <i>TGGGTCATTTGTCGCCCTCTCC</i> |

| Primers used to generate yeast two-hybrid constructs, all with a stop codon ^a | | |
|--|--------------------------------------|-----------------------------------|
| Amplified fragments | Forward primer (5'->3') | Reverse primer (5'->3') |
| BdELF3-stop | <u>CACCATGAGGAGGGCGGC</u> GG | <i>TTACGGATCATTCTGTTGCCCTCTCC</i> |
| SvELF3-stop | <u>CACCATGACGAGGGGAGGTG</u> | <i>CTATGGGTCA</i> TTTGTCGCCCTCTCC |
| AtELF4 | <u>CACCATGAAGAGGAACGGCGAGACGA</u> | <i>TTAAGCTCTAGTTCCGGCAGCAC</i> CC |
| AtLUX-Nt (amino acids 1-143) | <u>CACCATGGGAGAGGAAGTACAAA</u> | <i>CTATTTAAGTGT</i> TTTCCCAGATAG |
| AtLUX-Ct (amino acids 144-324) | <u>CACCATGCGACC</u> CGCGTTAGTGTGGACA | <i>TTAATTCTCATTGCGCTTCCACCT</i> |

| Primer sets for genotyping | | |
|----------------------------|--|--|
| Mutant name | for wild type PCR (5'->3') | for mutant PCR (5'->3') |
| <i>elf3-2</i> ^b | <i>TGAGTATTGTTCTTCGAGC</i> and CATATGGAGGAAAGTAGCCATTAC | <i>TGGTTATTATTCCTCCGCTTT</i> C and <i>TTGTTCCATTAGCTGTTAACCTA</i> |

^a CACC (underscored) were added to forward primers for cloning into the pENTR/D-TOP vector

^b (Nusinow et al., 2011)

Supplemental Table 2. A full list of At/Bd/SvELF3 associated proteins identified from AP-MS

| Total Unique Peptide Count | Accession Number | Molecular Weight | AtELF3-1 | AtELF3-2 | SvELF3#2 rep1 | SvELF3#2 rep2 | SvELF3#3 rep1 | SvELF3#3 rep2 | BdELF3#2 rep1 | BdELF3#2 rep2 | BdELF3#3 rep1 | BdELF3#3 rep2 |
|--|------------------|------------------|----------|----------|---------------|---------------|---------------|---------------|---------------|---------------|---------------|---------------|
| Identified Proteins (283) | ATG18790.1 | 129 kDa | 33 | 34 | 41 | 40 | 43 | 40 | 31 | 31 | 36 | 35 |
| Symbols: PHYB phytochrome D chr:9195602-9199486 REVERSE LENGTH=116 | ATG16250.1 | 129 kDa | 10 | 11 | 11 | 13 | 13 | 12 | 11 | 10 | 13 | 12 |
| Symbols: HSC70-1, HSP70-1, AT-HSC70-1, HSC70 heat shock cognate protein 70-1 chr:554055-556334 REVERSE LENGTH=651 | ATG02500.1 | 71 kDa | 15 | 12 | 25 | 22 | 24 | 30 | 12 | 12 | 7 | 9 |
| Symbols: heat shock protein 70 (Hsp 70) family protein chr:2903434-2905632 REVERSE LENGTH=649 | ATG09440.1 (+1) | 71 kDa | 16 | 15 | 22 | 21 | 22 | 26 | 15 | 14 | 6 | 10 |
| Symbols: HSP70, ATHSP70 heat shock protein 70 chr:33991487-3993689 REVERSE LENGTH=650 | ATG12580.1 | 71 kDa | 12 | 9 | 15 | 16 | 17 | 20 | 10 | 10 | 4 | 6 |
| Symbols: heat shock protein 70 (Hsp 70) family protein chr:550296-552565 REVERSE LENGTH=653 | ATG02490.1 | 71 kDa | 13 | 11 | 13 | 13 | 14 | 18 | 10 | 9 | 4 | 6 |
| Symbols: Hsp70 heat shock protein 70B chr:15502386-5504326 REVERSE LENGTH=646 | ATG16030.1 | 71 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: BdELF3_HFC | ATMGcustom02 | 86 kDa | 1 | 0 | 1 | 0 | 1 | 0 | 26 | 27 | 22 | 20 |
| Symbols: PHYC phytochrome C chr:514008049-14011619 FORWARD LENGTH=1111 | ATG35840.1 | 124 kDa | 22 | 23 | 27 | 32 | 27 | 33 | 20 | 18 | 19 | 22 |
| Symbols: SvELF3_HFC | ATMGcustom0 | 87 kDa | 1 | 0 | 20 | 29 | 23 | 33 | 1 | 1 | 1 | 1 |
| Symbols: AtELF3_HFC | ATMGcustom03 | 84 kDa | 21 | 19 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| Symbols: T2P zinc knuckle (CCHC-type) family protein chr:517527261-17530207 FORWARD LENGTH=831 | ATG43630.1 | 91 kDa | 14 | 12 | 13 | 20 | 13 | 24 | 12 | 13 | 14 | 14 |
| Symbols: RBC1 ribulose-bisphosphate carboxylases | ATCG00490.1 | 53 kDa | 14 | 13 | 13 | 18 | 11 | 19 | 14 | 14 | 9 | 10 |
| Symbols: PHYE phytochrome E chr:10042312-10045948 REVERSE LENGTH=1112 | ATG18130.1 | 123 kDa | 12 | 19 | 13 | 18 | 12 | 17 | 6 | 10 | 15 | 14 |
| Symbols: TUB2 tubulin beta chain 2 chr:525181560-25183501 FORWARD LENGTH=450 | ATG52690.1 (+1) | 51 kDa | 10 | 9 | 2 | 7 | 3 | 9 | 7 | 5 | 4 | 3 |
| Symbols: TUB5 tubulin beta-5 chain chr:16938933-6940481 REVERSE LENGTH=449 | ATG120010.1 | 50 kDa | 9 | 7 | 0 | 7 | 0 | 9 | 7 | 4 | 3 | 2 |
| Symbols: TUB6 tubulin beta-6 chain chr:53961317-3962971 REVERSE LENGTH=449 | ATG12250.1 | 51 kDa | 7 | 6 | 0 | 4 | 0 | 6 | 6 | 4 | 3 | 2 |
| Symbols: TUB9 tubulin beta-9 chain chr:411182218-11183840 FORWARD LENGTH=444 | ATG20890.1 | 50 kDa | 9 | 8 | 0 | 6 | 2 | 7 | 5 | 4 | 3 | 2 |
| Symbols: TUB7 tubulin beta-7 chain chr:21644258-12645932 REVERSE LENGTH=449 | ATG29550.1 | 51 kDa | 9 | 8 | 0 | 5 | 3 | 8 | 6 | 5 | 3 | 2 |
| Symbols: TUB8 tubulin beta chain 4 chr:517859442-17860994 REVERSE LENGTH=444 | ATG44340.1 | 50 kDa | 9 | 8 | 0 | 5 | 2 | 7 | 6 | 4 | 3 | 2 |
| Symbols: TUB8 tubulin beta 8 chr:58042962-8045428 FORWARD LENGTH=449 | ATG523860.1 (+1) | 51 kDa | 9 | 8 | 0 | 6 | 3 | 6 | 6 | 5 | 3 | 0 |
| Symbols: PCH1 I-box family protein chr:7074940-7079181 FORWARD LENGTH=778 | ATG16365.1 (+2) | 89 kDa | 9 | 9 | 9 | 14 | 11 | 16 | 9 | 9 | 11 | 11 |
| Symbols: GACP-2, GACP1 glyceraldehyde-3-phosphate dehydrogenase C2 chr:14608465-4610494 REVERSE LENGTH=338 | ATG13440.1 | 37 kDa | 8 | 7 | 4 | 15 | 6 | 12 | 4 | 3 | 6 | 2 |
| Symbols: GACP, GACP-1, GACP1 glyceraldehyde-3-phosphate dehydrogenase C subunit 1 chr:31081077-1083131 FORWARD LENGTH=338 | ATG04120.1 | 37 kDa | 7 | 7 | 4 | 15 | 6 | 12 | 4 | 3 | 6 | 2 |
| Symbols: ATPA ATP synthase subunit alpha chr:9938-11461 REVERSE LENGTH=507 | ATG00120.1 | 55 kDa | 12 | 9 | 1 | 10 | 0 | 13 | 9 | 8 | 7 | 4 |
| Symbols: TU4A, TOR2 tubulin alpha-4 chain chr:1356421-1358266 FORWARD LENGTH=450 | ATG04820.1 (+1) | 50 kDa | 6 | 7 | 5 | 9 | 6 | 10 | 2 | 5 | 2 | 1 |
| Symbols: TU3A tubulin alpha-3 chr:6682761-6684474 REVERSE LENGTH=450 | ATG19770.1 (+1) | 50 kDa | 4 | 4 | 3 | 6 | 3 | 8 | 1 | 3 | 1 | 0 |
| Symbols: TU6A Tubulin/Tfz2 family protein chr:8548753-8550319 REVERSE LENGTH=427 | ATG41960.1 | 47 kDa | 6 | 6 | 4 | 8 | 5 | 8 | 2 | 6 | 2 | 1 |
| Symbols: ACT8 actin 8 chr:18216539-18217947 FORWARD LENGTH=377 | ATG49240.1 (+1) | 42 kDa | 3 | 3 | 2 | 5 | 3 | 4 | 3 | 3 | 3 | 3 |
| Symbols: ACT7 actin 7 chr:53052809-3054220 FORWARD LENGTH=377 | ATG59980.1 | 42 kDa | 4 | 4 | 1 | 6 | 4 | 6 | 4 | 3 | 2 | 1 |
| Symbols: ACT1, AAC1 actin 1 chr:15779761-15781241 FORWARD LENGTH=377 | ATG37620.1 (+2) | 42 kDa | 1 | 0 | 0 | 4 | 1 | 2 | 0 | 0 | 0 | 0 |
| Symbols: ACT4 actin 4 chr:23950109-23951586 FORWARD LENGTH=377 | ATG59370.1 (+2) | 42 kDa | 0 | 0 | 0 | 4 | 0 | 3 | 1 | 1 | 1 | 0 |
| Symbols: Actin family protein chr:217578683-17580222 FORWARD LENGTH=329 | ATG42170.1 | 37 kDa | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 |
| Symbols: Actin-like ATPase superfamily protein chr:217560211-17561945 FORWARD LENGTH=378 | ATG42100.1 | 42 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: ATRABD8, ATRABE18, RAB18 RAB GTPase homolog E18 chr:41099036-10991466 FORWARD LENGTH=476 | ATG20360.1 | 52 kDa | 6 | 5 | 9 | 10 | 8 | 12 | 5 | 4 | 3 | 3 |
| Symbols: Ribosomal protein S5 family protein chr:217460016-17461398 REVERSE LENGTH=285 | ATG41840.1 | 31 kDa | 5 | 6 | 2 | 3 | 3 | 4 | 5 | 2 | 1 | 0 |
| Symbols: Ribosomal protein S5 family protein chr:211268911-21690085 FORWARD LENGTH=284 | ATG58380.1 (+3) | 31 kDa | 6 | 5 | 3 | 2 | 5 | 5 | 3 | 3 | 1 | 0 |
| Symbols: Ribosomal protein S5 family protein chr:21279824-21280887 REVERSE LENGTH=276 | ATG57490.1 | 30 kDa | 3 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: TIC time for coffee chr:7913181-791867 FORWARD LENGTH=1555 | ATG22380.2 | 165 kDa | 5 | 5 | 4 | 12 | 3 | 15 | 4 | 3 | 1 | 1 |
| Symbols: ELF4 Protein of unknown function (DUF1313) chr:216734545-16734880 REVERSE LENGTH=111 | ATG40080.1 | 12 kDa | 4 | 4 | 3 | 5 | 4 | 4 | 4 | 4 | 5 | 5 |
| Symbols: GAPA, GAPA-1 glyceraldehyde-3-phosphate dehydrogenase A subunit chr:3-979226-9795848 FORWARD LENGTH=396 | ATG26650.1 | 42 kDa | 11 | 8 | 3 | 13 | 4 | 15 | 5 | 4 | 3 | 2 |
| Symbols: GAP-2 glyceraldehyde-3-phosphate dehydrogenase A subunit 2 chr:14392634-439380 REVERSE LENGTH=350 | ATG12900.3 (+1) | 38 kDa | 11 | 8 | 3 | 11 | 4 | 12 | 5 | 3 | 2 | 1 |
| Symbols: Ribosomal protein L6 family chr:12010986-12012223 FORWARD LENGTH=194 | ATG33120.1 (+1) | 22 kDa | 4 | 4 | 6 | 10 | 5 | 9 | 4 | 5 | 5 | 5 |
| Symbols: Ribosomal protein L6 family chr:46463201-6464458 REVERSE LENGTH=194 | ATG41050.1 | 22 kDa | 1 | 2 | 0 | 3 | 0 | 3 | 0 | 2 | 2 | 2 |
| Symbols: COP1, ATCOP1, DET40, FUS1, EMBL168 Transducin GTPase-like superfamily protein chr:213978000-13983282 FORWARD LENGTH=675 | ATG23290.1 | 76 kDa | 8 | 9 | 6 | 4 | 3 | 5 | 1 | 2 | 6 | 4 |
| Symbols: IMPA-2 importin alpha isoform 2 chr:9134450-9137134 FORWARD LENGTH=535 | ATG416143.1 (+1) | 59 kDa | 2 | 2 | 1 | 8 | 0 | 8 | 10 | 9 | 2 | 4 |
| Symbols: ATB-1MP, ATKAP, ALPHAL-1, IMP ALPHAE, IMPA1 importin alpha isoform 1 chr:3-2120559-2123555 FORWARD LENGTH=532 | ATG06720.1 (+1) | 59 kDa | 0 | 0 | 0 | 2 | 0 | 2 | 2 | 1 | 0 | 0 |
| Symbols: IMPA-0 importin alpha isoform 6 chr:584397-587036 FORWARD LENGTH=538 | ATG02690.1 (+1) | 59 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: IMPA-4 importin alpha isoform 4 chr:2994505-2997833 FORWARD LENGTH=538 | ATG09270.1 (+2) | 59 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: MTO3, SAMS3, MAT4 S-adenosylmethionine synthetase family protein chr:5952484-5953665 REVERSE LENGTH=393 | ATG173790.1 | 43 kDa | 9 | 7 | 2 | 5 | 0 | 6 | 1 | 0 | 0 | 0 |
| Symbols: MAT3 methionine adenosyltransferase 3 chr:2-15479721-15480893 REVERSE LENGTH=390 | ATG36880.1 (+1) | 42 kDa | 4 | 2 | 2 | 1 | 0 | 2 | 0 | 0 | 0 | 0 |
| Symbols: SAM-2, MATZ2, SAM2, ATSAM2 S-adenosylmethionine synthetase 2 chr:4-796298-797479 REVERSE LENGTH=393 | ATG01850.1 (+1) | 43 kDa | 5 | 2 | 0 | 1 | 0 | 2 | 0 | 0 | 0 | 0 |
| Symbols: SAM1, SAM-1, MAT1, ATSAM1 S-adenosylmethionine synthetase 1 chr:1519037-520218 FORWARD LENGTH=393 | ATG02500.1 (+1) | 43 kDa | 4 | 1 | 0 | 2 | 0 | 3 | 0 | 0 | 0 | 0 |
| Symbols: RCB ribosucinate chr:216570951-16573435 REVERSE LENGTH=474 | ATG39730.1 | 52 kDa | 7 | 7 | 3 | 4 | 3 | 6 | 7 | 6 | 3 | 2 |
| Symbols: PLCL1, LUX Homeodomain-like superfamily protein chr:17183248-17184219 FORWARD LENGTH=323 | ATG46640.1 (+1) | 35 kDa | 1 | 1 | 3 | 6 | 3 | 7 | 1 | 1 | 1 | 3 |
| Symbols: GS2, GLN2, ATGSL1 glutamine synthetase 2 chr:13831220-13833239 FORWARD LENGTH=430 | ATG53650.1 (+2) | 47 kDa | 6 | 5 | 3 | 8 | 3 | 7 | 5 | 4 | 1 | 1 |
| Symbols: CAT3, SEN2, ATCAT3 catalase 3 chr:17143142-71646193 FORWARD LENGTH=485 | ATG20620.5 | 56 kDa | 13 | 11 | 2 | 8 | 1 | 9 | 7 | 4 | 1 | 1 |
| Symbols: Clathrin, heavy chain chr:3-2842575-3491667 REVERSE LENGTH=1705 | ATG11130.1 | 193 kDa | 16 | 10 | 0 | 2 | 0 | 5 | 2 | 1 | 0 | 0 |
| Symbols: Clathrin, heavy chain chr:2587171-2595411 REVERSE LENGTH=1703 | ATG20580.1 | 193 kDa | 15 | 9 | 0 | 2 | 0 | 5 | 2 | 1 | 0 | 0 |
| Symbols: Ribosomal protein S3 family protein chr:19951547-19952782 FORWARD LENGTH=249 | ATG53870.1 | 27 kDa | 4 | 4 | 3 | 4 | 3 | 5 | 2 | 2 | 2 | 1 |
| Symbols: Ribosomal protein S3 family protein chr:2-13450384-13451669 FORWARD LENGTH=250 | ATG231610.1 | 28 kDa | 5 | 5 | 3 | 4 | 3 | 6 | 3 | 2 | 1 | 1 |
| Symbols: Ribosomal protein S3 family protein chr:5-13710355-13712192 REVERSE LENGTH=248 | ATG53530.1 | 27 kDa | 5 | 5 | 3 | 4 | 3 | 5 | 3 | 1 | 1 | 1 |
| Symbols: EIF4A1, RH4, TIF4A1 eukaryotic translation initiation factor 4A1 chr:3-4592635-4594128 REVERSE LENGTH=412 | ATG13190.1 (+1) | 47 kDa | 7 | 6 | 3 | 5 | 5 | 7 | 3 | 2 | 2 | 2 |
| Symbols: EIF4A2-1, EIF4A2-2 eIF4A2 chr:1-20260495-20262018 FORWARD LENGTH=412 | ATG14270.1 | 47 kDa | 5 | 4 | 3 | 5 | 5 | 7 | 3 | 2 | 2 | 2 |
| Symbols: EIF4A3-III eukaryotic initiation factor 4A-III chr:3-6863790-6866242 FORWARD LENGTH=408 | ATG319760.1 | ? | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: BIP, BIP2 Heat shock protein 70 (Hsp 70) family protein chr:5-1680769-16810480 REVERSE LENGTH=668 | ATG42020.1 | 74 kDa | 3 | 5 | 5 | 9 | 7 | 11 | 1 | 2 | 3 | 2 |
| Symbols: DAYSLLEEPER BED zinc finger hAT domain chr:3-14321838-14323928 FORWARD LENGTH=696 | ATG42170.1 | 79 kDa | 8 | 5 | 0 | 7 | 0 | 12 | 3 | 4 | 2 | 0 |
| Symbols: Protein kinase family protein chr:3-1014412-1018244 REVERSE LENGTH=701 | ATG03940.1 | 78 kDa | 3 | 4 | 0 | 3 | 0 | 1 | 8 | 6 | 6 | 5 |
| Symbols: MLK1 Protein kinase family protein chr:5-6010215-6013724 REVERSE LENGTH=691 | ATG18190.1 | 77 kDa | 5 | 5 | 0 | 2 | 0 | 1 | 6 | 6 | 5 | 5 |
| Symbols: SPA1 SPA (suppressor of pha-Y105) protein family chr:2-19022572-19026821 REVERSE LENGTH=1029 | ATG46340.1 | 115 kDa | 8 | 7 | 2 | 4 | 2 | 4 | 0 | 0 | 0 | 6 |
| Symbols: SPA1 SPA (suppressor of pha-Y105) protein family chr:5-15377501-15378306 REVERSE LENGTH=181 | ATG38410.1 | 20 kDa | 5 | 4 | 4 | 7 | 5 | 7 | 5 | 3 | 3 | 2 |
| Symbols: Ribulose bisphosphate carboxylase (small chain) family protein chr:5-15384350-15385155 REVERSE LENGTH=181 | ATG38430.1 | 20 kDa | 4 | 3 | 2 | 3 | 2 | 3 | 3 | 1 | 2 | 1 |
| Symbols: Ribulose bisphosphate carboxylase (small chain) family protein chr:5-15384350-15385162 REVERSE LENGTH=1122 | ATG09570.1 | 125 kDa | 1 | 1 | 7 | 5 | 7 | 2 | 0 | 2 | 6 | 3 |
| Symbols: Ribosomal protein L4/L1 family chr:3-2953813-2955444 FORWARD LENGTH=406 | ATG09630.1 (+1) | 45 kDa | 1 | 1 | 1 | 2 | 1 | 7 | 2 | 1 | 1 | 0 |
| Symbols: Ribosomal protein L4/L1 family chr:5-657830-659526 FORWARD LENGTH=407 | ATG02870.1 (+1) | 45 kDa | 2 | 2 | 1 | 2 | 1 | 6 | 2 | 1 | 0 | 0 |
| Symbols: PSCS1, ATPCS1 delta1-pyrrolidine-5-carboxylate synthase 1 chr:2-16598516-16602939 REVERSE LENGTH=717 | ATG29800.1 (+1) | 78 kDa | 7 | 6 | 1 | 4 | 1 | 9 | 4 | 3 | 2 | 0 |
| Symbols: PSCS2 delta1-pyrrolidine-5-carboxylate synthase 2 chr:3-20624278-20628989 REVERSE LENGTH=726 | ATG355610.1 | 79 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: RBCS1A ribulose bisphosphate carboxylase small chain 1A chr:1-2504865-25049249 REVERSE LENGTH=180 | ATG1667090.1 | 20 kDa | 5 | 5 | 4 | 7 | 5 | 7 | 4 | 3 | 1 | 3 |
| Symbols: ATCM5, ATMETS, ATMS Cobalamin-independent synthase family protein chr:5-5935771-5939195 FORWARD LENGTH=765 | ATG17920.1 (+1) | 84 kDa | 4 | 5 | 3 | 2 | 0 | 0 | 2 | 1 | 0 | 0 |
| Symbols: ATMS3, MS3 methionine synthase 3 chr:5-7124397-7128353 REVERSE LENGTH=812 | ATG520980.1 (+1) | 91 kDa | 2 | 2 | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 0 |

