

A CRISPR-based sequence proximity binding protein labelling system for scanning upstream regulatory proteins

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Supplementary Methods | The detail methods of CSPL.

Vector Availability

We have generated dCas9-TD, dCas9-TDmo, and OsU6pt in this work.

dCas9-TD-Tag and dCas9-TDmo-Tag, which have an HA or Flag tag in the N-terminal of dCas9, are also available for your consideration for IP assay. All the vectors are available from the corresponding author upon request.

Target selection

Design a 20 bp target on CRISPOR website (<https://crispor.gi.ucsc.edu/>). Designing two independent targets for the same region is recommended for making the results more credible. Using an unrelated region as target is also useful for filtering the negative proteins.

Please note that this target site was not intended to directly cover your specific region of interest.

Vector construction

dCas9-TD-GOI: Primers were synthesized according to the table below using pCBC and pHSE401¹ as templates to amplify three fragments: the promoter, gRNA, and terminator regions. These fragments were subsequently assembled into the dCas9-TD destination vector using Golden Gate assembly.

Fragments amplification:

Fragment	Primers	template
gRNA-F	ATATATGGTCTCGATTGNNN...20bp target...NNNGTTT TAGAGCT AGAAATAGC	pCBC
gRNA-R	ATTATTGGTCTCGAAACNNN...The reverse complement sequence of 20bp target...NNN CAATCTCTTAGTCGACTCTAC	
Promoter-F	TGCTCTTCACGCCGACTTGCCTTCCGCACAATAC	pHSE401
Promoter-R	ATGCAAGGTCTCACAATCACTACTTCGACTCTAGCTG	
Terminator-F	ATGTCGGTCTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAT AAGGC	pHSE401
Terminator-R	ACGCTCTTCAGACGTTGACCTGCAGGCATGCAAG	

Ligation system:

Component	Amount	Ligation program
Fragments	15 ng	(37°C 5 min+25°C 10 min) × 20 cycle + 37°C 30 min + 4°C hold
dCas9-TD	100 ng	
SapI enzyme	0.5 µL	
BsaI-HF enzyme	1 µL	
T7 ligase	1 µL	
2 × T7 ligase Buffer	10 µL	
ddH ₂ O	Up to 20 µL	

dCas9-TDmo-GOI: Primers were synthesized according to the table below using OsU6pt as templates to amplify two fragments: the promoter and gRNA-terminator regions. These fragments were subsequently assembled into the linearized dCas9-TD (SpeI+KpnI) destination vector.

Fragments amplification:

Fragment	Primers	template
U6-F	GATCCCCCGAATTACTGCggtacAAGAACGAACTAAGCCGGACAAGA AAAGG	OsU6pt
U6-R	CNNN...The reverse complement sequence of 20bp target...NNN AACACAAGCGGCAGCGCGCGG	
gRNA-F	GTGTTNNN...20bp target...NNNGTTTCAGAGCTATGCTGGAAACAGC	
gRNA-R	CGTGAGGATCCACTGAGACTAGTATTGGTTTATCTCATCGGAACTG C	

Ligation system:

Component	Amount	Ligation program
Fragments	15 ng	50°C 30 min + 4°C hold
Linearized dCas9-TDmo	100 ng	
2 × CE ligase mix	10 µL	
ddH ₂ O	Up to 20 µL	

Plant transformation

The constructions were transformed into the *Agrobacterium Tumefaciens* GV3101 strain for the transformation of both Arabidopsis and cabbage. The dipping flower method was used for Arabidopsis transformation as previously described². The homozygous transgenic T2 lines were used for biotin treatment. The cabbage accession ‘JZS’ was used for *Agrobacterium*-mediated transformation according to

Aneta's description³. The transgenic plants were selected using a Basta test strip (Agene, Beijing, China) and used to produce the T1 generation for further experimentation. *Oryza sativa* L. spp. *japonica* was transformed with *Agrobacterium tumefaciens*-mediated transformation and selected at Edgene Bio (Wuhan, China).

For other crops, genetic transformation and screening should be performed following their respective established transformation methods.

Biotin infection

For the biotin treatment of Arabidopsis, the leaves of three-week-old transgenic Arabidopsis were sprayed with a 0 or 100 μ M biotin solution containing 0.005% Silwet L-77 once every hour for a total treatment time of three hours. For the biotin treatment of