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|---|------------------|----------|----|---|---|---|---|---|----|---|---|---|
| Symbols: PGK1 phosphoglycerate kinase 1 chr3:4061127-4063140 REVERSE LENGTH=481 | AT3G12780.1 | 50 kDa | 5 | 4 | 0 | 6 | 0 | 9 | 3 | 2 | 1 | 0 |
| Symbols: PGK1 phosphoglycerate kinase 1 chr1:29924347-2996295 REVERSE LENGTH=401 | AT1G79550.1 (+) | 42 kDa | 2 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 0 |
| Symbols: Phosphoglycerate kinase family protein chr1:21028622-21030454 FORWARD LENGTH=405 | AT1G56190.2 | 43 kDa | 3 | 0 | 0 | 3 | 0 | 4 | 0 | 0 | 0 | 0 |
| Symbols: LOS1 Ribosomal protein S5/Elongation factor G/I/V family protein chr1:20968245-20971077 REVERSE LENGTH=843 | AT1G56070.1 | 94 kDa | 4 | 3 | 1 | 3 | 2 | 9 | 1 | 1 | 0 | 0 |
| Symbols: structural constituent of ribosome chrC:82826-83482 REVERSE LENGTH=218 | ATCG00800.1 | 25 kDa | 6 | 4 | 1 | 4 | 1 | 6 | 1 | 0 | 0 | 0 |
| Symbols: CAT2 catalase 2 chr4:16700937-16703215 REVERSE LENGTH=492 | AT4G35090.1 | 57 kDa | 10 | 6 | 2 | 8 | 1 | 7 | 4 | 4 | 1 | 1 |
| Symbols: Ribosomal protein S27a / ubiquitin family protein chr1:8314940-8315410 FORWARD LENGTH=156 | AT1G23410.1 (+) | 18 kDa | 3 | 3 | 1 | 2 | 1 | 2 | 3 | 2 | 1 | 2 |
| Symbols: UBQ9 ubiquitin chr5:14952782-14953750 REVERSE LENGTH=322 | AT5G37640.1 | 36 kDa | 0 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: UBQ12 ubiquitin 12 chr1:2054953-2055025 FORWARD LENGTH=230 | AT1G55060.1 | 26 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: UBQ8 ubiquitin 8 chr3:300411-3006005 REVERSE LENGTH=631 | AT3G09790.1 | 72 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: GTP binding Elongation factor Tu family protein chr1:2455559-2457001 FORWARD LENGTH=449 | AT1G07920.1 (+) | 50 kDa | 4 | 3 | 1 | 4 | 1 | 6 | 3 | 1 | 2 | 1 |
| Symbols: Ribosomal protein L13 family protein chr3:9054613-905871 FORWARD LENGTH=206 | AT3G24830.1 | 23 kDa | 1 | 1 | 1 | 1 | 2 | 1 | 1 | 2 | 0 | 0 |
| Symbols: Ribosomal protein L13 family protein chr5:19771315-19772686 REVERSE LENGTH=206 | AT3G07110.1 (+) | 23 kDa | 2 | 3 | 1 | 1 | 0 | 1 | 2 | 3 | 0 | 0 |
| Symbols: Ribosomal protein L13 family protein chr7:4655133-7656542 REVERSE LENGTH=206 | AT5G48760.1 (+) | 24 kDa | 0 | 0 | 0 | 1 | 0 | 1 | 1 | 1 | 0 | 0 |
| Symbols: HOG1, EMB1395, SAHH1, MEES5, ATSAH1 S-adenosyl-L-homocysteine hydrolase chr4:8054931-8056676 FORWARD LENGTH=485 | AT4G13170.1 | 24 kDa | 0 | 2 | 0 | 1 | 0 | 0 | 0 | 2 | 0 | 0 |
| Symbols: SAHH2, ATSAH2 S-adenosyl-L-homocysteine hydrolase 2 chr3:8588013-8589671 REVERSE LENGTH=485 | AT4G13940.1 | 53 kDa | 3 | 4 | 1 | 3 | 1 | 5 | 1 | 2 | 0 | 0 |
| Symbols: HOG1, SAHH1 S-adenosyl-L-homocysteine hydrolase chr4:8054931-8056763 FORWARD LENGTH=325 | AT3G23810.1 | 53 kDa | 2 | 2 | 0 | 1 | 0 | 3 | 0 | 1 | 0 | 0 |
| Symbols: CRB, CSP18, HIP1.3 chloroplast RNA binding chr1:3015473-3018035 FORWARD LENGTH=378 | AT4G13940.4 | 36 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: ACC1, AT-ACC1, EMB22, GK, PASY3 acetyl-CoA carboxylase 1 chr1:13534195-13543773 FORWARD LENGTH=2254 | AT1G09340.1 | 43 kDa | 4 | 3 | 1 | 1 | 1 | 4 | 1 | 1 | 0 | 0 |
| Symbols: Ribosomal protein S5 domain 2-like superfamily protein chr5:6090253-6090693 REVERSE LENGTH=146 | AT1G36160.1 (+) | 251 kDa | 12 | 1 | 0 | 1 | 0 | 2 | 0 | 0 | 0 | 0 |
| Symbols: Ribosomal protein S5 domain 2-like superfamily protein chr5:23781442-3781882 FORWARD LENGTH=146 | AT5G18380.1 (+) | 17 kDa | 3 | 4 | 1 | 3 | 1 | 2 | 3 | 3 | 0 | 0 |
| Symbols: CA1 carbonic anhydrase 1 chr3:194853-197873 REVERSE LENGTH=344 | AT2G09990.1 | 17 kDa | 2 | 3 | 0 | 2 | 0 | 1 | 2 | 2 | 0 | 0 |
| Symbols: CA2, CA18, BETA C2 carbonic anhydrase 2 chr2:475827-4762382 FORWARD LENGTH=331 | AT3G01500.2 (+) | 37 kDa | 2 | 2 | 1 | 3 | 1 | 5 | 3 | 1 | 0 | 0 |
| Symbols: ATAN11, LWD1 Transducin/WD40 repeat-like superfamily protein chr1:4395114-4396154 REVERSE LENGTH=346 | AT5G14740.1 (+) | 37 kDa | 1 | 1 | 1 | 3 | 1 | 6 | 1 | 0 | 0 | 0 |
| Symbols: RPL4, RPL56A ribosomal protein S6 chr4:15346306-15347714 REVERSE LENGTH=250 | AT1G2910.1 | 39 kDa | 5 | 7 | 5 | 8 | 4 | 5 | 5 | 5 | 3 | 3 |
| Symbols: RPL4, RPL56A ribosomal protein S6 chr4:15346306-15347714 REVERSE LENGTH=250 | AT3G13670.1 | 79 kDa | 5 | 6 | 0 | 0 | 0 | 1 | 10 | 6 | 7 | 7 |
| Symbols: RPL4, RPL56A ribosomal protein S6 chr4:15346306-15347714 REVERSE LENGTH=250 | AT4G31700.1 | 28 kDa | 2 | 4 | 0 | 1 | 0 | 4 | 4 | 4 | 2 | 1 |
| Symbols: Ribosomal protein L30/L7 family protein chr2:132943-134264 REVERSE LENGTH=242 | AT2G02150.1 | 28 kDa | 4 | 3 | 1 | 0 | 1 | 2 | 1 | 2 | 1 | 0 |
| Symbols: Ribosomal protein L30/L7 family protein chr2:18249227-18250417 REVERSE LENGTH=247 | AT2G44120.2 | 29 kDa | 2 | 3 | 0 | 1 | 0 | 2 | 0 | 1 | 0 | 0 |
| Symbols: Ribosomal protein L30/L7 family protein chr3:4438809-4435109 FORWARD LENGTH=244 | AT3G13580.1 (+) | 28 kDa | 1 | 2 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 |
| Symbols: Coatomer, alpha subunit chr2:12919814-22923728 FORWARD LENGTH=1218 | AT2G21390.1 (+) | 136 kDa | 2 | 0 | 0 | 2 | 0 | 9 | 0 | 0 | 0 | 0 |
| Symbols: Coatomer, alpha subunit chr2:12919814-22923728 FORWARD LENGTH=1216 | AT1G62020.1 | 137 kDa | 2 | 1 | 0 | 0 | 0 | 5 | 0 | 0 | 0 | 0 |
| Symbols: Coatomer, alpha subunit chr2:12919814-22923728 FORWARD LENGTH=1218 | AT1G29910.1 (+) | 28 kDa | 2 | 2 | 2 | 2 | 2 | 2 | 1 | 1 | 1 | 0 |
| Symbols: CAB3, AB140, CAB140, LHC81.3 chlorophyll A/B binding protein 3 chr1:10472443-10473246 REVERSE LENGTH=267 | AT2G05070.1 (+) | 29 kDa | 1 | 1 | 2 | 1 | 1 | 1 | 0 | 0 | 0 | 0 |
| Symbols: LHC82.2, LHC82.2 photosystem II light harvesting complex gene 2,2 chr2:1799436-1800329 REVERSE LENGTH=265 | AT1G29930.1 | 28 kDa | 2 | 2 | 2 | 2 | 2 | 2 | 1 | 1 | 1 | 0 |
| Symbols: HSP60-2 heat shock protein 60-2 chr2:14075093-14078568 REVERSE LENGTH=585 | AT2G33210.1 (+) | 62 kDa | 1 | 3 | 1 | 3 | 1 | 2 | 1 | 0 | 0 | 0 |
| Symbols: HSP60-3B heat shock protein 60 chr3:8669013-8672278 FORWARD LENGTH=577 | AT2G33990.1 | 61 kDa | 1 | 3 | 0 | 3 | 0 | 3 | 2 | 1 | 0 | 0 |
| Symbols: Ribosomal protein S34e chr3:1329751-1331418 FORWARD LENGTH=262 | AT3G04840.1 | 30 kDa | 2 | 2 | 1 | 1 | 1 | 3 | 1 | 1 | 1 | 0 |
| Symbols: Ribosomal protein S34e chr4:16548724-1655222 FORWARD LENGTH=262 | AT4G34670.1 | 30 kDa | 2 | 2 | 1 | 2 | 1 | 3 | 1 | 0 | 0 | 0 |
| Symbols: UBP12 ubiquitin-specific protease 12 chr5:2019545-2027834 REVERSE LENGTH=1116 | AT5G06600.1 (+) | 131 kDa | 0 | 0 | 0 | 3 | 0 | 3 | 1 | 1 | 0 | 0 |
| Symbols: UBP13 ubiquitin-specific protease 13 chr3:3761758-3770290 REVERSE LENGTH=1115 | AT3G11910.1 (+) | 131 kDa | 0 | 0 | 0 | 3 | 1 | 2 | 1 | 0 | 0 | 0 |
| Symbols: NIT1, ATN1, NIT1 nitrate reductase 1 chr3:15986901-15988841 FORWARD LENGTH=346 | AT3G44310.1 (+) | 38 kDa | 2 | 1 | 0 | 4 | 1 | 4 | 1 | 1 | 1 | 1 |
| Symbols: ARP1, emb2207, RPL3A, RP1 ribosomal protein 1 chr1:16266992-16268631 FORWARD LENGTH=389 | AT1G43170.1 (+) | 45 kDa | 2 | 1 | 0 | 2 | 0 | 1 | 1 | 1 | 0 | 0 |
| Symbols: RD212, RD212A Granulin repeat cysteine protease family protein chr1:17283139-17285609 REVERSE LENGTH=462 | AT1G47128.1 | 51 kDa | 4 | 3 | 0 | 2 | 0 | 2 | 0 | 2 | 0 | 0 |
| Symbols: ATPB, PB ATP synthase subunit beta chrC:52660-54156 REVERSE LENGTH=498 | ATCG00480.1 | 54 kDa | 4 | 5 | 0 | 3 | 0 | 3 | 2 | 2 | 1 | 0 |
| Symbols: PYK10, PSR3.1, BGLU23, LEB Glycosyl hydrolase superfamily protein chr3:2840657-2843730 REVERSE LENGTH=524 | AT3G09260.1 | ? | 1 | 1 | 1 | 3 | 0 | 3 | 1 | 1 | 0 | 0 |
| Symbols: KASI, KASI 3-ketoacyl-acyl carrier protein synthase chr5:18774439-18776629 REVERSE LENGTH=473 | AT5G46290.1 | 50 kDa | 4 | 3 | 0 | 1 | 2 | 3 | 2 | 2 | 0 | 0 |
| Symbols: RPL2.1 ribosomal protein L2 chrC:84347-85843 REVERSE LENGTH=274 | ATCG00830.1 (+) | 30 kDa | 3 | 2 | 0 | 2 | 0 | 3 | 3 | 4 | 0 | 0 |
| Symbols: ASN2 asparagine synthetase 2 chr5:25969224-25972278 FORWARD LENGTH=578 | AT5G65010.1 (+) | 65 kDa | 3 | 2 | 0 | 1 | 0 | 4 | 2 | 0 | 0 | 0 |
| Symbols: ASN1, DIN6, AT-ASN1 glutamine-dependent asparagine synthase 1 chr3:1743845-1744103 REVERSE LENGTH=512 | AT3G74340.2 | 58 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: ASN3, DIN6, AT-ASN1 glutamine synthetase 3 chr3:3212934-3216148 REVERSE LENGTH=578 | AT2G0240.1 (+) | 65 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: PIP2A, PIP2, PIP2.1 plasma membrane intrinsic protein 2 chr3:19803906-19805454 REVERSE LENGTH=287 | AT3G53420.1 (+) | 30 kDa | 4 | 4 | 0 | 1 | 0 | 1 | 2 | 1 | 0 | 0 |
| Symbols: RIBOSOMAL PROTEIN S10/S20e family protein chr3:16471606-16472312 REVERSE LENGTH=124 | AT3G45030.1 (+) | 14 kDa | 2 | 1 | 1 | 1 | 1 | 2 | 1 | 1 | 1 | 1 |
| Symbols: RIBOSOMAL PROTEIN S10/S20e family protein chr3:17453671-17454437 REVERSE LENGTH=122 | AT3G47370.1 (+) | 14 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: Coatomer, beta subunit chr1:15264145-15272693 FORWARD LENGTH=948 | AT4G31490.1 | 105 kDa | 5 | 2 | 0 | 1 | 0 | 4 | 0 | 0 | 0 | 0 |
| Symbols: Coatomer, beta subunit chr1:15264145-15272693 FORWARD LENGTH=948 | AT4G31480.1 (+) | 105 kDa | 5 | 2 | 0 | 1 | 0 | 3 | 0 | 0 | 0 | 0 |
| Symbols: MLK3 Protein kinase family protein chr2:10985118-10988652 REVERSE LENGTH=673 | AT2G25760.1 | 76 kDa | 2 | 3 | 0 | 1 | 0 | 1 | 5 | 4 | 4 | 4 |
| Symbols: RPT3 regulatory particle triple-A chr3:23569155-23571110 FORWARD LENGTH=408 | AT5G58290.1 | 46 kDa | 3 | 3 | 1 | 1 | 1 | 2 | 1 | 1 | 0 | 0 |
| Symbols: CPN60B, LEN1 chaperonin 60 beta chr1:20715717-20718673 REVERSE LENGTH=600 | AT1G55490.1 (+) | 64 kDa | 2 | 4 | 0 | 3 | 0 | 2 | 2 | 0 | 1 | 0 |
| Symbols: CPN60B chaperonin 60 beta chr1:22874058-22876966 FORWARD LENGTH=597 | AT5G56500.1 (+) | 63 kDa | 0 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: ATARCA, RACK1A, AT, RACK1A Transducin/WD40 repeat-like superfamily protein chr1:6222325-6223901 FORWARD LENGTH=327 | AT1G18080.1 | 36 kDa | 1 | 1 | 0 | 2 | 0 | 3 | 1 | 0 | 0 | 0 |
| Symbols: RACK1B, AT receptor for activated kinase 18 chr1:17981977-1798268 REVERSE LENGTH=326 | AT1G48630.1 | 36 kDa | 3 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 0 | 0 |
| Symbols: RACK1C, AT receptor for activated kinase 18 chr3:6211109-6212371 REVERSE LENGTH=326 | AT2G18130.1 | 36 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: AHA2, PM2, HA2 H(+)-ATPase 2 chr4:14770820-14775920 REVERSE LENGTH=948 | AT4G30190.1 (+) | 104 kDa | 4 | 3 | 0 | 1 | 0 | 2 | 0 | 0 | 0 | 0 |
| Symbols: AHA1, PMA, OST2, HA1 H(+)-ATPase 1 chr2:8221858-8227268 FORWARD LENGTH=949 | AT2G18960.1 | 104 kDa | 4 | 2 | 0 | 1 | 0 | 2 | 0 | 0 | 0 | 0 |
| Symbols: AHA7, HA7 H(+)-ATPase 7 chr3:22298763-2230509 FORWARD LENGTH=961 | AT3G00330.1 (+) | 106 kDa | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: AHA4, HA4 H(+)-ATPase 4 chr3:17693015-17697801 FORWARD LENGTH=960 | AT3G47950.1 | 105 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: AHA3, ATAH3, AHA3 H(+)-ATPase 3 chr5:23231208-23236381 REVERSE LENGTH=949 | AT5G7350.1 (+) | 104 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: AHA10 autoinhibited H(+)-ATPase isoform 10 chr1:5904058-5908989 FORWARD LENGTH=947 | AT1G17260.1 | 105 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: ATPase, F1 complex, alpha subunit protein chr2:3361474-3361428 FORWARD LENGTH=777 | AT2G07698.1 | 86 kDa | 2 | 2 | 1 | 3 | 1 | 4 | 1 | 0 | 0 | 0 |
| Symbols: ATPase, F1 complex, alpha subunit protein chr2:3361474-3361428 FORWARD LENGTH=777 | AT3G26640.1 | 39 kDa | 5 | 5 | 3 | 5 | 3 | 5 | 6 | 4 | 3 | 3 |
| Symbols: ATPase, V1 complex, subunit B protein chr1:7016971-7020290 FORWARD LENGTH=487 | AT1G20260.1 (+) | 54 kDa | 3 | 3 | 0 | 2 | 0 | 2 | 1 | 2 | 0 | 0 |
| Symbols: ATGSTF8, ATGSTF5, GST6, GSTF6 glutathione S-transferase phi 8 chr2:19558213-19559266 FORWARD LENGTH=263 | AT2G47730.1 | 29 kDa | 3 | 2 | 0 | 0 | 0 | 0 | 4 | 0 | 0 | 0 |
| Symbols: ATPC1 ATPase, F1 complex, gamma subunit protein chr4:2350761-2351882 REVERSE LENGTH=373 | AT4G04640.1 | 41 kDa | 5 | 3 | 0 | 2 | 1 | 2 | 1 | 2 | 1 | 0 |
| Symbols: FBZ42 fructose-bisphosphate aldolase 2 chr4:18163714-18165659 REVERSE LENGTH=398 | AT4G38970.1 | 43 kDa | 2 | 2 | 0 | 3 | 1 | 3 | 2 | 1 | 0 | 0 |
| Symbols: RPL16A ribosomal protein large subunit 16A chr2:17791794-17792946 FORWARD LENGTH=182 | AT2G42740.1 (+) | 21 kDa | 2 | 2 | 1 | 1 | 1 | 1 | 2 | 2 | 2 | 1 |
| Symbols: Transketolase chr3:22454004-22456824 FORWARD LENGTH=741 | AT3GG60750.1 (+) | 80 kDa | 3 | 2 | 0 | 0 | 0 | 0 | 7 | 1 | 0 | 0 |
| Symbols: Binding chr5:19317899-19327014 FORWARD LENGTH=1606 | AT5G47690.2 (+) | 181 kDa | 6 | 0 | 0 | 2 | 0 | 6 | 0 | 0 | 0 | 0 |
| Symbols: SAC52, RPL10, RPL10A Ribosomal protein L16/L10e family protein chr1:4888270-4889408 FORWARD LENGTH=220 | AT1G14320.1 | 25 kDa | 1 | 2 | 1 | 1 | 0 | 1 | 2 | 2 | 1 | 1 |
| Symbols: CAC3 acetyl Co-enzyme A carboxylase carboxytransferase alpha subunit chr2:15917612-15920749 FORWARD LENGTH=769 | AT2G38040.1 (+) | 85 kDa | 3 | 1 | 0 | 0 | 0 | 4 | 0 | 0 | 0 | 0 |
| Symbols: RAN1, RAN1, ATRAN1 RAN-related nuclear protein 1 chr5:17670364-1767147 FORWARD LENGTH=221 | AT5G20010.1 (+) | 25 kDa</ | | | | | | | | | | |

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|--|------------------|---------|---|---|---|---|---|---|---|---|---|---|---|
| Symbols: Histone superfamily protein chr:1:2369212-2369523 FORWARD LENGTH=103 | AT1G07660_1 (+8) | 11 kDa | 1 | 1 | 1 | 3 | 1 | 3 | 1 | 1 | 1 | 1 | 1 |
| Symbols: oxidoreductases, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor;copper ion binding chr:2:8613168-8615649 FORWARD LENGTH=401 | AT2G19940_1 (+1) | 44 kDa | 5 | 1 | 0 | 1 | 0 | 3 | 1 | 0 | 0 | 0 | 0 |
| Symbols: ATRP5B, RPS5B ribosomal protein S8 chr:2:15647883-15649042 REVERSE LENGTH=207 | AT2G37270_1 (+3) | 23 kDa | 3 | 1 | 0 | 0 | 0 | 0 | 2 | 2 | 2 | 2 | 1 |
| Symbols: Thioredoxin superfamily protein chr:3:3672189-3673937 FORWARD LENGTH=266 | AT3G11630_1 | 29 kDa | 0 | 1 | 0 | 0 | 0 | 0 | 2 | 1 | 2 | 0 | 0 |
| Symbols: PIP1B, TMP-A, ATH2, PIPI2 plasma membrane intrinsic protein 1B chr:2:1891045-18911703 FORWARD LENGTH=286 | AT2G45960_1 (+2) | 31 kDa | 1 | 1 | 0 | 2 | 1 | 2 | 1 | 1 | 0 | 0 | 0 |
| Symbols: RPL27A, RPL27AB Ribosomal protein L18e/L15 superfamily protein chr:1:8263007-8263447 FORWARD LENGTH=146 | AT1G23290_1 (+1) | 16 kDa | 1 | 1 | 0 | 1 | 0 | 1 | 2 | 1 | 1 | 1 | 0 |
| Symbols: Ribosomal protein L18ae/L18 family protein chr:2:1452916-14534161 REVERSE LENGTH=176 | AT2G34480_1 | 21 kDa | 2 | 1 | 0 | 2 | 0 | 1 | 1 | 0 | 1 | 0 | 0 |
| Symbols: Ribosomal protein L18ae/L18 family protein chr:3:4910773-4911933 FORWARD LENGTH=178 | AT3G14600_1 | 21 kDa | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: EMB2719, HAP15 PAM domain (PC/PINT associated module) protein chr:1:7001409-7004154 REVERSE LENGTH=488 | AT1G20200_1 | 56 kDa | 3 | 3 | 0 | 1 | 0 | 3 | 0 | 0 | 0 | 0 | 0 |
| Symbols: PAM domain (PC/PINT associated module) protein chr:1:28524623-28526718 REVERSE LENGTH=487 | AT1G75990_1 | 56 kDa | 3 | 0 | 0 | 1 | 0 | 3 | 0 | 0 | 0 | 0 | 0 |
| Symbols: APS1 ATP sulfurylase 1 chr:3:8112837-8114734 FORWARD LENGTH=463 | AT3G28890_1 | 51 kDa | 3 | 1 | 0 | 2 | 0 | 3 | 0 | 0 | 0 | 0 | 0 |
| Symbols: APS2, ASA1 Pseudouridine synthase/archaeosine transglycosylase-like family protein chr:6:914825-6916657 REVERSE LENGTH=476 | AT1G19920_1 | 54 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: APS4 Pseudouridine synthase/archaeosine transglycosylase-like family protein chr:4:8413443-8415311 REVERSE LENGTH=465 | AT1G14680_1 | 52 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: Tetraacopteptide repeat (TPR)-like superfamily protein chr:3:22565440-22566678 REVERSE LENGTH=412 | AT3G0980_1 | 47 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 5 | 5 | 0 | 0 | 0 |
| Symbols: SPA2 SPA1-related 2 chr:4:6772163-6776765 FORWARD LENGTH=103 | AT4G1110_1 | 115 kDa | 5 | 6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: PORB prochlorophyllide oxidoreductase B chr:1:13725648-13727107 FORWARD LENGTH=401 | AT4G27440_1 (+1) | 43 kDa | 3 | 2 | 0 | 1 | 0 | 1 | 1 | 0 | 0 | 0 | 0 |
| Symbols: ATP8 ATP synthase epsilon chain chr:5:S225-S2663 REVERSE LENGTH=132 | ATCG00470_1 | 14 kDa | 2 | 2 | 0 | 1 | 0 | 1 | 1 | 2 | 0 | 0 | 0 |
| Symbols: RPL14 ribosomal protein L14 chr:C80696-81064 REVERSE LENGTH=122 | ATCG00780_1 | 14 kDa | 2 | 2 | 0 | 1 | 0 | 2 | 1 | 2 | 0 | 0 | 0 |
| Symbols: C2 calcium/lipid-binding plant phosphoribosyltransferase family protein chr:5:2127200-2129584 REVERSE LENGTH=794 | AT5G06850_1 | 91 kDa | 0 | 0 | 0 | 2 | 0 | 5 | 0 | 0 | 0 | 0 | 0 |
| Symbols: FDH formate dehydrogenase chr:5:477043-4779190 FORWARD LENGTH=384 | AT5G14780_1 | 42 kDa | 2 | 1 | 0 | 1 | 0 | 3 | 0 | 1 | 0 | 0 | 0 |
| Symbols: TOCI, APRK1, PRKR1, ATTOCI CCT motif-containing response regulator protein chr:5:24675540-24678176 FORWARD LENGTH=618 | AT5G61380_1 | 69 kDa | 2 | 2 | 2 | 0 | 3 | 0 | 1 | 0 | 1 | 1 | 1 |
| Symbols: ELF4-L2 ELF4-like 2 chr:2:7349498-2734547 FORWARD LENGTH=119 | AT1G72630_1 | 13 kDa | 0 | 1 | 0 | 1 | 0 | 1 | 2 | 2 | 2 | 1 | 1 |
| Symbols: STV1, RPL24A RPL24 Ribosomal protein L24 family protein chr:3:19660749-19661912 REVERSE LENGTH=163 | AT3G53020_1 | 19 kDa | 2 | 2 | 0 | 1 | 0 | 1 | 2 | 2 | 0 | 0 | 0 |
| Symbols: glycine-rich protein chr:4:11944050-11945656 REVERSE LENGTH=356 | AT4G22740_1 (+1) | 39 kDa | 2 | 2 | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 0 | 0 |
| Symbols: Ribosomal L28e family protein chr:8:851752-851995 FORWARD LENGTH=143 | AT2G19730_1 (+2) | 16 kDa | 1 | 1 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | 0 |
| Symbols: Ribosomal protein S11 family protein chr:2:15169295-15171159 FORWARD LENGTH=150 | AT2G36160_1 | 16 kDa | 2 | 2 | 1 | 3 | 1 | 3 | 0 | 0 | 0 | 0 | 0 |
| Symbols: Ribosomal protein S11 family protein chr:3:3623757-3624866 REVERSE LENGTH=150 | AT3G11510_1 | 16 kDa | 1 | 2 | 1 | 2 | 1 | 2 | 0 | 0 | 0 | 0 | 0 |
| Symbols: Coatomer, beta' subunit chr:3:5411699-5418312 REVERSE LENGTH=909 | AT3G15980_1 (+3) | 102 kDa | 3 | 1 | 0 | 0 | 0 | 4 | 0 | 0 | 0 | 0 | 0 |
| Symbols: structural molecules chr:1:30084522-30091949 FORWARD LENGTH=1135 | AT1G7990_1 (+2) | 129 kDa | 2 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 0 | 0 | 0 |
| Symbols: XIK, ATIXX, XI-1 Myosin family protein with Dil domain chr:5:6927064-6936825 REVERSE LENGTH=1545 | AT5G20490_1 (+1) | 175 kDa | 1 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: MYA1, ATMYA1, XI-1 myosin 1 chr:1:6039453-6049309 FORWARD LENGTH=1520 | AT1G17580_1 | 173 kDa | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: XIC, ATIXC Myosin family protein with Dil domain chr:1:2779963-2788325 FORWARD LENGTH=1538 | AT1G08730_1 | 175 kDa | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: HSP18-2, ERD8, HSP90_2, AtHsp90_2-1 heat shock protein 81-2 chr:5:22668923-22689433 FORWARD LENGTH=699 | AT5G56030_1 (+1) | 80 kDa | 3 | 2 | 0 | 1 | 0 | 1 | 1 | 1 | 0 | 0 | 0 |
| Symbols: PIP3A, PIP2, SIMP Plasma membrane intrinsic protein 3 chr:4:16708672-16709958 FORWARD LENGTH=280 | AT4G35100_1 (+1) | 30 kDa | 3 | 3 | 1 | 2 | 1 | 0 | 2 | 0 | 0 | 0 | 0 |
| Symbols: RPS4 chloroplast ribosomal protein S4 chr:5:45223-45828 REVERSE LENGTH=201 | ATCG00380_1 | 23 kDa | 1 | 1 | 0 | 0 | 0 | 0 | 2 | 2 | 0 | 0 | 0 |
| Symbols: LOS2, ENO2 Enolase chr:2:15321081-15323786 REVERSE LENGTH=444 | AT2G36530_1 | 48 kDa | 1 | 1 | 0 | 1 | 0 | 2 | 1 | 0 | 1 | 0 | 0 |
| Symbols: ATPase, V0/A0 complex, subunit C/I chr:3:10778025-10780350 FORWARD LENGTH=351 | AT3G28715_1 | 41 kDa | 2 | 1 | 0 | 1 | 0 | 1 | 1 | 0 | 0 | 0 | 0 |
| Symbols: ATPase, V0/A0 complex, subunit C/D chr:3:10773144-10775594 FORWARD LENGTH=351 | AT3G28710_1 | 41 kDa | 1 | 1 | 0 | 2 | 0 | 2 | 0 | 0 | 0 | 0 | 0 |
| Symbols: cpHsc70-1 chloroplast heat shock protein 70-1 chr:4:12590949-12593437 FORWARD LENGTH=718 | AT4G24280_1 | 77 kDa | 0 | 0 | 0 | 2 | 0 | 5 | 1 | 0 | 0 | 0 | 0 |
| Symbols: CPHC570-2 SEAT SHOCK PROTEIN 70-2, HSP70-7, cpHsc70-2 chloroplast heat shock protein 70-2 chr:5:20303470-20306295 FORWARD LENGTH=718 | AT5G49910_1 | 77 kDa | 0 | 0 | 0 | 3 | 0 | 4 | 1 | 0 | 0 | 0 | 0 |
| Symbols: LUH LEUNIG_homolog chr:2:1387235-13871844 FORWARD LENGTH=787 | AT2G37200_1 (+6) | 86 kDa | 0 | 0 | 0 | 1 | 0 | 3 | 0 | 0 | 0 | 0 | 0 |
| Symbols: emb11238 DEAD box RNA helicase (R3H) chr:9:59285540-5928871 REVERSE LENGTH=747 | AT5G26742_1 (+1) | 81 kDa | 3 | 2 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: RPS11 ribosomal protein S11 chr:7:78960-79767 REVERSE LENGTH=138 | ATCG00750_1 | 15 kDa | 2 | 2 | 0 | 1 | 0 | 1 | 2 | 2 | 0 | 0 | 0 |
| Symbols: Ribosomal protein S4 (RPS4) family protein chr:2:7546598-7548138 FORWARD LENGTH=261 | AT2G17360_1 (+3) | 30 kDa | 2 | 0 | 1 | 1 | 0 | 1 | 1 | 0 | 0 | 0 | 0 |
| Symbols: PFL_RPS18A, PFL1 Ribosomal protein S13/S18 family chr:1:8067990-8069163 FORWARD LENGTH=152 | AT1G22780_1 (+2) | 18 kDa | 0 | 1 | 1 | 2 | 0 | 1 | 0 | 1 | 1 | 0 | 0 |
| Symbols: P40, AP40, RPSAA 40S ribosomal protein SA chr:1:27243148-27244842 FORWARD LENGTH=298 | AT1G27370_1 (+1) | 32 kDa | 1 | 3 | 0 | 2 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| Symbols: RPSAB 40S ribosomal protein SA chr:3:1309544-1310846 REVERSE LENGTH=280 | AT5G04770_2 | 31 kDa | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: CLPC, ATHP93-II, HSP93-V, DCA1, CLPC1 CLPC homolog chr:5:20715710-20719800 REVERSE LENGTH=929 | AT5G50920_1 | ? | 4 | 2 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| Symbols: ATPLC, ATHP93-II, HSP93-VII Clp ATPase chr:3:8122363-18126000 REVERSE LENGTH=952 | AT3G48870_1 (+1) | 106 kDa | 3 | 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| Symbols: SPA1 SPA1-related 1 chr:1:19783748-19786690 FORWARD LENGTH=794 | AT1G3090_1 (+1) | 89 kDa | 3 | 6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: SPA1 SPA1-related 2 chr:2:8692736-8694837 FORWARD LENGTH=443 | AT2G20140_1 (+1) | 49 kDa | 5 | 3 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| Symbols: RPT6A, ATSG1 regulatory particle triple-4 ATPase 6A chr:5:6752144-6754918 FORWARD LENGTH=419 | AT5G19990_1 (+1) | 47 kDa | 1 | 1 | 0 | 1 | 0 | 2 | 1 | 1 | 0 | 0 | 0 |
| Symbols: Lactate/malate dehydrogenase family protein chr:1:1189418-1191267 REVERSE LENGTH=332 | AT1G04410_1 | 36 kDa | 0 | 2 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| Symbols: Aldolase superfamily protein chr:3:19627383-19628874 REVERSE LENGTH=358 | AT3G52930_1 | 39 kDa | 0 | 1 | 0 | 1 | 0 | 3 | 1 | 0 | 0 | 1 | 0 |
| Symbols: Aldolase superfamily protein chr:5:963389-964982 REVERSE LENGTH=359 | AT5G0360_2 | 39 kDa | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: Aldolase superfamily protein chr:4:13391566-13392937 FORWARD LENGTH=358 | AT4G26530_1 (+1) | 38 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| Symbols: CHU1, CH42, CH42, CHU1, CHU1 P-loop containing nucleoside triphosphate hydrolases superfamily protein chr:4:10201897-10203361 REVERSE LENGTH=424 | AT4G18480_1 | 46 kDa | 2 | 1 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 0 | 0 |
| Symbols: CHU2, CHL2, CHU2 magnesium chelatase 2 chr:5:18628095-18629565 FORWARD LENGTH=418 | AT5G45930_1 | 46 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: tRNA translucin family protein / WD-40 repeat family protein chr:3:23431009-23437241 REVERSE LENGTH=1104 | AT3G63460_1 (+2) | 120 kDa | 1 | 1 | 0 | 1 | 0 | 2 | 0 | 0 | 0 | 0 | 0 |
| Symbols: vacuolar ATP synthase subunit H family protein chr:3:14228846-14232228 REVERSE LENGTH=441 | AT3G42050_1 | 50 kDa | 2 | 1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| Symbols: RPL18 ribosomal protein L18 chr:3:1621511-1622775 FORWARD LENGTH=187 | AT3G05590_1 (+1) | 21 kDa | 2 | 1 | 1 | 1 | 0 | 2 | 1 | 1 | 0 | 0 | 0 |
| Symbols: RPT5A, ATSG2 regulatory particle triple-4 ATPase 5A chr:3:1603540-1605993 FORWARD LENGTH=424 | AT3G05530_1 | 47 kDa | 3 | 2 | 0 | 0 | 0 | 0 | 1 | 2 | 2 | 0 | 0 |
| Symbols: AGT, AGT1, SGAT alanine:glyoxylate aminotransferase chr:2:5329417-5540902 REVERSE LENGTH=401 | AT2G1360_1 (+1) | 44 kDa | 1 | 1 | 1 | 1 | 0 | 2 | 0 | 0 | 0 | 0 | 0 |
| Symbols: Ribosomal protein L22p/L17e family protein chr:1:9515230-9516725 FORWARD LENGTH=176 | AT1G27400_1 (+1) | 20 kDa | 0 | 1 | 2 | 0 | 0 | 1 | 2 | 0 | 0 | 0 | 0 |
| Symbols: VHA-A vacuolar ATP synthase subunit A chr:1:296900463-29664575 FORWARD LENGTH=623 | AT1G78900_1 (+1) | 69 kDa | 1 | 0 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 0 | 0 |
| Symbols: RPT1A regulatory particle triple-1A chr:1:20065921-20068324 REVERSE LENGTH=426 | AT1G53750_1 | 48 kDa | 2 | 1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| Symbols: AT1J2, AT2 DNAJI homologue 2 chr:5:7303798-7305668 REVERSE LENGTH=419 | AT5G2260_1 | 46 kDa | 2 | 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| Symbols: AT1J3, AT1 DNAJI homologous 3 chr:3:1586115-1587109 REVERSE LENGTH=420 | AT3G4410_1 (+1) | 46 kDa | 2 | 2 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 0 | 0 |
| Symbols: RPS1, ARRP1 ribosomal protein S1 chr:5:11619262-11621223 REVERSE LENGTH=416 | AT5G03510_1 | 45 kDa | 1 | 0 | 0 | 3 | 0 | 4 | 0 | 0 | 0 | 0 | 0 |
| Symbols: ACCD acetyl-CoA carboxylase carboxyl transferase subunit beta chr:C57075-58541 FORWARD LENGTH=488 | ATCG00500_1 | 56 kDa | 2 | 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| Symbols: RPS15A ribosomal protein S15A chr:2:408413-2409065 REVERSE LENGTH=134 | ATCG00770_1 | 15 kDa | 1 | 2 | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 0 | 0 |
| Symbols: SSR16 small subunit ribosomal protein 16 chr:1:16535084-16536092 REVERSE LENGTH=113 | AT4G34620_1 | 13 kDa | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: Sucrose-6P-phosphate phosphohydrolase family protein chr:2:15053952-15055776 FORWARD LENGTH=422 | AT2G35840_1 (+2) | 48 kDa | 1 | 0 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 0 | 0 |
| Symbols: GTP binding Elongation factor Tu family protein chr:4:1295751-1298354 REVERSE LENGTH=454 | AT4G02930_1 | 49 kDa | 3 | 0 | 0 | 1 | 0 | 3 | 0 | 0 | 0 | 0 | 0 |
| Symbols: ECT2 evolutionarily conserved C-terminal region 2 chr:3:4385274-4388220 FORWARD LENGTH=667 | AT3G13460_1 (+3) | 72 kDa | 3 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: NOP56 homolog of nuclear protein NOP56 chr:1:20984544-2098693 REVERSE LENGTH=522 | AT1G1860_1 (+2) | 44 kDa | 1 | 1 | 0 | 1 | 0 | 1 | 2 | 0 | 0 | 0 | 0 |
| Symbols: RPS15A ribosomal protein S15A chr:2:408413-2409065 REVERSE LENGTH= | | | | | | | | | | | | | |

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|--|------------------|---------|---|---|---|---|---|---|---|---|---|---|---|
| Symbols: RPL16 ribosomal protein L16 chr:81189-82652 REVERSE LENGTH=135 | ATCG00790.1 | 15 kDa | 1 | 0 | 0 | 1 | 0 | 2 | 0 | 0 | 0 | 0 | 0 |
| Symbols: PUB12, ATPUB12 PLANT U-BOX 12 chr:212370608-12370608 REVERSE LENGTH=962 | AT2G28830.1 | 107 kDa | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| Symbols: NAD(P)-binding Rossmann-fold superfamily protein chr:3:11193767-11194948 REVERSE LENGTH=298 | AT3G29250.1 | 32 kDa | 0 | 0 | 0 | 1 | 0 | 3 | 0 | 0 | 0 | 0 | 0 |
| Symbols: ILA IUTYHHA chr:1:24065232-24081908 REVERSE LENGTH=2610 | AT1G64790.1 (+1) | 285 kDa | 3 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: APUM5, PUM5 pumilio 5 chr:3:0759098-706260 REVERSE LENGTH=961 | AT3G20250.1 | 107 kDa | 3 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: ATPP57, TP57, ATPPSA trehalose-phosphatase/synthase 7 chr:1:1955413-1958153 FORWARD LENGTH=851 | AT1G06410.1 | 97 kDa | 1 | 0 | 0 | 0 | 0 | 3 | 0 | 0 | 0 | 0 | 0 |
| Symbols: transcription regulators chr:1:37335-38668 FORWARD LENGTH=2431 | AT1G02080.1 (+1) | 270 kDa | 2 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: ATGST9, GLUTR, ATGST7, GST9 glutathione S-transferase PHI 9 chr:2:13139132-13140057 FORWARD LENGTH=215 | AT2G30860.1 (+1) | 24 kDa | 0 | 2 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: Ribosomal protein L35ae family protein chr:1:27928415-27929466 REVERSE LENGTH=112 | AT1G74270.1 | 13 kDa | 1 | 0 | 0 | 2 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| Symbols: ATU2AF35B, U2AF35B Zinc finger Cx8-Cx5-Cx3-H type family protein chr:5:17170445-17171296 REVERSE LENGTH=283 | AT5G42820.1 (+1) | 33 kDa | 2 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| Symbols: ATU2AF35A U2 snRN auxiliary factor small subunit, putative chr:6:9615302-9616042 FORWARD LENGTH=246 | AT1G7650.2 | 29 kDa | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| Symbols: Zinc finger Cx8-Cx5-Cx3-H type family protein chr:3:16328211-16328448 REVERSE LENGTH=75 | AT3G44785.1 | 9 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: PIbL, PIbS phytochrome interacting factor 3-like 6 chr:3:21828189-2182895 REVERSE LENGTH=442 | AT5G59060.1 (+3) | 49 kDa | 0 | 0 | 1 | 0 | 0 | 0 | 2 | 0 | 0 | 0 | 0 |
| Symbols: PIb4, SRL2, ATPb4 phytochrome interacting factor 4 chr:2:17887003-1788823 FORWARD LENGTH=430 | AT2G43010.1 (+1) | 48 kDa | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| Symbols: Ribosomal protein L31e family protein chr:2:851377-8514346 FORWARD LENGTH=119 | AT2G19740.1 (+2) | 14 kDa | 0 | 0 | 0 | 2 | 0 | 2 | 0 | 0 | 0 | 0 | 0 |
| Symbols: Ribosomal protein L31e family protein chr:5:22944003-22944767 REVERSE LENGTH=85 | AT5G56710.2 | 10 kDa | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| Symbols: Coatomer epsilon subunit chr:1:1085846-10860173 REVERS LENGTH=292 | AT1G30630.1 | 33 kDa | 0 | 0 | 0 | 2 | 0 | 2 | 0 | 0 | 0 | 0 | 0 |
| Symbols: SHM4 serine hydroxymethyltransferase 4 chr:8048013-8050021 REVERSE LENGTH=471 | AT4G13930.1 | 52 kDa | 2 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: RP22 ribosomal protein L22 chr:3:83467-83949 REVERSE LENGTH=160 | ATCG00810.1 | 19 kDa | 0 | 0 | 0 | 1 | 0 | 2 | 0 | 0 | 0 | 0 | 0 |
| Symbols: PBE1 20S proteasome beta subunit E1 chr:14452641-4454663 FORWARD LENGTH=274 | AT1G13060.1 (+2) | 30 kDa | 0 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: PSB8 photosystem II reaction center protein B chr:72371-73897 FORWARD LENGTH=508 | ATCG00680.1 | 56 kDa | 1 | 1 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 0 | 0 |
| Symbols: NRPB1, RPBP1 RNA_POL_II_LSRNA_POL_II_LS RNA polymerase II large subunit chr:4:16961115-16967892 REVERSE LENGTH=1839 | AT4G35800.1 | 205 kDa | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: EMB82761 threonyl-tRNA synthetase, putative / threonine-tRNA ligase, putative chr:16846466-1701271 REVERSE LENGTH=650 | AT2G04842.1 | 75 kDa | 0 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 0 | 0 | 0 |
| Symbols: ELF4-L4 ELF4-like 4 chr:5997932-5998276 FORWARD LENGTH=114 | AT1G17455.1 (+1) | 13 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 0 | 0 |
| Symbols: AAA-type ATPase family protein chr:1:7009220-17011607 FORWARD LENGTH=399 | AT1G45000.1 (+2) | 45 kDa | 2 | 2 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 0 | 0 |
| Symbols: PHOT1, NPH1, JK224, RTP1 phototropin 1 chr:3:1681857-16823960 FORWARD LENGTH=996 | AT3G45780.1 (+1) | 112 kDa | 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| Symbols: PHOT2, NP1, NP1 phototropin 2 chr:23524771-23529993 FORWARD LENGTH=915 | AT5G58140.1 (+3) | 102 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: ZFN1 zinc finger protein 1 chr:3:614075-615916 FORWARD LENGTH=397 | AT3G02830.1 | 44 kDa | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: Ribosomal protein L35Ae family protein chr:1:15651585-15652427 REVERSE LENGTH=111 | AT1G41880.1 | 13 kDa | 0 | 0 | 2 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: SPA3 SPA1-related chr:3:5169327-5172480 REVERSE LENGTH=837 | AT3G15354.1 | 93 kDa | 1 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: PRP39 Tetra peptide repeat (TPR)-like superfamily protein chr:1:051803-1056550 FORWARD LENGTH=768 | AT1G04080.1 (+1) | 85 kDa | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: ABA1, LOS6, NPQ2, ATABA1, ZEP, IB53, ATZEP zeaxanthin epoxidase (ZEP) (ABA1) chr:26753745-26757090 REVERSE LENGTH=667 | AT5G67030.1 (+1) | 74 kDa | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

Percent Coverage

| Accession Number | Molecular Weight | AfELF3-1 | AfELF3-2 | SvELF3#2 rep1 | SvELF3#2 rep2 | SvELF3#3 rep1 | SvELF3#3 rep2 | BdELF3#2 rep1 | BdELF3#2 rep2 | BdELF3#3 rep1 | BdELF3#3 rep2 |
|------------------|------------------|----------|----------|---------------|---------------|---------------|---------------|---------------|---------------|---------------|---------------|
| AT2G18790.1 | 129 kDa | 36.80% | 37.40% | 54.20% | 42.20% | 49.60% | 45.00% | 33.70% | 32.90% | 39.80% | 37.30% |
| AT4G16250.1 | 129 kDa | 10.10% | 11.00% | 11.90% | 11.70% | 14.70% | 11.90% | 11.10% | 10.10% | 13.60% | 11.80% |
| AT5G02500.1 | 71 kDa | 36.10% | 28.40% | 55.60% | 51.00% | 53.80% | 58.70% | 28.40% | 28.10% | 16.70% | 22.60% |
| AT3G09440.1 (+1) | 71 kDa | 37.30% | 33.60% | 49.90% | 44.40% | 51.00% | 47.80% | 33.60% | 31.70% | 12.80% | 24.50% |
| AT3G12580.1 | 71 kDa | 27.80% | 20.80% | 31.20% | 36.90% | 37.50% | 41.70% | 22.60% | 22.30% | 8.77% | 15.10% |
| AT5G02490.1 | 71 kDa | 31.70% | 24.50% | 29.60% | 28.20% | 31.40% | 39.20% | 22.70% | 20.80% | 8.73% | 15.00% |
| AT1G16030.1 | 71 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| ATMGCustom02 | 86 kDa | 2.38% | 0 | 1.00% | 0.00% | 1.00% | 0.00% | 41.70% | 42.70% | 35.30% | 33.10% |
| AT5G35840.1 | 124 kDa | 29.40% | 28.90% | 37.40% | 38.70% | 37.10% | 42.10% | 24.10% | 22.00% | 22.70% | 25.80% |
| ATMGCustom01 | 87 kDa | 2.38% | 0 | 40.20% | 48.00% | 42.40% | 54.40% | 1.00% | 1.00% | 2.38% | 2.51% |
| ATMGCustom03 | 84 kDa | 35.80% | 31.40% | 0 | 0 | 0 | 0 | 0.00% | 0 | 0 | 0 |
| AT4G3630.1 | 91 kDa | 21.40% | 17.00% | 22.50% | 32.50% | 22.00% | 36.10% | 17.80% | 19.30% | 20.20% | 21.70% |
| ATCG00490.1 | 53 kDa | 32.20% | 30.10% | 39.20% | 34.20% | 29.00% | 46.10% | 32.20% | 32.20% | 21.50% | 22.80% |
| AT4G18130.1 | 123 kDa | 16.00% | 26.60% | 18.30% | 23.20% | 18.50% | 23.50% | 7.46% | 14.10% | 19.20% | 18.40% |
| AT5G62690.1 (+1) | 51 kDa | 31.10% | 27.10% | 9.78% | 23.10% | 12.90% | 28.90% | 20.70% | 16.00% | 13.30% | 11.10% |
| AT1G20010.1 | 50 kDa | 25.60% | 20.90% | 0 | 21.60% | 0 | 27.60% | 20.90% | 10.20% | 7.57% | 5.35% |
| AT5G12250.1 | 51 kDa | 20.70% | 18.30% | 0 | 14.30% | 0 | 20.30% | 18.30% | 10.20% | 7.57% | 5.35% |
| AT4G20890.1 | 50 kDa | 28.40% | 24.30% | 0 | 20.90% | 7.21% | 23.20% | 15.80% | 10.40% | 7.66% | 5.41% |
| AT2G29550.1 | 51 kDa | 27.40% | 23.40% | 0 | 16.70% | 12.90% | 26.30% | 18.30% | 16.00% | 7.57% | 5.35% |
| AT4G4340.1 | 50 kDa | 28.40% | 24.30% | 0 | 18.20% | 7.21% | 26.60% | 18.50% | 10.40% | 7.66% | 5.41% |
| AT5G23860.1 (+1) | 51 kDa | 28.70% | 24.70% | 0 | 20.50% | 12.90% | 20.30% | 18.30% | 16.00% | 7.57% | 0 |
| AT2G16365.1 (+2) | 89 kDa | 14.90% | 14.90% | 17.50% | 25.10% | 21.00% | 28.70% | 15.40% | 16.60% | 18.60% | 18.60% |
| AT1G13440.1 | 37 kDa | 37.30% | 31.70% | 22.50% | 58.60% | 34.90% | 52.70% | 20.70% | 12.70% | 27.20% | 10.40% |
| AT3G04120.1 | 37 kDa | 37.30% | 31.70% | 22.50% | 58.60% | 34.90% | 52.70% | 20.70% | 12.70% | 27.20% | 10.40% |
| ATCG00120.1 | 55 kDa | 31.60% | 20.90% | 0.27% | 26.60% | 0 | 35.70% | 22.70% | 20.90% | 18.30% | 9.86% |
| AT1G04820.1 (+1) | 50 kDa | 20.20% | 21.30% | 18.70% | 32.90% | 21.30% | 35.60% | 8.44% | 16.90% | 6.44% | 4.44% |
| AT5G19770.1 (+1) | 50 kDa | 11.10% | 10.90% | 11.10% | 20.70% | 9.11% | 26.40% | 4.00% | 12.70% | 2.00% | 0 |
| AT4G14960.1 | 47 kDa | 21.20% | 19.20% | 16.40% | 31.40% | 19.20% | 32.30% | 8.90% | 21.10% | 6.79% | 4.68% |
| AT1G49240.1 (+1) | 42 kDa | 12.50% | 12.50% | 9.02% | 18.30% | 11.90% | 15.10% | 12.50% | 12.50% | 12.50% | 12.50% |
| AT5G09810.1 | 42 kDa | 16.70% | 16.70% | 4.24% | 22.50% | 16.20% | 22.30% | 16.70% | 12.50% | 9.02% | 4.24% |
| AT5G59370.1 (+1) | 42 kDa | 0 | 0 | 0 | 13.30% | 0 | 10.30% | 4.77% | 4.77% | 0 | 0 |
| AT2G42170.1 | 37 kDa | 5.47% | 5.47% | 6.99% | 5.47% | 5.47% | 5.47% | 5.47% | 5.47% | 5.47% | 0 |
| AT2G42100.1 | 42 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| AT4G20360.1 | 52 kDa | 17.60% | 14.10% | 32.10% | 34.70% | 30.50% | 40.50% | 14.10% | 11.60% | 9.03% | 9.03% |
| AT2G1840.1 | 31 kDa | 23.90% | 28.40% | 9.12% | 14.00% | 15.10% | 20.00% | 23.90% | 23.90% | 10.50% | 5.26% |
| AT1G58380.1 (+3) | 31 kDa | 27.80% | 23.60% | 13.40% | 9.51% | 23.90% | 24.30% | 14.10% | 14.10% | 5.28% | 0.00% |
| AT3G57490.1 | 30 kDa | 12.70% | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| AT3G22380.2 | 165 kDa | 5.47% | 5.47% | 4.18% | 12.20% | 2.96% | 15.30% | 4.05% | 3.02% | 1.29% | 1.29% |
| AT2G40080.1 | 12 kDa | 49.50% | 49.50% | 42.30% | 67.60% | 60.40% | 49.50% | 49.50% | 49.50% | 67.60% | 67.60% |
| AT3G26650.1 | 42 kDa | 36.60% | 30.60% | 11.40% | 46.20% | 14.90% | 48.20% | 20.20% | 16.70% | 14.10% | 10.10% |
| AT1G12900.3 (+1) | 38 kDa | 39.40% | 34.60% | 12.90% | 39.40% | 16.90% | 39.40% | 22.90% | 14.30% | 11.40% | 4.29% |
| AT1G33120.1 (+1) | 22 kDa | 24.70% | 21.10% | 34.00% | 56.20% | 34.00% | 47.40% | 25.80% | 29.90% | 29.90% | 29.90% |
| AT4G10450.1 | 22 kDa | 4.12% | 9.28% | 0 | 14.40% | 0 | 14.40% | 0 | 9.28% | 9.28% | 9.28% |
| AT2G32950.1 | 76 kDa | 15.70% | 16.90% | 17.20% | 8.44% | 6.22% | 11.90% | 1.78% | 4.30% | 11.30% | 7.85% |
| AT4G16143.1 (+1) | 59 kDa | 6.36% | 6.36% | 2.24% | 23.40% | 0.00% | 26.40% | 28.80% | 26.70% | 6.36% | 10.70% |
| AT3G06720.1 (+1) | 59 kDa | 0 | 0 | 0 | 5.08% | 0 | 5.26% | 5.08% | 3.01% | 0 | 0.00% |
| AT1G02690.1 | 59 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| AT1G09270.1 (+2) | 59 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| AT3G17390.1 | 43 kDa | 39.20% | 29.80% | 9.92% | 15.00% | 0 | 24.40% | 4.33% | 0 | 0 | 0 |

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|--|------------------|---------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|-------|
| Symbols: MAT3 methionine adenosyltransferase 3 chr2:15479721-15480893 REVERSE LENGTH=390 | AT2G36880_1 (+1) | 42 kDa | 20.50% | 11.50% | 10.00% | 3.85% | 0 | 10.00% | 0 | 0 | 0 | 0 | 0 |
| Symbols: SAM-2, MAT2, SAM2, ATSAM2 S-adenosylmethionine synthetase 2 chr4:796298-797479 REVERSE LENGTH=393 | AT4G01850_1 (+1) | 43 kDa | 23.70% | 9.16% | 0 | 3.82% | 0 | 9.41% | 0 | 0 | 0 | 0 | 0 |
| Symbols: SAM1, SAM-1, MAT1, ATSAM1 S-adenosylmethionine synthetase 1 chr1:519037-520218 FORWARD LENGTH=393 | AT1G02500_1 (+1) | 43 kDa | 19.80% | 5.34% | 0 | 6.62% | 0 | 12.20% | 0 | 0 | 0 | 0 | 0 |
| Symbols: RCA rubisco activase chr2:16570951-16573345 REVERSE LENGTH=474 | AT2G39730_1 | 52 kDa | 23.80% | 21.50% | 10.80% | 15.60% | 13.30% | 23.20% | 21.50% | 19.60% | 12.00% | 8.02% | |
| Symbols: PCL1, LUX Homeodomain-like superfamily protein chr1:17183248-17184219 FORWARD LENGTH=323 | AT3G46640_1 (+1) | 35 kDa | 3.10% | 3.10% | 10.20% | 18.90% | 10.20% | 22.90% | 3.10% | 3.10% | 3.10% | 10.50% | |
| Symbols: GS2, GLN2, ATGLS1 glutamine synthetase 2 chr5:13831220-13833239 FORWARD LENGTH=485 | AT1G20620_5 | 56 kDa | 37.30% | 32.00% | 4.74% | 24.70% | 2.89% | 28.00% | 23.70% | 11.50% | 2.27% | 2.27% | |
| Symbols: CAT3, SEN2, ATCAT3 catalase 3 chr1:17183248-17184219 FORWARD LENGTH=485 | AT1G11130_1 (+1) | 47 kDa | 22.80% | 17.70% | 16.50% | 33.00% | 16.50% | 22.60% | 17.70% | 14.00% | 3.49% | 3.49% | |
| Symbols: Clathrin, heavy chain chr3:342575-3491667 REVERSE LENGTH=1705 | AT3G11130_1 | 193 kDa | 13.30% | 8.68% | 0 | 1.94% | 0 | 5.04% | 2.17% | 1.29% | 0 | 0 | |
| Symbols: Clathrin, heavy chain chr3:2587171-2595411 REVERSE LENGTH=1703 | AT3G08530_1 | 193 kDa | 12.40% | 7.99% | 0 | 1.94% | 0 | 5.05% | 2.17% | 1.29% | 0 | 0 | |
| Symbols: Ribosomal protein S3 family protein chr3:19951547-19952782 FORWARD LENGTH=249 | AT3G53870_1 | 27 kDa | 16.90% | 16.90% | 16.90% | 22.50% | 16.90% | 25.70% | 10.40% | 10.40% | 10.40% | 10.40% | 5.22% |
| Symbols: Ribosomal protein S3 family protein chr2:13450284-13451669 FORWARD LENGTH=250 | AT2G1610_1 | 28 kDa | 20.00% | 20.00% | 16.80% | 22.40% | 16.80% | 30.80% | 13.60% | 10.40% | 5.20% | 5.20% | |
| Symbols: Ribosomal protein S3 family protein chr5:13710355-13712192 REVERSE LENGTH=248 | AT5G5530_1 | 27 kDa | 20.60% | 20.60% | 16.90% | 22.60% | 16.90% | 25.80% | 14.10% | 5.24% | 5.24% | 5.24% | |
| Symbols: EIF4A1, R44, TIF4A1 eukaryotic translation initiation factor 4A1 chr3:4592635-4594128 REVERSE LENGTH=412 | AT1G13920_1 (+1) | 47 kDa | 14.60% | 12.60% | 10.90% | 12.10% | 12.60% | 16.70% | 8.25% | 5.83% | 5.83% | 5.83% | |
| Symbols: EIF4A2-1, EIF4A2-2 elif4a-2 chr1:20260495-20262018 FORWARD LENGTH=412 | AT1G54270_1 | 47 kDa | 10.20% | 8.25% | 10.90% | 12.10% | 12.60% | 17.50% | 8.25% | 5.83% | 5.83% | 5.83% | |
| Symbols: EIF4A2-1 eukaryotic initiation factor 4A-II chr3:6863790-6866242 FORWARD LENGTH=408 | AT3G19760_1 | ? | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| Symbols: BIP, BIPP Heat shock protein 70 (Hsp 70) family protein chr5:16807697-16810480 REVERSE LENGTH=668 | AT5G42020_1 | 74 kDa | 5.99% | 10.30% | 7.78% | 19.50% | 15.60% | 23.20% | 2.40% | 4.64% | 6.59% | 4.49% | |
| Symbols: DAYSLLEEPER BED zinc finger hAT family dimerisation domain chr3:14321838-14323928 FORWARD LENGTH=696 | AT3G42170_1 | 79 kDa | 19.00% | 11.40% | 0 | 15.90% | 0 | 27.20% | 7.18% | 8.19% | 4.02% | 0 | |
| MLK2 Symbols: Protein kinase family protein chr3:1014412-1018244 REVERSE LENGTH=701 | AT3G03940_1 | 78 kDa | 8.27% | 7.99% | 0 | 6.56% | 0 | 1.57% | 19.80% | 13.00% | 13.40% | 9.42% | |
| MLK1 Symbols: Protein kinase family protein chr5:6010215-6013724 REVERSE LENGTH=691 | AT5G18190_1 | 77 kDa | 12.40% | 10.70% | 0 | 4.92% | 0 | 1.59% | 14.00% | 14.00% | 10.70% | 10.70% | |
| Symbols: GAPB glyceraldehyde-3-phosphate dehydrogenase B subunit chr1:16127552-16129584 FORWARD LENGTH=447 | AT1G42970_1 | 48 kDa | 26.00% | 21.70% | 3.36% | 34.70% | 3.36% | 40.50% | 16.30% | 12.30% | 9.62% | 3.36% | |
| Symbols: SPA1 SPA (suppressor of pha-105) protein family chr2:1902572-19026821 REVERSE LENGTH=1029 | AT2G46340_1 | 115 kDa | 13.50% | 8.84% | 2.43% | 8.07% | 2.82% | 8.55% | 0 | 8.16% | 5.83% | | |
| Symbols: Ribosomal phosphoprotein carboxyals (small chain) family protein chr5:15377501-15378306 REVERSE LENGTH=181 | AT5G38410_1 | 20 kDa | 26.50% | 22.10% | 36.50% | 39.20% | 37.00% | 39.20% | 26.50% | 17.70% | 21.50% | 17.10% | |
| Symbols: Ribosomal phosphoprotein carboxyals (small chain) family protein chr5:15384350-15385155 REVERSE LENGTH=181 | AT5G38400_1 | 20 kDa | 26.00% | 21.50% | 16.60% | 18.80% | 16.60% | 18.80% | 16.60% | 7.73% | 12.20% | 7.73% | |
| Symbols: PHYA, FHY2, EFL1, HYB phytochrome A chr3:2953813-2955444 FORWARD LENGTH=406 | AT1G09570_1 | 125 kDa | 1.16% | 1.34% | 11.30% | 5.17% | 11.20% | 2.41% | 0.00% | 2.23% | 7.40% | 4.37% | |
| Symbols: Ribosomal protein L4/L1 family chr3:2953813-2955265 FORWARD LENGTH=407 | AT3G09630_1 (+1) | 45 kDa | 3.69% | 3.69% | 3.45% | 6.65% | 3.45% | 21.70% | 7.14% | 3.69% | 3.69% | 0 | |
| Symbols: Ribosomal protein L4/L1 family chr5:657830-6595265 FORWARD LENGTH=407 | AT5G02870_1 (+1) | 45 kDa | 6.88% | 6.88% | 3.44% | 7.13% | 3.44% | 18.20% | 6.63% | 3.69% | 0 | 0 | |
| Symbols: PSC51, ATPCS delta1-pyrrole-5-carboxylate synthase 1 chr2:16598516-16602939 REVERSE LENGTH=717 | AT2G39800_1 (+1) | 78 kDa | 12.10% | 13.20% | 3.35% | 5.72% | 3.35% | 18.50% | 7.81% | 6.00% | 3.21% | 0 | |
| Symbols: PSC52 delta1-pyrrole-5-carboxylate synthase 2 chr3:20624278-20628989 REVERSE LENGTH=726 | AT2G55610_1 | 79 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| Symbols: RBCS1A ribulose bisphosphate carboxylase small chain 1A chr1:25048465-2504249 FORWARD LENGTH=180 | AT1G67090_1 | 20 kDa | 26.70% | 26.70% | 26.70% | 38.90% | 27.20% | 38.90% | 22.20% | 17.80% | 7.78% | 17.80% | |
| Symbols: ATCM5, ATMTS, ATM1 Cobalamin-independent synthase family protein chr5:5957355-5939195 FORWARD LENGTH=765 | AT5G17920_1 (+1) | 84 kDa | 7.06% | 9.93% | 7.06% | 8.76% | 5.75% | 12.70% | 3.92% | 1.83% | 0 | 0 | |
| Symbols: ATM53, MS3 methionine synthase 3 chr5:7124397-7128353 REVERSE LENGTH=812 | AT5G20980_1 (+1) | 91 kDa | 2.34% | 3.20% | 0 | 0 | 0 | 3.20% | 1.97% | 0 | 0 | 0 | |
| Symbols: PGK1 phosphoglycerate kinase 1 chr3:4061127-4063140 REVERSE LENGTH=481 | AT3G12780_1 | 50 kDa | 16.20% | 12.50% | 0 | 17.30% | 0 | 25.20% | 10.40% | 7.28% | 3.53% | 0 | |
| Symbols: PGK phosphoglycerate kinase 1 chr2:29924347-29926295 REVERSE LENGTH=401 | AT1G79550_1 (+1) | 42 kDa | 8.73% | 0 | 0 | 0 | 0 | 0 | 4.24% | 4.24% | 4.24% | 0 | |
| Symbols: Phosphoglycerate kinase family protein chr1:21028622-21030454 FORWARD LENGTH=405 | AT1G56190_2 | 43 kDa | 11.10% | 0 | 0 | 11.40% | 0 | 13.60% | 0 | 0 | 0 | 0 | |
| Symbols: LOSS1 Ribosomal protein S5/Elongation factor GII/V family protein chr1:20968245-20971077 REVERSE LENGTH=843 | AT1G56070_1 | 94 kDa | 5.93% | 4.98% | 2.73% | 6.52% | 4.15% | 18.70% | 2.14% | 2.14% | 0 | 0 | |
| Symbols: structural constituent of ribosome chr2:82826-83482 REVERSE LENGTH=218 | AT2G00800_1 | 25 kDa | 30.70% | 22.50% | 9.17% | 22.50% | 9.17% | 31.20% | 4.13% | 0 | 0 | 0 | |
| CAT2 Catalase 2 chr4:16700937-16703215 REVERSE LENGTH=492 | AT4G35090_1 | 57 kDa | 27.40% | 17.90% | 6.91% | 24.60% | 2.85% | 19.50% | 12.40% | 12.20% | 2.24% | 2.24% | |
| Symbols: Ribosomal protein S27a / Ubiquitin family protein chr1:8319490-8315410 FORWARD LENGTH=230 | AT1G23410_1 (+3) | 18 kDa | 21.20% | 21.20% | 10.30% | 15.40% | 10.30% | 15.40% | 21.20% | 16.00% | 5.77% | 16.00% | |
| Symbols: UBO9 ubiquitin 9 chr5:1495282-14953750 REVERSE LENGTH=322 | AT5G37640_1 | 36 kDa | 0 | 7.76% | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| Symbols: UBO12 ubiquitin 12 chr2:10549533-20552025 FORWARD LENGTH=230 | AT1G55060_1 | 26 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| Symbols: UBO8 ubiquitin 8 chr3:3004111-300606 REVERSE LENGTH=631 | AT3G09790_1 | 72 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| Symbols: GTP binding elongation factor Tu family protein chr1:2455559-2457001 FORWARD LENGTH=449 | AT1G7920_1 (+5) | 50 kDa | 8.91% | 6.90% | 2.45% | 8.91% | 2.45% | 14.30% | 7.13% | 2.45% | 4.23% | 2.45% | |
| Symbols: Ribosomal protein L13 family protein chr3:9064613-9065871 FORWARD LENGTH=206 | AT3G24830_1 | 23 kDa | 5.83% | 5.83% | 6.80% | 6.80% | 6.80% | 12.60% | 5.83% | 11.70% | 0.00% | 0 | |
| Symbols: Ribosomal protein L13 family protein chr3:2252092-2253322 FORWARD LENGTH=206 | AT3G07110_1 (+1) | 23 kDa | 11.70% | 12.10% | 6.80% | 6.80% | 6.80% | 11.70% | 17.50% | 0 | 0 | 0 | |
| Symbols: Ribosomal protein L13 family protein chr5:1977135-19772685 REVERSE LENGTH=206 | AT5G48760_1 (+1) | 24 kDa | 0 | 0 | 0 | 6.80% | 0 | 6.80% | 5.83% | 0 | 0 | 0 | |
| Symbols: Ribosomal protein L13 family protein chr4:7655133-7656542 REVERSE LENGTH=206 | AT4G13170_1 | 24 kDa | 0 | 6.31% | 0 | 6.80% | 0 | 0 | 0 | 11.70% | 0 | 0 | |
| Symbols: HOG1, EMB1395, SAHH1, MEE58, ATSAH1 S-adenosyl-L-homocysteine hydrolase chr4:8054931-8056676 FORWARD LENGTH=485 | AT4G13940_1 | 53 kDa | 6.39% | 10.50% | 5.98% | 8.66% | 5.98% | 17.10% | 2.06% | 4.54% | 0 | 0 | |
| Symbols: SAHH2, ATSAH2 S-adenosyl-L-homocysteine (SAH) hydrolase 2 chr3:8588013-8589671 REVERSE LENGTH=485 | AT3G23810_1 | 53 kDa | 4.33% | 4.33% | 0 | 1.86% | 0 | 10.30% | 0 | 2.47% | 0 | 0 | |
| Symbols: HOG1, SAHH1 S-adenosyl-L-homocysteine hydrolase chr4:8054931-8056735 FORWARD LENGTH=325 | AT4G13940_4 | 36 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| Symbols: CRB, CSP418, HIP1,3 chloroplast RNA binding chr1:3015473-3018035 FORWARD LENGTH=378 | AT1G09340_1 | 43 kDa | 16.10% | 11.60% | 3.70% | 4.23% | 3.70% | 18.00% | 3.70% | 3.70% | 0 | 0 | |
| Symbols: ACC1, AT-ACC1, EMB22, GK, PASS1 acetyl-CoA carboxylase 1 chr1:13534196-13543773 FORWARD LENGTH=2254 | AT1G36160_1 (+1) | 251 kDa | 8.07% | 0.80% | 0 | 1.06% | 0 | 2.09% | 0 | 0 | 0 | 0 | |
| Symbols: Ribosomal protein S5 domain 2-like superfamily protein chr5:609253-6090693 REVERSE LENGTH=146 | AT5G18380_1 (+1) | 17 kDa | 22.60% | 28.10% | 6.85% | 22.60% | 6.85% | 13.00% | 22.60% | 22.60% | 0.00% | 0 | |
| Symbols: Ribosomal protein S5 domain 2-like superfamily protein chr2:3781442-3781882 FORWARD LENGTH=146 | AT2G050990_1 | 17 kDa | 15.80% | 21.20% | 0 | 15.80% | 0 | 6.16% | 15.80% | 15.80% | 0.00% | 0 | |
| Symbols: CA1 carbonic anhydrase 1 chr3:194853-197873 REVERSE LENGTH=347 | AT4G13170_1 (+1) | 37 kDa | 8.36% | 8.36% | 4.90% | 13.80% | 4.90% | 18.40% | 11.00% | 4.61% | 0.00% | 0 | |
| Symbols: CA2, C18, BETA CA2 carbonic anhydrase 2 chr5:4758245-4762382 FORWARD LENGTH=331 | AT4G13940_4 | 36 kDa | 3.93% | 3.93% | 5.14% | 14.50% | 5.14% | 23.60% | 3.93% | 0.00% | 0 | 0 | |
| ATAN11, LW01 LW01 Transducin/WD40-repeat-like superfamily protein chr1:4395114-4396154 REVERSE LENGTH=346 | AT1G2910_1 | 39 kDa | 21.40% | 29.50% | 21.10% | 30.90% | 16.80% | 21.10% | 21.70% | 19.40% | 11.00% | 11.00% | |
| Symbols: MLK4 Protein kinase family protein chr3:4469434-4473234 FORWARD LENGTH=703 | AT3G13670_1 | 79 kDa | 10.20% | 12.70% | 0 | 0 | 0 | 1.71% | 21.20% | 9.82% | 10.80% | 13.40% | |
| Symbols: RPS6, RPS6A ribosomal protein S6 chr4:15346306-1534774 REVERSE LENGTH=250 | AT4G31700_1 | 28 kDa | 10.80% | 24.00% | 0.00% | 3.60% | 0 | 20.80% | 24.00% | 20.80% | 10.80% | 4.80% | |
| Symbols: Ribosomal protein L30/L7 family protein chr2:1293493-1342462 REVERSE LENGTH=242 | AT2G01250_1 | 28 kDa | 19.00% | 15.30% | 4.96% | 0 | 4.96% | 10.30% | 6.20% | 9.92% | 6.20% | 0 | |
| Symbols: Ribosomal protein L30/L7 family protein chr2:18249227-18250417 REVERSE LENGTH=247 | AT2G44120_2 | 29 kDa | 9.72% | 15.00% | 0 | 6.07% | 0 | 10.10% | 0.00% | 3.64% | 0 | 0 | |
| Symbols: Ribosomal protein L30/L7 family protein chr3:4433809-4435109 FORWARD LENGTH=244 | AT2G33210_1 (+2) | 28 kDa | 6.15% | 11.50% | 0 | 0 | 0 | 4.10% | 6.15% | 0.00% | 0 | 0 | |
| Symbols: Coatomer, alpha subunit chr2:152428-1532178 FORWARD LENGTH=1218 | AT2G23190_1 | 136 kDa | 2.13% | 0.00% | 0 | 2.46% | 0 | 10.00% | 0 | 0 | 0 | 0 | |
| Symbols: Coatomer, alpha subunit chr1:22919814-22923728 FORWARD LENGTH=1216 | AT1G62020_1 | 137 kDa | 2.55% | 1.23% | 0 | 0.00% | 0 | 5.26% | 0 | 0 | 0 | 0 | |
| Symbols: CAB3, AB180, LHCBI_2 chlorophyll A/B binding protein 3 chr1:10472443-10473246 REVERSE LENGTH=267 | AT1G29910_1 (+1) | 28 kDa | 7.49% | 7.49% | 13.90% | 7.49% | 13.90% | 7.49% | 4.49% | 4.49% | 4.49% | 0 | |
| Symbols: LHCBI_2, LHCBI_2 photosystem II light harvesting complex gene 2 chr2:1794936-1800329 REVERSE LENGTH=265 | AT2G05070_1 (+2) | 29 kDa | 3.02% | 3.02% | 16.20% | 3.02% | 3.02% | 3.02% | 0 | 0.00% | 0 | 0 | |
| Symbols: CAB1, AB140, CAB140, LHCBI_3 chlorophyll A/B binding protein 1 chr1:10478071-10478874 FORWARD LENGTH=267 | AT1G29930_1 | 28 kDa | 7.49% | 7.49% | 13.90% | 7.49% | 13.90% | 7.49% | 4.49% | 4.49% | 4.49% | | |
| Symbols: HSP60, HSP60-3B heat shock protein 60 chr3:8669013-8672278 FORWARD LENGTH=577 | AT2G3390_1 | 61 kDa | 2.08% | 7.80% | 0 | 7.80% | 0</ | | | | | | |

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|--|------------------|---------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
| Symbols: Coatomer, beta subunit chr4:15269460-15272693 FORWARD LENGTH=948 | AT4G31490.1 | 106 kDa | 10.10% | 5.91% | 0 | 3.90% | 0 | 7.81% | 0.00% | 0 | 0 | 0 |
| Symbols: Coatomer, beta subunit chr4:15264145-15267384 FORWARD LENGTH=948 | AT4G31480.1 (+1) | 106 kDa | 10.10% | 5.91% | 0 | 3.90% | 0 | 6.22% | 0 | 0 | 0 | 0 |
| Symbols: MLK3 Protein kinase family protein chr2:10985118-10988652 REVERSE LENGTH=673 | AT2G25760.1 | 76 kDa | 4.90% | 6.39% | 0 | 3.71% | 0 | 3.71% | 12.50% | 8.77% | 9.06% | 9.06% |
| Symbols: RPT3 regulatory particle triple-A ATPase 3 chr5:23569155-23571116 FORWARD LENGTH=408 | AT5G58290.1 | 46 kDa | 9.80% | 10.00% | 4.66% | 4.66% | 4.66% | 8.05% | 2.94% | 2.94% | 0 | 0.00% |
| Symbols: CPN60B, LEN1 chaperonin 60 beta chr1:20715717-20718673 REVERSE LENGTH=600 | AT1G55490.1 (+1) | 64 kDa | 4.17% | 10.70% | 0 | 6.33% | 0 | 4.00% | 4.33% | 0 | 2.17% | 0 |
| Symbols: TCP-1/cpn60 chaperonin family protein chr5:22874058-22876966 FORWARD LENGTH=597 | AT5G56500.1 (+1) | 63 kDa | 0 | 4.52% | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: ATARCA, RACK1A_AT, RACK1A Transducin/WD40 repeat-like superfamily protein chr1:6222325-6223901 FORWARD LENGTH=327 | AT1G18080.1 | 36 kDa | 2.75% | 8.26% | 0 | 8.56% | 0 | 11.30% | 3.98% | 0 | 0 | 0 |
| Symbols: RACK1C_AT receptor for activated C kinase 18 chr1:17981977-17982628 REVERSE LENGTH=326 | AT1G18130.1 | 36 kDa | 15.00% | 0.00% | 0 | 0 | 0 | 6.13% | 0 | 8.28% | 0 | 0 |
| Symbols: AH2, PMA2, HA2 H(+)-ATPase 2 chr4:14770820-14775920 REVERSE LENGTH=948 | AT4G30190.1 (+1) | 104 kDa | 4.75% | 3.90% | 0 | 1.58% | 0 | 3.27% | 0 | 0 | 0 | 0 |
| Symbols: AH1, PMA, OST2, HA1 H(+)-ATPase 1 chr2:8221858-8227268 FORWARD LENGTH=949 | AT2G18960.1 | 104 kDa | 4.74% | 2.74% | 0 | 1.58% | 0 | 3.27% | 0 | 0 | 0 | 0 |
| Symbols: AH4, HA7 H(+)-ATPase 2 chr3:22298763-22303509 FORWARD LENGTH=961 | AT3G60330.1 (+1) | 105 kDa | 1.04% | 0 | 0 | 0 | 0 | 0 | 0.00% | 0 | 0 | 0 |
| Symbols: AH4A, HA4 H(+)-ATPase 4 chr3:7693015-17697801 FORWARD LENGTH=960 | AT1G47950.1 | 105 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: AH3A, ATAH3, HA3 H(+)-ATPase 3 chr5:22331206-22336381 REVERSE LENGTH=949 | AT5G57350.1 (+1) | 104 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: AH10 autoinhibited H(+)-ATPase isoform 10 chr1:5904058-5908989 FORWARD LENGTH=947 | AT1G17260.1 | 105 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: ATPase, F1 complex, alpha subunit protein chr2:3361474-3361428 FORWARD LENGTH=777 | AT2G07698.1 | 86 kDa | 2.70% | 2.70% | 2.83% | 5.66% | 2.83% | 7.08% | 1.42% | 0.00% | 0 | 0 |
| Symbols: LWD2 Transducin/WD40 repeat-like superfamily protein chr3:7932726-794316 FORWARD LENGTH=346 | AT3G26640.1 | 39 kDa | 21.40% | 21.10% | 11.00% | 15.90% | 11.00% | 21.70% | 27.20% | 15.90% | 11.00% | 11.00% |
| Symbols: ATPase, VI complex, subunit B protein chr1:7016971-7020290 FORWARD LENGTH=487 | AT1G20260.1 (+2) | 54 kDa | 10.10% | 10.10% | 0 | 6.16% | 0 | 7.19% | 3.08% | 7.19% | 0 | 0 |
| Symbols: ATGST8, ATGST5, GST6, GST8 glutathione S-transferase alpha ph 8 chr2:19558213-1955266 FORWARD LENGTH=263 | AT2G47730.1 | 29 kDa | 15.60% | 10.60% | 0 | 0.00% | 0 | 27.00% | 0 | 0 | 0 | 0 |
| Symbols: ATPC1 ATPase, F1 complex, gamma subunit protein chr4:2350761-2351882 REVERSE LENGTH=373 | AT4G04640.1 | 41 kDa | 18.00% | 9.12% | 0 | 6.17% | 7.24% | 6.17% | 3.49% | 6.17% | 2.68% | 0 |
| Symbols: FBPA2 fructose-bisphosphate aldolase 2 chr1:1816374-1816569 REVERSE LENGTH=398 | AT4G38970.1 | 43 kDa | 10.10% | 10.80% | 0 | 13.80% | 7.04% | 14.60% | 10.80% | 7.04% | 0 | 0 |
| Symbols: RPL16A ribosomal protein large subunit 16A chr1:17791794-17792946 FORWARD LENGTH=182 | AT2G42740.1 (+4) | 21 kDa | 12.10% | 12.10% | 7.69% | 7.69% | 7.69% | 7.69% | 7.69% | 12.10% | 12.10% | 7.69% |
| Symbols: Transektolease chr2:22454004-2245682 FORWARD LENGTH=741 | AT3G60750.1 (+1) | 80 kDa | 6.21% | 4.18% | 0 | 0.00% | 0 | 18.60% | 2.43% | 0 | 0 | 0 |
| Symbols: I binding chr3:1917899-1937014 FORWARD LENGTH=1606 | AT5G47690.2 (+1) | 181 kDa | 5.35% | 0 | 0 | 2.37% | 0 | 5.98% | 0 | 0 | 0 | 0 |
| Symbols: SACS2, RP1L0, RP1L0A Ribosomal protein L16p/L16o family protein chr1:4888270-4889408 FORWARD LENGTH=220 | AT1G14320.1 | 25 kDa | 5.45% | 10.50% | 5.45% | 5.00% | 0 | 5.00% | 10.50% | 10.50% | 5.45% | 5.45% |
| Symbols: CAC3 acetyl Co-enzyme A carboxylase carboxyltransferase alpha subunit chr2:15917612-15920749 FORWARD LENGTH=769 | AT2G38040.1 (+1) | 85 kDa | 6.63% | 2.47% | 0 | 0 | 0 | 7.41% | 0 | 0 | 0 | 0 |
| Symbols: RAN-1, RAN1, ATRAN1 RAS-related nuclear protein-1 chr5:6760364-6761747 FORWARD LENGTH=221 | AT5G20010.1 (+2) | 25 kDa | 10.40% | 15.40% | 0 | 11.30% | 0 | 31.20% | 5.88% | 0 | 0 | 0 |
| Symbols: Ribosomal protein S4 chr5:4935124-4936334 REVERSE LENGTH=198 | AT5G15200.1 | 23 kDa | 9.60% | 9.60% | 7.58% | 13.10% | 7.58% | 13.10% | 4.55% | 0 | 0 | 0 |
| Symbols: Ribosomal protein S26e family protein chr2:16918506-16919623 FORWARD LENGTH=133 | AT2G40510.1 (+2) | 15 kDa | 18.00% | 18.00% | 0 | 18.00% | 0 | 18.00% | 18.00% | 6.77% | 0 | 0 |
| Symbols: EMB2296 Ribosomal protein L2 family chr2:7837151-7838160 FORWARD LENGTH=258 | AT2G18020.1 | 28 kDa | 12.00% | 7.36% | 7.36% | 4.65% | 7.36% | 7.36% | 7.36% | 7.36% | 0.00% | 0 |
| Symbols: Ribosomal protein L2 family chr4:17097613-17098656 FORWARD LENGTH=258 | AT4G36130.1 | 28 kDa | 12.00% | 7.36% | 0 | 4.65% | 0 | 0 | 7.36% | 0 | 0 | 0 |
| Symbols: Histone superfamily protein chr1:2369212-2369523 FORWARD LENGTH=103 | AT1G07660.1 (+8) | 11 kDa | 9.71% | 9.71% | 7.77% | 29.10% | 7.77% | 29.10% | 9.71% | 9.71% | 9.71% | 9.71% |
| Symbols: oxidoreductases, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor; copper ion binding chr2:8613168-8615649 FORWARD LENGTH=401 | AT2G19940.1 (+1) | 44 kDa | 19.70% | 3.99% | 0 | 3.99% | 0 | 8.98% | 3.99% | 0 | 0 | 0 |
| Symbols: ATP5SB, RPS5B ribosomal protein S8 chr1:15674883-15649042 REVERSE LENGTH=207 | AT2G37270.1 (+3) | 23 kDa | 17.90% | 6.28% | 0 | 0 | 0 | 13.50% | 13.50% | 13.50% | 13.50% | 13.50% |
| Symbols: Thioredoxin superfamily protein chr3:3672189-3673937 FORWARD LENGTH=266 | AT3G11630.1 | 29 kDa | 0 | 6.39% | 0 | 0.00% | 0 | 12.40% | 6.39% | 10.90% | 0 | 0 |
| Symbols: PIP1B, TMP-A, ATH2, PIP2_1 plasma membrane intrinsic protein 18 chr2:18918504-18911703 FORWARD LENGTH=286 | AT2G45960.1 (+2) | 31 kDa | 3.50% | 3.50% | 0.00% | 9.79% | 6.29% | 9.79% | 3.50% | 3.50% | 0 | 0 |
| Symbols: RPL27A, RPL27AB Ribosomal protein L18e/L15 superfamily protein chr1:8263007-8263447 FORWARD LENGTH=146 | AT1G23290.1 (+1) | 16 kDa | 10.30% | 10.30% | 0.00% | 6.85% | 0 | 8.22% | 17.10% | 10.30% | 10.30% | 0 |
| Symbols: Ribosomal protein L18e/L18x family protein chr2:14532916-14534161 REVERSE LENGTH=178 | AT2G34480.1 | 21 kDa | 8.99% | 4.49% | 0 | 9.55% | 0 | 4.49% | 4.49% | 0.00% | 4.49% | 0 |
| Symbols: Ribosomal protein L18e/L18x family protein chr3:491073-491193 FORWARD LENGTH=178 | AT3G14600.1 | 21 kDa | 0 | 0 | 0 | 5.06% | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: EM82719, HAP15 PAM domain (PCI/PIN associated module) protein chr1:28524623-28526178 FORWARD LENGTH=487 | AT1G27590.1 | 56 kDa | 8.20% | 8.81% | 0 | 2.66% | 0 | 9.02% | 0 | 0 | 0 | 0 |
| Symbols: PAM domain (PCI/PIN associated module) protein chr1:28524623-28526178 FORWARD LENGTH=487 | AT1G28290.1 | 51 kDa | 9.07% | 2.59% | 0 | 6.70% | 0 | 9.29% | 0 | 0 | 0 | 0 |
| Symbols: APS1 Pseudouridine synthase/Archaeosine transglycosylase-III family protein chr1:6914835-6916657 REVERSE LENGTH=476 | AT1G19920.1 | 54 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: APS2, ASA1 Pseudouridine synthase/archaeosine transglycosylase-III family protein chr4:8413443-8415311 REVERSE LENGTH=465 | AT4G14680.1 | 52 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: Tetra peptide repeat (TPR) like superfamily protein chr2:22565440-22566678 REVERSE LENGTH=412 | AT3G60980.1 | 47 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 13.80% | 14.10% | 0 | 0 |
| Symbols: SPA2 SPA1-related 2 chr4:6772163-6776675 FORWARD LENGTH=1036 | AT4G11110.1 | 115 kDa | 10.60% | 11.60% | 0 | 13.10% | 0 | 23.80% | 13.10% | 21.30% | 0.00% | 0.00% |
| Symbols: PORB1 protocochloryl oxidoreductase B chr4:13725648-13727107 FORWARD LENGTH=401 | AT4G27440.1 (+1) | 43 kDa | 12.50% | 7.48% | 0 | 2.99% | 0 | 2.99% | 0 | 0 | 0 | 0 |
| Symbols: ATPC ATP synthase epsilon chain chr5:52265-52663 REVERSE LENGTH=132 | ATCG00470.1 | 14 kDa | 27.30% | 27.30% | 0 | 11.40% | 0 | 15.90% | 27.30% | 0 | 0 | 0 |
| Symbols: RPL14 ribosomal protein L14 chr4:80696-8106 REVERSE LENGTH=122 | ATCG00780.1 | 14 kDa | 21.30% | 21.30% | 0 | 13.10% | 0 | 23.80% | 13.10% | 21.30% | 0.00% | 0.00% |
| Symbols: C2 calcium/lipid-binding plant phosphotransferase family protein chr5:2127200-2129584 FORWARD LENGTH=794 | ATCG06850.1 | 91 kDa | 0 | 0 | 0 | 4.66% | 0 | 8.44% | 0 | 0 | 0 | 0 |
| Symbols: FDH formate dehydrogenase chr5:4777043-4779190 FORWARD LENGTH=384 | AT5G14780.1 | 42 kDa | 9.38% | 3.12% | 0 | 7.03% | 0 | 16.40% | 0 | 7.03% | 0 | 0 |
| Symbols: TOC1, APR1, PR1, ATTOC1 CCT motif-containing response regulator protein chr5:24675540-24678176 FORWARD LENGTH=618 | AT5G61380.1 | 69 kDa | 4.05% | 4.05% | 5.34% | 0 | 7.28% | 0 | 1.94% | 0 | 2.10% | 2.10% |
| Symbols: ELF4-L2 ELF4-L2 chr2:17349488-17345347 FORWARD LENGTH=412 | AT1G2630.1 | 13 kDa | 0 | 10.90% | 0 | 12.60% | 0 | 10.90% | 21.80% | 21.80% | 21.80% | 10.90% |
| Symbols: STV1, RPL24B, RPL24 Ribosomal protein L14 family protein chr3:19606749-19616192 FORWARD LENGTH=163 | AT5G33020.1 | 19 kDa | 14.70% | 14.70% | 0 | 7.36% | 0 | 7.36% | 14.70% | 0 | 0 | 0 |
| Symbols: glycine-rich protein chr4:11944050-11945655 REVERSE LENGTH=356 | AT4G22740.1 (+1) | 39 kDa | 12.10% | 12.10% | 0 | 0 | 0 | 12.10% | 7.58% | 0.00% | 0 | 0 |
| Symbols: Ribosomal protein L28 protein family chr2:851752-8517935 FORWARD LENGTH=143 | AT2G19730.1 (+2) | 16 kDa | 13.30% | 13.30% | 0 | 0 | 0 | 24.50% | 0.00% | 0.00% | 24.50% | 0 |
| Symbols: Ribosomal protein S11 family protein chr2:1516925-1517159 FORWARD LENGTH=150 | AT2G36160.1 | 16 kDa | 16.00% | 16.00% | 8.67% | 23.30% | 8.67% | 23.30% | 0 | 0 | 0 | 0 |
| Symbols: Ribosomal protein S11 family protein chr3:3623757-3624866 REVERSE LENGTH=150 | AT3G1510.1 | 16 kDa | 8.67% | 16.00% | 8.67% | 16.00% | 8.67% | 16.00% | 0 | 0 | 0 | 0 |
| Symbols: Coatomer, beta' subunit chr5:514699-5418313 REVERSE LENGTH=909 | AT3G15980.1 (+3) | 102 kDa | 3.74% | 1.10% | 0 | 0.00% | 0 | 5.28% | 0 | 0 | 0 | 0 |
| Symbols: structural molecular chr1:30084522-30091949 FORWARD LENGTH=1135 | AT1G79990.1 (+2) | 129 kDa | 2.11% | 0 | 0 | 0 | 0 | 1.76% | 0 | 0 | 0 | 0 |
| Symbols: XIK, ATTIX, XI-17 Myosin family protein with Dil domain chr5:6927064-6936825 REVERSE LENGTH=1545 | AT5G20490.1 (+1) | 175 kDa | 0.91% | 2.20% | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: MYA1, ATMYA1, XI-1 myosin 1 protein chr1:6039453-6049309 FORWARD LENGTH=1520 | AT1G17580.1 | 173 kDa | 1.38% | 1.32% | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: XIC, ATXIC Myosin family protein with Dil domain chr1:2779963-278825 FORWARD LENGTH=1538 | AT1G08720.1 | 175 kDa | 0 | 1.30% | 0 | 0.00% | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: HSP81-2, ERD8, HSP90.2, AtHsp80.2 heat shock protein 81-2 chr5:22686923-2268943 FORWARD LENGTH=699 | AT5G56030.1 (+1) | 80 kDa | 5.72% | 4.01% | 0 | 2.00% | 0 | 2.00% | 2.00% | 0 | 0 | 0 |
| Symbols: PIP3, PIP3A, PIP2, SIMP1 plasma membrane intrinsic protein 3 chr4:16708672-16709958 FORWARD LENGTH=280 | AT4G35100.1 (+1) | 30 kDa | 17.10% | 17.10% | 6.79% | 11.10% | 6.79% | 0 | 11.10% | 0 | 0 | 0 |
| Symbols: PIP3 chloroplast ribosomal protein S4 chr4:45223-45228 REVERSE LENGTH=201 | ATCG0380.1 | 23 kDa | 3.98% | 3.98% | 0 | 0 | 0 | 0.00% | 8.96% | 8.96% | 0 | 0 |
| Symbols: LOS2, ENO2 Enolase chr2:152321081-15232786 REVERSE LENGTH=444 | AT2G36530.1 | 48 kDa | 3.38% | 3.38% | 0 | 3.38% | 0 | 7.88% | 3.38% | 0 | 3.60% | 0 |
| Symbols: ATPase, VO/A complex, subunit C/D chr2:10778025-10780350 FORWARD LENGTH=351 | AT3G28715.1 | 41 kDa | 9.12% | 5.70% | 0 | 4.27% | 0 | 4.27% | 5.70% | 0 | 0 | 0 |
| Symbols: ATPase, VO/A complex, subunit C/D chr3:10773144-10775594 REVERSE LENGTH=351 | AT2G22870.1 | 41 kDa | 5.70% | 5.70% | 0 | 9.97% | 0 | 9.97% | 0 | 0 | 0 | 0 |
| Symbols: cPhsC70-2 chloroplast heat shock protein 70-2 chr4:12590094-12593437 FORWARD LENGTH=718 | AT4G24280.1 | 77 kDa | 0 | 0 | 0 | 2.92% | 0 | 8.77% | 1.95% | 0 | 0 | 0 |
| Symbols: CPHSC70-2EAT SHOCK PROTEIN 70-2, HSC70-2 chloroplast heat shock protein 70-2 chr5:20303470-20306295 FORWARD LENGTH=718 | AT5G49910.1 | 77 kDa | 0 | 0 | 0 | 5.15% | 0 | 6.55% | 1.95% | 0 | 0 | 0 |
| Symbols: LUH LEUNIG homolog chr2:1386723-13871844 FORWARD LENGTH=787 | AT2G32700.1 (+6) | 86 kDa | 0 | 0 | 0 | 1.52% | 0 | 6.48% | 0 | 0 | 0 | 0 |
| Symbols: emb1138 DEAD box RNA helicase (RH3) chr5:9288540-9288871 REVERSE LENGTH=747 | AT5G26742.1 (+1) | 81 kDa | 5.62% | 6.02% | 0 | 1.87% | 0 | 0.00% | 0 | 0 | 0 | 0 |
| Symbols: RPS11 ribosomal protein S11 chr2:78960-79376 REVERSE LENGTH=139 | ATCG00750.1 | 15 kDa | 15.90% | 15.90% | 0 | | | | | | | |

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|--|------------------|---------|--------|--------|--------|--------|--------|--------|--------|--------|--------|-------|-------|
| Symbols: Aldolase superfamily protein chr5:963389-964982 REVERSE LENGTH=359 | AT5G03690.2 | 39 kDa | 0 | 0 | 0 | 3.90% | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: Aldolase superfamily protein chr4:13931566-13292937 FORWARD LENGTH=358 | AT4G26530.1 (+1) | 38 kDa | 0 | 0 | 0 | 0 | 0 | 3.91% | 0 | 0 | 0 | 0 | 0 |
| Symbols: CHL1, CH42, CHL11, CHL-1 P-loop containing nucleoside triphosphate hydrolases superfamily protein chr4:10201897-10203361 REVERSE LENGTH=424 | AT4G18480.1 | 46 kDa | 8.49% | 4.95% | 0 | 0.00% | 0 | 7.31% | 0 | 0 | 0 | 0 | 0 |
| Symbols: CHL12, CHL12, CHL-2 magnesium chelatase I2 chr5:18628095-18629565 FORWARD LENGTH=418 | AT5G45930.1 | 46 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: transducin family protein / WD-40 repeat family protein chr3:23431009-23437241 REVERSE LENGTH=1104 | ATGG3460.1 (+2) | 120 kDa | 1.18% | 1.18% | 0 | 1.36% | 0 | 2.54% | 0 | 0 | 0 | 0 | 0 |
| Symbols: vacuolar ATP synthase subunit H family protein chr3:14228846-14232228 REVERSE LENGTH=441 | AT3G42050.1 | 50 kDa | 6.35% | 2.95% | 0 | 4.08% | 0 | 2.95% | 0 | 0 | 0 | 0 | 0 |
| Symbols: RPL18 ribosomal protein L18 chr3:1621511-1622775 FORWARD LENGTH=187 | AT3G05590.1 (+1) | 21 kDa | 12.80% | 5.88% | 6.95% | 5.88% | 0 | 13.40% | 5.88% | 5.88% | 0 | 0 | 0 |
| Symbols: RPTSA, AT56A2 regulatory particle triple-A ATPase 5A chr3:1603540-1605993 FORWARD LENGTH=424 | AT3G05530.1 | 47 kDa | 13.70% | 7.55% | 0 | 0 | 0 | 4.72% | 7.55% | 7.55% | 0 | 0 | 0.00% |
| Symbols: AGT, AGT1, SGAT alanine:glyoxylate aminotransferase chr2:5539417-5540902 REVERSE LENGTH=401 | AT2G13360.1 (+1) | 44 kDa | 3.99% | 3.99% | 4.24% | 0 | 4.24% | 6.98% | 0 | 0 | 0 | 0 | 0 |
| Symbols: ribosomal protein L22p/L17e family protein chr1:9515230-9516725 FORWARD LENGTH=176 | AT1G27400.1 (+1) | 20 kDa | 0 | 5.11% | 10.80% | 0.00% | 5.68% | 15.90% | 0 | 0 | 0 | 0 | 0 |
| Symbols: VHA-A vacuolar ATP synthase subunit A chr1:29660463-29664575 FORWARD LENGTH=623 | AT1G78900.1 (+1) | 69 kDa | 1.77% | 0.00% | 0 | 0 | 0 | 4.33% | 0 | 0 | 0 | 0 | 0 |
| Symbols: RPT1A regulatory particle triple-A 1A chr1:20065921-20068324 REVERSE LENGTH=426 | AT1G53750.1 | 48 kDa | 5.63% | 2.11% | 0 | 3.05% | 0 | 3.05% | 0.00% | 0 | 0 | 0 | 0 |
| Symbols: AT1J2, J2 DNAJ homologue 2 chr5:7303798-730568 REVERSE LENGTH=419 | AT5G22060.1 | 46 kDa | 6.21% | 6.21% | 0 | 0 | 0 | 2.86% | 0 | 0 | 0 | 0 | 0 |
| Symbols: AT13, AT1 DNAJ homologue 3 chr3:15869115-15871059 REVERSE LENGTH=420 | AT4G44100.1 (+1) | 46 kDa | 6.19% | 6.19% | 0 | 0 | 0 | 5.95% | 0 | 0 | 0 | 0 | 0 |
| Symbols: RP51, ARRP5 ribosomal protein S1 chr5:11619262-11621223 REVERSE LENGTH=416 | AT5G31010.1 | 45 kDa | 3.61% | 0 | 0 | 8.17% | 0 | 10.60% | 0 | 0 | 0 | 0 | 0 |
| Symbols: ACCD acetyl-CoA carboxylase carboxyl transferase subunit beta chr5:57075-58541 FORWARD LENGTH=488 | ATCG00500.1 | 56 kDa | 6.56% | 2.87% | 0 | 0 | 0 | 2.66% | 0 | 0 | 0 | 0 | 0 |
| Symbols: RP58 ribosomal protein S8 chr5:80068-80472 REVERSE LENGTH=134 | ATCG00770.1 | 15 kDa | 8.96% | 17.20% | 0 | 8.96% | 0 | 8.96% | 8.21% | 8.21% | 0 | 0 | 0 |
| Symbols: SSR16 small subunit ribosomal protein 16 chr5:16535084-16536092 REVERSE LENGTH=113 | AT4G34620.1 | 13 kDa | 13.30% | 13.30% | 0 | 13.30% | 0 | 13.30% | 13.30% | 13.30% | 25.70% | 0 | 0 |
| Symbols: Sucrose-6-phosphate phosphohydrolase family protein chr2:15053952-15055776 FORWARD LENGTH=422 | AT2G35840.1 (+2) | 48 kDa | 4.50% | 0 | 0 | 0 | 0 | 6.16% | 0 | 0 | 0 | 0 | 0 |
| Symbols: GTP binding elongation factor Tu family protein chr1:1295751-129854 REVERSE LENGTH=454 | AT4G02930.1 | 49 kDa | 8.15% | 0 | 0 | 3.52% | 0 | 8.37% | 0 | 0 | 0 | 0 | 0 |
| Symbols: ECT2 evolutionarily conserved C-terminal region 2 chr5:4385274-4388220 REVERSE LENGTH=667 | AT3G13460.1 (+3) | 72 kDa | 7.50% | 5.55% | 0 | 0.00% | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: Glycine cleavage T-protein family chr1:4001801-4003245 FORWARD LENGTH=408 | AT1G18860.1 (+2) | 44 kDa | 5.64% | 5.64% | 0 | 5.64% | 0 | 5.64% | 9.56% | 0 | 0 | 0 | 0 |
| Symbols: NOP56 homolog of nucleolar NOP56P chr1:20984544-2098689 REVERSE LENGTH=522 | AT1G56110.1 | 59 kDa | 2.87% | 0.00% | 0 | 0 | 0 | 5.94% | 0 | 0 | 0 | 0 | 0 |
| Symbols: RP51A ribosomal protein S15A chr1:2408413-2409065 REVERS LENGTH=130 | AT1G0770.1 (+2) | 15 kDa | 6.92% | 6.92% | 10.80% | 0 | 10.80% | 23.10% | 0 | 0 | 0 | 0 | 0 |
| Symbols: ribosomal protein S8 family protein chr2:16517588-16518265 REVERSE LENGTH=136 | AT2G39590.1 | 15 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: RP1N1A, ATRP1N1A 26S proteasome regulatory subunit S2 1A chr2:8859211-8864699 FORWARD LENGTH=891 | AT2G20580.1 | ? | 0.00% | 0.00% | 0 | 0 | 0 | 0.00% | 0 | 0 | 0 | 0 | 0 |
| Symbols: PAC1 20S proteasome alpha subunit C1 chr3:7792819-7793571 REVERSE LENGTH=250 | AT3G22110.1 | 27 kDa | 0 | 11.20% | 0 | 0 | 0 | 4.80% | 6.40% | 6.40% | 0 | 0 | 0 |
| Symbols: ATB8C1, BBC1, RSU2 breast basic conserved 1 chr3:18166971-18168047 REVERSE LENGTH=206 | AT3G49010.1 (+3) | 24 kDa | 0 | 0.00% | 0 | 11.70% | 0 | 17.00% | 11.70% | 0.00% | 0 | 0 | 0 |
| Symbols: Tetrapeptidopeptide repeat (TSPY)-like superfamily protein chr3:2253579-2253694 FORWARD LENGTH=403 | AT3G6060.1 | 46 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 2.23% | 4.71% | 0 | 0 | 0 |
| Symbols: CPN60A, CH-CPN60A, SLP chaperonin 60kDa chr2:11926603-11929184 FORWARD LENGTH=586 | AT2G28000.1 | 62 kDa | 4.44% | 2.22% | 0 | 0.00% | 0 | 0.00% | 0 | 0 | 0 | 0 | 0 |
| Symbols: ATIP49A, RIN1 P-loop containing nucleoside triphosphate hydrolase superfamily protein chr5:7391026-7394071 REVERSE LENGTH=458 | AT5G22330.1 | 50 kDa | 0.00% | 5.02% | 0 | 5.24% | 0 | 2.40% | 0 | 0 | 0 | 0 | 0 |
| Symbols: RPL16 ribosomal protein L16 chrC:81189-82652 REVERSE LENGTH=138 | ATCG00790.1 | 15 kDa | 10.40% | 0.00% | 0 | 10.40% | 0 | 20.70% | 0 | 0 | 0 | 0 | 0 |
| Symbols: PUB12, ATPUB12 PLANT U-BOX 12 chr2:12367001-12370608 REVERSE LENGTH=962 | AT2G28830.1 | 107 kDa | 1.46% | 0.00% | 0 | 1.46% | 0 | 1.46% | 0 | 0 | 0 | 0 | 0 |
| Symbols: NAD(P)H-binding Rossmann-fold superfamily protein chr3:11193767-11194948 REVERSE LENGTH=298 | AT3G29250.1 | 32 kDa | 0 | 0 | 0 | 4.03% | 0 | 18.10% | 0 | 0 | 0 | 0 | 0 |
| Symbols: LA LUTYHIA chr1:24065232-2408109 REVERSE LENGTH=2610 | AT1G4790.1 (+1) | 285 kDa | 2.07% | 0 | 0 | 0.00% | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: APUM5, PUM5 pumilio 5 chr3:1059098-7062660 REVERSE LENGTH=961 | AT2G20250.1 | 107 kDa | 3.75% | 1.04% | 0 | 1.04% | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: ATPP57, TP57, ATTPSA trehalose-phosphatase/synthase 7 chr1:1955413-1958153 FORWARD LENGTH=851 | AT1G06410.1 | 97 kDa | 1.29% | 0 | 0 | 0 | 0 | 3.41% | 0 | 0 | 0 | 0 | 0 |
| Symbols: transcription regulators chr1:373335-386682 FORWARD LENGTH=2431 | AT1G02080.1 (+1) | 270 kDa | 1.93% | 0.74% | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: ATGST9, GLUTR, ATGST7, GST9 glutathione S-transferase PH 9 chr2:13139132-13140057 FORWARD LENGTH=215 | AT2G30860.1 (+1) | 24 kDa | 0 | 16.70% | 0 | 3.72% | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: Ribosomal protein L35e family protein chr1:2982415-29929466 REVERSE LENGTH=112 | AT1G74270.1 | 13 kDa | 22.30% | 0 | 0 | 33.00% | 0 | 22.30% | 0 | 0 | 0 | 0 | 0 |
| Symbols: ATU2A2F35B, U2AF35B Zinc finger C-X5-C-X5-C-X3-X3 type family protein chr5:17170445-17171296 REVERSE LENGTH=283 | AT5G42820.1 (+1) | 33 kDa | 8.13% | 0 | 0 | 6.36% | 0 | 6.36% | 0 | 0 | 0 | 0 | 0 |
| Symbols: ATU2A2F35A U2 snRNP auxiliary small subunit, putative chr1:9615302-9616042 FORWARD LENGTH=246 | AT1G27650.2 | 29 kDa | 0 | 0 | 0 | 7.32% | 0 | 7.32% | 0 | 0 | 0 | 0 | 0 |
| Symbols: Zinc finger C-X8-C-X5-C-X3-X3 type family protein chr3:16328221-16328448 REVERSE LENGTH=75 | AT3G44785.1 | 9 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: PIL6, PI5 phytochrome interacting factor 3-like 6 chr3:21828189-2182895 REVERSE LENGTH=442 | AT3G59060.1 (+3) | 49 kDa | 0 | 0.00% | 2.71% | 0 | 0 | 0 | 9.95% | 0 | 0 | 0 | 0 |
| Symbols: PI4, SRL2, ATP1F4 phytochrome interacting factor 4 chr2:17887003-1788882 FORWARD LENGTH=430 | AT2G43010.1 (+1) | 48 kDa | 0 | 0 | 2.79% | 0 | 0 | 0.00% | 2.79% | 0 | 0 | 0 | 0 |
| Symbols: Ribosomal protein L31e family protein chr2:8513577-8514346 FORWARD LENGTH=119 | AT2G19740.1 (+2) | 14 kDa | 0 | 0 | 0 | 31.90% | 0 | 31.90% | 0 | 0 | 0 | 0 | 0 |
| Symbols: Ribosomal protein L31e family protein chr5:22944003-2294767 REVERSE LENGTH=85 | AT5G56710.2 | 10 kDa | 0 | 0 | 0 | 9.41% | 0 | 9.41% | 0 | 0 | 0 | 0 | 0 |
| Symbols: Coatomer epsilon subunit chr1:10858546-10860137 REVERSE LENGTH=292 | AT1G30630.1 | 33 kDa | 0 | 0 | 0 | 14.70% | 0 | 14.70% | 0 | 0 | 0 | 0 | 0 |
| Symbols: SHM4 serine hydroxymethyltransferase 4 chr4:8048013-8050022 REVERSE LENGTH=471 | AT4G13930.1 | 52 kDa | 6.37% | 3.40% | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: RPL22 ribosomal protein L22 chrC:83467-83949 REVERSE LENGTH=161 | ATCG00810.1 | 19 kDa | 0 | 0 | 0 | 8.12% | 0 | 14.40% | 0 | 0 | 0 | 0 | 0 |
| Symbols: PBEL1 20S proteasome subunit E1 chr1:4452641-4454663 FORWARD LENGTH=274 | AT1G13601.1 (+2) | 30 kDa | 0 | 14.20% | 0 | 0 | 0 | 0 | 0 | 0.00% | 0 | 0 | 0 |
| Symbols: PSB8 photosystem II reaction center protein B chrC:72371-73897 FORWARD LENGTH=508 | ATCG00680.1 | 56 kDa | 3.35% | 2.17% | 0 | 0 | 0 | 0 | 5.51% | 0 | 0 | 0 | 0 |
| Symbols: RP81, RP81, RNA_POL_II_LSRNA, RNA_POL_II_LSLRNA RNA polymerase II large subunit chr4:16961115-16967892 REVERSE LENGTH=1839 | AT4G35800.1 | 205 kDa | 1.96% | 0 | 0 | 0 | 0 | 0.00% | 0 | 0 | 0 | 0 | 0 |
| Symbols: EM82761 threonyl-tRNA synthetase, putative / threonine-tRNA ligase, putative chr2:1698466-1701271 REVERSE LENGTH=650 | AT2G04842.1 | 75 kDa | 0 | 0 | 0 | 0.00% | 0 | 4.00% | 0 | 0 | 0 | 0 | 0 |
| Symbols: ELF4-L4 ELF4-like 4 chr1:5997932-5998276 FORWARD LENGTH=114 | AT1G1755.1 (+1) | 13 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 22.80% | 22.80% | 11.40% | 0.00% | 0 |
| Symbols: AAA-type ATPase family protein chr1:17009220-1701607 FORWARD LENGTH=399 | AT1G45000.1 (+2) | 45 kDa | 6.02% | 6.02% | 0 | 0 | 0 | 0 | 6.02% | 0 | 0 | 0 | 0 |
| Symbols: PHOT1, NP1, JK224, RTP1 photoprotein 1 chr1:16818557-16823960 FORWARD LENGTH=996 | AT3G45780.1 | 112 kDa | 2.51% | 0 | 0 | 2.11% | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: PHOT2, NP1 photoprotein 2 chr5:2352477-2352993 FORWARD LENGTH=915 | AT5G58140.1 (+3) | 102 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: ZFN1 zinc finger protein 1 chr3:614075-615916 FORWARD LENGTH=397 | AT3G02830.1 | 44 kDa | 8.06% | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: Ribosomal protein L35e family protein chr1:1651585-16562427 REVERSE LENGTH=111 | AT1G18180.1 | 13 kDa | 0 | 0 | 0 | 33.30% | 0 | 22.50% | 0 | 0 | 0 | 0 | 0 |
| Symbols: SPA3 SPA1-related 3 chr3:5169327-5172480 REVERSE LENGTH=837 | AT3G15354.1 | 93 kDa | 2.03% | 3.70% | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: PRP39 Tetrapeptidopeptide repeat (TPR)-like superfamily protein chr1:1051803-1056550 FORWARD LENGTH=768 | AT1G04080.1 (+1) | 85 kDa | 4.95% | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: ABA1, LOS6, NPQ2, ATABA1, ZEP, IB53, ATZEP zeaxanthin epoxidase (ZEP) (ABA1) chr5:26753745-26757090 REVERSE LENGTH=667 | AT5G67030.1 (+1) | 74 kDa | 4.65% | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

Exclusive Unique Peptide Count

Identified Proteins (283)

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|--|------------------|---------|----|----|----|----|----|----|----|----|----|----|----|
| Symbols: PHB, HY, OOP1 phytochrome B chr2:8140079-8144151 FORWARD LENGTH=1172 | AT2G18790.1 | 129 kDa | 23 | 24 | 31 | 28 | 32 | 30 | 22 | 22 | 24 | 24 | 24 |
| Symbols: PHD phytochrome D chr4:195602-1959486 REVERSE LENGTH=164 | AT4G16250.1 | 129 kDa | 1 | 1 | 2 | 1 | 3 | 2 | 2 | 2 | 1 | 2 | 2 |
| Symbols: HSC70-1, HSP70-1, AT-HSC70-1, HSC70 heat shock cognate protein 70 chr5:554055-556334 REVERSE LENGTH=651 | AT5G02500.1 | 71 kDa | 3 | 2 | 9 | 7 | 9 | 9 | 2 | 2 | 2 | 2 | 2 |
| Symbols: Heat shock protein 70 (Hsp 70) family protein chr3:2903434-2905632 REVERSE LENGTH=649 | AT3G09440.1 (+1) | 71 kDa | 6 | 6 | 8 | 8 | 9 | 8 | 6 | 6 | 2 | 2 | 3 |
| Symbols: HSP70, ATHSP70 heat shock protein 70 chr3:3991487-3993689 REVERSE LENGTH=650 | AT3G12580.1 | 71 kDa | 2 | 1 | 1 | 4 | 2 | 4 | 2 | 1 | 0 | 0 | 0 |
| Symbols: Heat shock protein 70 (Hsp 70) family protein chr5:550296-552565 REVERSE LENGTH=653 | AT5G02490.1 | 71 kDa | 4 | 3 | 1 | 2 | 2 | 4 | 2 | 1 | 0 | 0 | 0 |
| Symbols: Hsp70b heat shock protein 70B chr5:1502386-5504326 REVERSE LENGTH=646 | AT1G16030.1 | 71 k | | | | | | | | | | | |

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|--|------------------|---------|---|---|---|---|---|---|---|---|---|---|
| Symbols: CA1 carbonic anhydrase 1 chr3:194853-197873 FORWARD LENGTH=347 | AT3G01500.2 (+1) | 37 kDa | 1 | 1 | 0 | 1 | 0 | 1 | 2 | 1 | 0 | 0 |
| Symbols: CA2, CA18, BETA CA2 carbonic anhydrase 2 chr5:4758257-4762382 FORWARD LENGTH=331 | AT5G14740.1 (+1) | 37 kDa | 0 | 0 | 0 | 1 | 0 | 2 | 0 | 0 | 0 | 0 |
| Symbols: ATAN11, LWD1 Transducin/WD40 repeat-like superfamily protein chr1:4395114-4396154 FORWARD LENGTH=346 | AT1G12910.1 | 39 kDa | 2 | 3 | 2 | 4 | 1 | 2 | 2 | 2 | 0 | 0 |
| Symbols: MLK4 Protein kinase family protein chr3:446934-4473234 FORWARD LENGTH=703 | AT3G13670.1 | 79 kDa | 3 | 3 | 0 | 0 | 0 | 1 | 6 | 3 | 3 | 5 |
| Symbols: RPS6A ribosomal protein S6 chr4:15346306-15347714 FORWARD LENGTH=250 | AT4G31700.1 | 28 kDa | 2 | 4 | 0 | 1 | 0 | 4 | 4 | 4 | 2 | 1 |
| Symbols: Ribosomal protein L30/17 family protein chr2:132943-134265 FORWARD LENGTH=242 | AT2G01250.1 | 28 kDa | 3 | 2 | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 0 |
| Symbols: Ribosomal protein L30/17 family protein chr2:18429227-18250417 FORWARD LENGTH=247 | AT2G44120.2 | 29 kDa | 1 | 1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| Symbols: Ribosomal protein L30/17 family protein chr3:4433809-4435109 FORWARD LENGTH=244 | AT3G13580.1 (+2) | 28 kDa | 1 | 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| Symbols: I Coatomer, alpha subunit chr2:1524248-9156577 FORWARD LENGTH=1218 | AT2G21390.1 | 136 kDa | 2 | 0 | 0 | 2 | 0 | 5 | 0 | 0 | 0 | 0 |
| Symbols: I Coatomer, alpha subunit chr1:22919814-22923728 FORWARD LENGTH=1216 | AT1G62020.1 | 137 kDa | 2 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| Symbols: CAB3, AB180, LHC81.2 chlorophyll A/B binding protein 3 chr1:10472443-10473246 FORWARD LENGTH=267 | AT1G29910.1 (+1) | 28 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: LHC82.2, LHC82.1 photosystem II light harvesting complex gene 2.2 chr2:2179436-1800329 FORWARD LENGTH=265 | AT2G05070.1 (+2) | 29 kDa | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: CAB18, AB140, CAB140, LHC81.1 chlorophyll A/B binding protein 1 chr1:10478071-10478874 FORWARD LENGTH=267 | AT1G29930.1 | 28 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: HSP60 heat shock protein 60-2 chr2:14075093-14708560 FORWARD LENGTH=585 | AT2G33210.1 (+1) | 62 kDa | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 0 | 0 | 0 |
| Symbols: HSP60, HSP60-3B heat shock protein 60 chr3:8669013-8672278 FORWARD LENGTH=577 | AT2G3390.1 | 61 kDa | 1 | 1 | 0 | 1 | 0 | 1 | 2 | 1 | 0 | 0 |
| Symbols: Ribosomal protein S3Ae chr3:1329751-1331414 FORWARD LENGTH=262 | AT3G04840.1 | 30 kDa | 1 | 1 | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 0 |
| Symbols: Ribosomal protein S3Ae chr4:16548724-16550222 FORWARD LENGTH=262 | AT4G34670.1 | 30 kDa | 1 | 1 | 0 | 1 | 0 | 1 | 1 | 0 | 0 | 0 |
| Symbols: UBP12 ubiquitin-specific protease 12 chr5:2019545-2027834 FORWARD LENGTH=1116 | AT5G06600.1 (+1) | 131 kDa | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 0 |
| Symbols: UBP13 ubiquitin-specific protease 13 chr3:3761758-3770290 FORWARD LENGTH=1115 | AT1G11910.1 (+1) | 131 kDa | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| Symbols: NIT1, ATNIT1, NIT1 nitriphile 1 chr3:15986901-15988841 FORWARD LENGTH=346 | AT3G44310.1 (+1) | 38 kDa | 2 | 1 | 0 | 4 | 1 | 4 | 1 | 1 | 1 | 1 |
| Symbols: ARP1, emb2207, RPL3A, RP1 ribosomal protein 1 chr1:16266992-16268631 FORWARD LENGTH=389 | AT1G43170.1 (+1) | 45 kDa | 2 | 1 | 0 | 2 | 0 | 1 | 1 | 1 | 0 | 0 |
| Symbols: RD21, RD21A Granulin repeat cysteine protease family protein chr1:17283139-17285609 FORWARD LENGTH=462 | AT1G47128.1 | 51 kDa | 4 | 3 | 0 | 2 | 0 | 2 | 0 | 2 | 0 | 0 |
| Symbols: ATP7B, PBP synthase subunit beta chr3:52660-54156 FORWARD LENGTH=498 | ATCG00480.1 | 54 kDa | 4 | 5 | 0 | 2 | 0 | 2 | 2 | 2 | 1 | 0 |
| Symbols: YK1, PBP1 ribosomal protein S3Ae chr3:2840657-2843730 FORWARD LENGTH=524 | ATCG09260.1 | ? | 1 | 1 | 1 | 3 | 0 | 3 | 1 | 1 | 0 | 0 |
| Symbols: KAS1, KAS1 3-ketoacyl-acyl carrier protein synthase I chr5:18774439-18776629 FORWARD LENGTH=473 | AT5G46290.1 | 50 kDa | 4 | 3 | 0 | 1 | 2 | 3 | 2 | 2 | 0 | 0 |
| Symbols: RPL2.1 ribosomal protein L2 chr3:84337-85843 FORWARD LENGTH=274 | ATCG00830.1 (+1) | 30 kDa | 3 | 2 | 0 | 2 | 0 | 3 | 3 | 4 | 0 | 0 |
| Symbols: ASN1, ASN1 asparagine synthetase 2 chr5:25969224-25972278 FORWARD LENGTH=578 | AT5G65010.1 (+1) | 65 kDa | 2 | 1 | 0 | 1 | 0 | 3 | 1 | 1 | 0 | 0 |
| Symbols: ASN1, DING, AT-ASN1 glutamine-dependent asparagine synthase 1 chr3:17438445-17441043 FORWARD LENGTH=512 | AT3G47420.2 | 58 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: ASN3 asparagine synthetase 3 chr3:3212934-321648 FORWARD LENGTH=578 | AT5G10240.1 (+1) | 65 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: PIP2A, PIP2, PIP2.1 plasma membrane intrinsic protein 2 chr3:19803906-19805454 FORWARD LENGTH=287 | AT3G53420.1 (+1) | 30 kDa | 4 | 4 | 0 | 1 | 0 | 1 | 2 | 1 | 0 | 0 |
| Symbols: RIBSOMAL PROTEIN S10P/S20E ribosomal protein S10P/S20E family protein chr3:16471606-16472312 FORWARD LENGTH=124 | AT3G45030.1 (+1) | 14 kDa | 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| Symbols: RIBSOMAL PROTEIN S10P/S20E ribosomal protein S10P/S20E family protein chr3:17453671-17454437 FORWARD LENGTH=122 | AT3G47370.1 (+2) | 14 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: Coatomer, beta subunit chr4:15264460-15272693 FORWARD LENGTH=948 | AT4G31490.1 | 106 kDa | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| Symbols: Coatomer, beta subunit chr4:15264415-15267383 FORWARD LENGTH=948 | AT4G31480.1 (+1) | 106 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: MLK3 protein kinase family protein chr2:1098518-10988652 FORWARD LENGTH=673 | AT2G25760.1 | 76 kDa | 1 | 1 | 0 | 1 | 0 | 1 | 3 | 2 | 2 | 2 |
| Symbols: RPT7 regulatory particle triple-A ATPase 3 chr5:23569155-23571116 FORWARD LENGTH=408 | AT5G58290.1 | 46 kDa | 2 | 2 | 1 | 1 | 1 | 2 | 0 | 0 | 0 | 0 |
| Symbols: CPN60, LEN1 chaperonin 60 beta chr1:20715717-20718673 FORWARD LENGTH=600 | AT1G55490.1 (+1) | 64 kDa | 1 | 2 | 0 | 1 | 0 | 1 | 1 | 0 | 0 | 0 |
| Symbols: TCP1 cpn60 chaperonin family protein chr5:22874058-22876566 FORWARD LENGTH=597 | AT5G56500.1 (+1) | 63 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: ATARCA, RACK1A, AT, RACK1A Transducin/WD40 repeat-like superfamily protein chr1:6222325-6223901 FORWARD LENGTH=327 | AT1G18080.1 | 36 kDa | 0 | 1 | 0 | 2 | 0 | 2 | 1 | 0 | 0 | 0 |
| Symbols: RACK1C, AT receptor for activated C kinase 18 chr3:6211109-6212371 FORWARD LENGTH=326 | AT1G18130.1 | 36 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: RACK1A, PMA2, PM2, H(+)-ATPase 2 chr4:17470820-17477522 FORWARD LENGTH=948 | AT4G30190.1 (+1) | 104 kDa | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: AAH1, PMA, OST2, HA1 H(+)-ATPase 1 chr2:8221858-8227268 FORWARD LENGTH=949 | AT2G18960.1 | 104 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: AAH7, HA7 H(+)-ATPase 7 chr3:22298763-23203509 FORWARD LENGTH=961 | AT3GG0330.1 (+1) | 105 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: AAH4, HA4 H(+)-ATPase 4 chr3:17693015-17697801 FORWARD LENGTH=960 | AT3G47950.1 | 105 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: AHA3, ATAH3, HA3 H(+)-ATPase 3 chr3:23231208-23236381 FORWARD LENGTH=949 | AT5G57350.1 (+1) | 104 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: AAH10 autoinhibited H(+)-ATPase isoform 10 chr1:5904058-5908998 FORWARD LENGTH=947 | AT1G17260.1 | 105 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: ATPase, F1 complex, alpha subunit chr2:3361474-3364028 FORWARD LENGTH=777 | AT2G07698.1 | 86 kDa | 2 | 2 | 1 | 3 | 1 | 4 | 1 | 0 | 0 | 0 |
| Symbols: LWD2 Transducin/WD40 repeat-like superfamily protein chr3:7939276-7949316 FORWARD LENGTH=346 | AT3G26640.1 | 39 kDa | 2 | 1 | 0 | 1 | 0 | 2 | 3 | 1 | 0 | 0 |
| Symbols: ATPase, VI complex, subunit B protein chr1:7016971-7020290 FORWARD LENGTH=487 | AT1G20260.1 (+2) | 54 kDa | 3 | 3 | 0 | 2 | 0 | 2 | 1 | 2 | 0 | 0 |
| Symbols: ATGST8, ATGST5, GST6, GST7 glutathione S-transferase alpha subunit 1 chr1:219558213-21955266 FORWARD LENGTH=263 | AT2G47730.1 | 29 kDa | 3 | 2 | 0 | 0 | 0 | 4 | 0 | 0 | 0 | 0 |
| Symbols: ATPC1 ATPase, gamma subunit chr4:2350761-2351882 FORWARD LENGTH=373 | AT4G04640.1 | 41 kDa | 5 | 3 | 0 | 2 | 1 | 2 | 1 | 2 | 1 | 0 |
| Symbols: FB42 fructose-bisphosphate aldolase 2 chr2:1816314-18165659 FORWARD LENGTH=398 | AT4G38970.1 | 43 kDa | 2 | 2 | 0 | 3 | 1 | 3 | 2 | 1 | 0 | 0 |
| Symbols: RPL16A ribosomal protein large subunit 16 chr2:17791794-17792946 FORWARD LENGTH=182 | AT2G42740.1 (+4) | 21 kDa | 2 | 2 | 1 | 1 | 1 | 1 | 1 | 2 | 2 | 1 |
| Symbols: Transketolase chr3:22454004-22456824 FORWARD LENGTH=741 | AT3G60750.1 (+1) | 80 kDa | 3 | 2 | 0 | 0 | 0 | 0 | 7 | 1 | 0 | 0 |
| Symbols: binding chr5:19317899-19327014 FORWARD LENGTH=1606 | AT5G47690.2 (+1) | 181 kDa | 6 | 0 | 0 | 2 | 0 | 6 | 0 | 0 | 0 | 0 |
| Symbols: SACS2, RPL11, RPL10A ribosomal protein L16p/L10e family protein chr1:4888270-4889408 FORWARD LENGTH=220 | AT1G14320.1 | 25 kDa | 1 | 2 | 1 | 1 | 0 | 1 | 2 | 2 | 1 | 1 |
| Symbols: CAC3 acetyl Co-enzyme A carboxylase carboxytransferase alpha subunit chr2:15917612-15920749 FORWARD LENGTH=769 | AT2G38040.1 (+1) | 85 kDa | 3 | 1 | 0 | 0 | 0 | 4 | 0 | 0 | 0 | 0 |
| Symbols: RAM-1, RAN1, ATRAN1 RAS-related nuclear protein-1 chr5:6760364-6761747 FORWARD LENGTH=221 | AT5G20010.1 (+2) | 25 kDa | 2 | 3 | 0 | 2 | 0 | 5 | 1 | 0 | 0 | 0 |
| Symbols: Ribosomal protein S4 chr5:495124-4936334 FORWARD LENGTH=198 | AT5G15200.1 | 23 kDa | 2 | 2 | 1 | 2 | 1 | 2 | 1 | 0 | 0 | 0 |
| Symbols: Ribosomal protein S26 family protein chr2:16918506-16919623 FORWARD LENGTH=133 | AT2G40510.1 (+2) | 15 kDa | 2 | 2 | 0 | 2 | 0 | 2 | 2 | 2 | 1 | 0 |
| Symbols: EM82296 Ribosomal protein L2 family chr2:7837151-7838160 FORWARD LENGTH=258 | AT2G18020.1 | 28 kDa | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 0 |
| Symbols: Ribosomal protein L2 family chr2:17097613-17098656 FORWARD LENGTH=258 | AT3G36130.1 | 28 kDa | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: Histone superfamily protein chr1:2369212-2369523 FORWARD LENGTH=103 | AT1G07660.1 (+8) | 11 kDa | 1 | 1 | 1 | 3 | 1 | 3 | 1 | 1 | 1 | 1 |
| Symbols: oxidoreductases, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor; copper ion binding chr2:8613168-8615649 FORWARD LENGTH=401 | AT2G19940.1 (+1) | 44 kDa | 5 | 1 | 0 | 1 | 0 | 3 | 1 | 0 | 0 | 0 |
| Symbols: ATP5B, RP5B ribosomal protein S8 chr2:15647883-15649042 FORWARD LENGTH=207 | AT2G37270.1 (+3) | 23 kDa | 3 | 1 | 0 | 0 | 0 | 0 | 2 | 2 | 2 | 1 |
| Symbols: Thioredoxin superfamily protein chr3:3672189-3673937 FORWARD LENGTH=266 | AT3G16130.1 | 29 kDa | 0 | 1 | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 0 |
| Symbols: PIP1B, TMP-A, ATH2, PIP1,2 plasma membrane intrinsic protein 1B chr2:1891450-18911703 FORWARD LENGTH=286 | AT2G45960.1 (+2) | 31 kDa | 1 | 1 | 0 | 2 | 1 | 2 | 1 | 1 | 0 | 0 |
| Symbols: RPL27A, RPL27AB ribosomal protein L18e/L18e' superfamily protein chr1:8263007-8263447 FORWARD LENGTH=146 | AT1G23290.1 (+1) | 16 kDa | 1 | 1 | 0 | 1 | 0 | 1 | 2 | 1 | 1 | 0 |
| Symbols: Ribosomal protein L18e/L18e' family protein chr2:14532916-14534161 FORWARD LENGTH=178 | AT2G34480.1 | 21 kDa | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: Ribosomal protein L18e/LX family protein chr3:4910773-4911933 FORWARD LENGTH=178 | AT3G14600.1 | 21 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: EM8219, HAP15 PAM domain (PC/PINT associated module) protein chr1:7001409-7004154 FORWARD LENGTH=488 | AT1G20200.1 | 56 kDa | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: PAM domain (PC/PINT associated module) protein chr1:28524623-2852618 FORWARD LENGTH=487 | AT1G57990.1 | 56 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: AP51 ATP sulfurylase 1 chr3:8112837-8114734 FORWARD LENGTH=463 | AT3G22890.1 | 51 kDa | 2 | 0 | 0 | 2 | 0 | 2 | 0 | 0 | 0 | 0 |
| Symbols: AP52, ASA1 Pseudouridine synthase/archaeosine transglycosylase-like family protein chr1:6914835-6916657 FORWARD LENGTH=476 | AT1G19920.1 | 54 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: AP53 Pseudouridine synthase/archaeosine transglycosylase-like family protein chr4:8413443-8415311 FORWARD LENGTH=465 | AT4G14680.1 | 52 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: Tetra peptide repeat (TPR)-like superfamily protein chr3:22565440-2256679 FORWARD LENGTH=412 | AT3G60980.1 | 47 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 5 | 5 | 0 | 0 |
| Symbols: SPA2 SPA1-related 2 chr4:6772163-6776675 FORWARD LENGTH=1036 | AT4G1110.1 | 115 kDa | 5 | 6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: PORB protoclorophyllide oxidoreductase B chr4:13725648-1372710 FORWARD LENGTH=401 | AT4G27440.1 (+1) | 43 kDa | 3 | 2 | 0 | 1 | 0 | 1 | 1 | 0 | 0 | 0 |
| Symbols: APE ATP synthase epsilon chain chr5:52265-52663 FORWARD LENGTH=132 | ATCG00470.1 | 14 kDa | 2 | 2 | 0 | 1 | 0 | 1 | 1 | 2 | 0 | 0 |
| Symbols: RPL14 ribosomal protein L14 chrC:8086-8104 FORWARD LENGTH=122 | ATCG00780.1 | 14 kDa | 2 | 2 | 0 | 1 | 0 | 2 | 1 | 2 | 0 | 0 |
| Symbols: C calcium/lipid-binding plant phosphorous/transferase family protein chr5:2127200-2129584 FORWARD LENGTH=794 | AT5G06850.1 | 91 kDa | 0 | 0 | | | | | | | | |

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|--|------------------|---------|---|---|---|---|---|---|---|---|---|---|
| Symbols: STV1, RPL24B, RPL24 Ribosomal protein L24e family protein chr3:19660749-19661912 REVERSE LENGTH=163 | AT3G53020.1 | 19 kDa | 2 | 2 | 0 | 1 | 0 | 1 | 2 | 2 | 0 | 0 |
| Symbols: glycine-rich protein chr4:11944050-1194565 REVERSE LENGTH=356 | AT4G22740.1 (+1) | 39 kDa | 2 | 2 | 0 | 0 | 0 | 2 | 1 | 0 | 0 | 0 |
| Symbols: Ribosomal L28e protein family chr2:8517528-8512995 FORWARD LENGTH=143 | AT2G19730.1 (+2) | 16 kDa | 1 | 1 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | 0 |
| Symbols: Ribosomal protein S11 family protein chr2:15169925-1517159 FORWARD LENGTH=150 | AT2G36160.1 | 16 kDa | 1 | 1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| Symbols: Ribosomal protein S11 family protein chr3:3623757-3624866 REVERSE LENGTH=150 | AT3G11510.1 | 16 kDa | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: Coatomer, beta' subunit chr3:5411699-5418313 REVERSE LENGTH=909 | AT3G15980.1 (+3) | 102 kDa | 1 | 1 | 0 | 0 | 0 | 2 | 0 | 0 | 0 | 0 |
| Symbols: structural molecular chaperone chr1:30084522-30091949 FORWARD LENGTH=1135 | AT1G79990.1 (+2) | 129 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: XIK, ATXIX, XI-17 Myosin family protein with Dil domain chr5:6927064-6936825 REVERSE LENGTH=1545 | AT5G20490.1 (+1) | 175 kDa | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: MYA1, ATMYA1, XI-1 myosin 1 chr2:6039453-6049309 FORWARD LENGTH=1520 | AT1G17580.1 | 173 kDa | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: XIC, ATXIC Myosin family protein with Dil domain chr1:2779963-2788325 FORWARD LENGTH=1538 | AT1G08730.1 | 175 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: HSP81-2, ERD8, HSP90-2, AtHsp90.2 heat shock protein 81-2 chr5:22686923-2268943 FORWARD LENGTH=699 | AT5G56030.1 (+1) | 80 kDa | 3 | 2 | 0 | 1 | 0 | 1 | 1 | 0 | 0 | 0 |
| Symbols: PIP3, PIP3A, PIP2, SIMP plasma membrane intrinsic protein 3 chr4:16708672-16709958 FORWARD LENGTH=280 | AT4G35100.1 (+1) | 30 kDa | 2 | 2 | 1 | 1 | 1 | 0 | 1 | 0 | 0 | 0 |
| Symbols: RPS4 chloroplast ribosomal protein S4 chr5:45223-45828 REVERSE LENGTH=201 | AT1G0380.1 | 23 kDa | 1 | 1 | 0 | 0 | 0 | 2 | 2 | 0 | 0 | 0 |
| Symbols: LOS2, ENO2 Enolase chr2:15321081-15323786 REVERSE LENGTH=444 | AT2G36530.1 | 48 kDa | 1 | 1 | 0 | 1 | 0 | 2 | 1 | 0 | 1 | 0 |
| Symbols: ATPase, VO/ATP complex, subunit C/D chr3:10778025-10780350 FORWARD LENGTH=351 | AT3G28715.1 | 41 kDa | 2 | 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| Symbols: ATPase, VO/ATP complex, subunit C/D chr3:10773144-10775594 REVERSE LENGTH=351 | AT3G28710.1 | 41 kDa | 1 | 1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| Symbols: cPhsc70-2 chloroplast heat shock protein 70-1 chr4:12590094-12593437 FORWARD LENGTH=718 | AT4G24280.1 | 77 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| Symbols: cPhsc70-2-ATAT PROTEIN 70-2, HSC70-7, cPhsc70-2 chloroplast heat shock protein 70-2 chr5:20303470-20306295 FORWARD LENGTH=718 | AT5G49910.1 | 77 kDa | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: LUH LEUNIG, homolog chr2:13867235-13871844 FORWARD LENGTH=787 | AT2G32700.1 (+6) | 86 kDa | 0 | 0 | 0 | 1 | 0 | 3 | 0 | 0 | 0 | 0 |
| Symbols: emb1138 DEAD box RNA helicase (RH3) chr5:928540-9288871 REVERSE LENGTH=747 | AT5G26742.1 (+1) | 81 kDa | 3 | 2 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: RPS11 ribosomal protein S11 chrC:78960-79376 REVERSE LENGTH=138 | ATCG00750.1 | 15 kDa | 2 | 2 | 0 | 1 | 0 | 1 | 2 | 2 | 0 | 0 |
| Symbols: Ribosomal protein S4 (RPS4) family protein chr2:546598-7548138 FORWARD LENGTH=261 | AT2G17360.1 (+3) | 30 kDa | 2 | 0 | 1 | 1 | 0 | 1 | 1 | 0 | 0 | 0 |
| Symbols: PFL, RPS18A, PFL1 Ribosomal protein S13/S18 family chr1:8067990-8069163 FORWARD LENGTH=152 | AT1G22780.1 (+2) | 18 kDa | 0 | 1 | 1 | 2 | 0 | 1 | 0 | 1 | 0 | 0 |
| Symbols: P40, AP40, RPSAA 40S ribosomal protein S4 chr1:27243148-27244842 REVERSE LENGTH=298 | AT1G72370.1 (+1) | 32 kDa | 1 | 2 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| Symbols: RPSab 40S ribosomal protein S8 chr3:1309544-1310846 REVERSE LENGTH=280 | AT3G04770.2 | 31 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: CLPC, ATHSP93-V, HSP93-3, DC1, CLPC CLPC homolog chr1:520715710-20719800 REVERSE LENGTH=929 | AT5G50920.1 | ? | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: ATCLPC, ATHSP93-III, HSP93-11 Clp ATPase chr3:18122363-18126008 REVERSE LENGTH=952 | AT3G48870.1 (+1) | 106 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: SPA4 SPA1-related 4 chr1:19783748-19786690 FORWARD LENGTH=794 | AT1G53090.1 (+1) | 89 kDa | 2 | 5 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: AAA-type ATPase family protein chr2:8629736-8694837 FORWARD LENGTH=443 | AT2G20140.1 (+1) | 49 kDa | 5 | 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| Symbols: RPT6A, ATSG1 regulatory particle triple-A ATPase 6A chr5:6752144-6754918 FORWARD LENGTH=419 | AT5G19990.1 (+1) | 47 kDa | 0 | 0 | 0 | 1 | 0 | 2 | 0 | 0 | 0 | 0 |
| Symbols: Lactate/malate dehydrogenase family protein chr1:1189418-1191267 REVERSE LENGTH=332 | AT1G04410.1 | 36 kDa | 0 | 2 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| Symbols: Aldolase superfamily protein chr3:19627383-19628874 REVERS LENGTH=358 | AT3G52930.1 | 39 kDa | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 |
| Symbols: Aldolase superfamily protein chr5:963389-964986 REVERSE LENGTH=359 | AT5G03690.2 | 39 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: Aldolase superfamily protein chr4:13931566-13329397 FORWARD LENGTH=358 | AT4G26530.1 (+1) | 38 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: CHU1, CH42, CH11, CHL1 P-loop containing nucleoside triphosphatases superfamily protein chr4:10201897-10203361 REVERSE LENGTH=424 | AT4G18480.1 | 46 kDa | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| Symbols: CHU2, CHL2, CHU2 magnesium chelatase I2 chr5:18628095-18629565 FORWARD LENGTH=418 | AT5G45930.1 | 46 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: transducin family protein / WD-40 repeat family protein chr3:23431009-2347241 REVERSE LENGTH=1104 | AT3G63460.1 (+2) | 120 kDa | 1 | 1 | 0 | 1 | 0 | 2 | 0 | 0 | 0 | 0 |
| Symbols: vacuolar ATP synthase subunit A chr3:14228846-14232228 REVERSE LENGTH=441 | AT3G42050.1 | 50 kDa | 2 | 1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| Symbols: RPL18 ribosomal protein L18 chr3:1621511-1622773 FORWARD LENGTH=187 | AT3G05590.1 (+1) | 21 kDa | 2 | 1 | 1 | 1 | 0 | 2 | 1 | 1 | 0 | 0 |
| Symbols: RPT5A, AT562-2 regulatory particle triple-A ATPase SA chr3:1603540-1605993 FORWARD LENGTH=424 | AT3G05530.1 | 47 kDa | 2 | 1 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 |
| Symbols: AGT, AGT1, SGAT alanine:glyoxylate aminotransferase chr2:5359417-5540902 REVERSE LENGTH=401 | AT2G13360.1 (+1) | 44 kDa | 1 | 1 | 1 | 0 | 1 | 2 | 0 | 0 | 0 | 0 |
| Symbols: RPS1 ribosomal protein L22/P17e family protein chr5:1951520-9516725 FORWARD LENGTH=176 | AT1G27400.1 (+1) | 20 kDa | 0 | 1 | 2 | 0 | 0 | 1 | 2 | 0 | 0 | 0 |
| Symbols: VHA-A vacuolar ATP synthase subunit A chr1:29660463-29664575 FORWARD LENGTH=623 | AT1G78900.1 (+1) | 69 kDa | 1 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 0 | 0 |
| Symbols: RPT1A regulatory particle triple-A 1A chr1:20065921-20068324 REVERSE LENGTH=426 | AT1G53750.1 | 48 kDa | 2 | 1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| Symbols: AT1J2, J2 DNAI homologue 2 chr5:7303798-7305668 REVERSE LENGTH=419 | AT2G22060.1 | 46 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: AT13, AT1 DNAI homologue 3 chr3:15869115-15871059 REVERSE LENGTH=420 | AT3G44110.1 (+1) | 46 kDa | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| Symbols: RPS1, ARRP51 ribosomal protein S1 chr5:1161962-11621223 REVERSE LENGTH=416 | AT3G03510.1 | 45 kDa | 1 | 0 | 0 | 3 | 0 | 4 | 0 | 0 | 0 | 0 |
| Symbols: ACCD acetyl-CoA carboxylase carboxyl transferase subunit beta chrC:57075-58541 FORWARD LENGTH=488 | ATCG00500.1 | 56 kDa | 2 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| Symbols: RPS18 ribosomal protein S8 chr2:80068-80472 REVERSE LENGTH=134 | ATCG00770.1 | 15 kDa | 1 | 2 | 0 | 1 | 0 | 1 | 1 | 1 | 0 | 0 |
| Symbols: SSR16 small subunit ribosomal protein 16 chr4:16535084-16536092 REVERSE LENGTH=113 | AT4G34620.1 | 13 kDa | 1 | 1 | 0 | 0 | 1 | 1 | 1 | 2 | 0 | 0 |
| Symbols: 6'-deoxy-phosphate phosphohydrolase family protein chr2:15053952-15055776 FORWARD LENGTH=422 | AT2G35840.1 (+2) | 48 kDa | 1 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 0 | 0 |
| Symbols: GTP binding Elongation Factor Tu family protein chr4:1295751-1298354 REVERSE LENGTH=454 | AT4G02930.1 | 49 kDa | 3 | 0 | 0 | 1 | 0 | 3 | 0 | 0 | 0 | 0 |
| Symbols: ECT2 evolutionarily conserved C-terminal region 2 chr4:4385274-4388220 REVERSE LENGTH=667 | AT3G13460.1 (+3) | 72 kDa | 3 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: Glycine cleavage T-protein family chr1:4001801-4003245 FORWARD LENGTH=408 | AT1G1860.1 (+2) | 44 kDa | 1 | 1 | 0 | 1 | 0 | 1 | 2 | 0 | 0 | 0 |
| Symbols: NOP56 homolog of nucleolar protein NOP56 chr1:20984544-20986893 REVERSE LENGTH=522 | AT1G56110.1 | 59 kDa | 1 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 0 | 0 |
| Symbols: RPS15A ribosomal protein S15A chr1:2408413-2409065 FORWARD LENGTH=130 | AT1G07770.1 (+2) | 15 kDa | 1 | 1 | 1 | 0 | 1 | 3 | 0 | 0 | 0 | 0 |
| Symbols: RPS16 ribosomal protein S8 family protein chr2:16517588-16518265 REVERSE LENGTH=136 | AT2G39590.1 | 15 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: RPN1A, ATPRN1A 26S proteasome regulatory subunit S2 A1 chr2:8859211-8864699 FORWARD LENGTH=891 | AT2G20580.1 | ? | 2 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: PAC1 20S proteasome alpha subunit C1 chr3:7792819-7793571 REVERSE LENGTH=250 | AT2G22110.1 | 27 kDa | 0 | 2 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 |
| Symbols: ATBBC1, BBC1, RSU2 breast basic conserving 1 chr3:1816971-18168047 REVERSE LENGTH=206 | AT3G49010.1 (+3) | 24 kDa | 0 | 0 | 0 | 1 | 0 | 2 | 1 | 0 | 0 | 0 |
| Symbols: Tetrastricopeptid repeat (TPR) like superfamily protein chr3:22535729-22536940 FORWARD LENGTH=403 | AT2G60960.1 | 46 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 2 | 0 | 0 |
| Symbols: CPN60A, CH-CPN60A, SLP chaperonin-60A chr2:11926603-11929491 FORWARD LENGTH=586 | AT2G28000.1 | 62 kDa | 2 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: ATTIP9A, RIN1 P-loop containing nucleoside triphosphatases superfamily protein chr5:7391026-7394071 REVERSE LENGTH=458 | AT2G22330.1 | 50 kDa | 0 | 2 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| Symbols: RPL16 ribosomal protein L16 chrC:81189-82652 REVERSE LENGTH=135 | ATCG00790.1 | 15 kDa | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| Symbols: PUB12, ATPUB12 PLANT UBX BOX 12 chr2:12370608-12370608 REVERSE LENGTH=962 | AT2G28800.1 | 107 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: NAD(P)-binding Rossmann-fold superfamily protein chr3:11193767-11194948 REVERSE LENGTH=298 | AT3G2950.1 | 32 kDa | 0 | 0 | 0 | 1 | 0 | 3 | 0 | 0 | 0 | 0 |
| Symbols: ILA ILTUYHA chr1:24065238-24081908 REVERSE LENGTH=2610 | AT1G64790.1 (+1) | 285 kDa | 3 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: APUM5, PUM5 pumilio 5 chr3:7059098-7062660 REVERSE LENGTH=961 | AT2G20250.1 | 107 kDa | 2 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: ATP5, TP57, ATPPS5 trehalose-phosphatase/synthase 7 chr1:1955413-1958153 FORWARD LENGTH=851 | AT1G06410.1 | 97 kDa | 1 | 0 | 0 | 0 | 0 | 3 | 0 | 0 | 0 | 0 |
| Symbols: I transcription regulator chr1:373335-386682 REVERSE LENGTH=2431 | AT1G20280.1 (+1) | 270 kDa | 2 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: ATGST9, GLUT9, ATGST7, GST9 glutathione S-transferase PHI 9 chr2:13139132-13140057 FORWARD LENGTH=215 | AT2G30860.1 (+1) | 24 kDa | 0 | 2 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: Ribosomal protein L35e family protein chr2:8513577-8514346 FORWARD LENGTH=119 | AT1G74270.1 | 13 kDa | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| Symbols: ATU2AF35B, U2AF35B Zinc finger C-x8-C-x5-C-x3-H type family protein chr5:1710445-17171296 REVERSE LENGTH=112 | AT5G42820.1 (+1) | 33 kDa | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: ATU2AF35A 5' snrNP auxiliary factor small subunit, putative chr1:9615302-9616042 FORWARD LENGTH=246 | AT1G27650.2 | 29 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: Zinc finger C-x8-C-x5-C-x3-H type family protein chr3:16328221-16328448 REVERSE LENGTH=75 | AT3G44785.1 | 9 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: PIL6, PI5 phytochrome interacting factor 3-like 6 chr3:21828189-21828985 REVERSE LENGTH=442 | AT3G59060.1 (+3) | 49 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| Symbols: PIF4, SRL2, ATP1F4 phytochrome interacting factor 4 chr2:17887003-1788823 FORWARD LENGTH=430 | AT2G43010.1 (+1) | 48 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: Ribosomal protein L31e family protein chr2:8513577-8514346 FORWARD LENGTH=119 | AT2G19740.1 (+2) | 14 kDa | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| Symbols: Ribosomal protein L31e family protein chr5:22944003-22944767 REVERSE LENGTH=85 | AT5G56710.2 | 10 kDa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Symbols: Coatomer epsilon subunit chr1:10858546-10860173 REVERSE LENGTH=292 | AT1G30630.1 | 33 kDa | 0 | 0 | 0 | 2 | 0 | 0 | 2 | 0 | 0 | 0 |
| Symbols: SHM4 serine hydroxymethyltransferase 4 chr4:8048013 | | | | | | | | | | | | |

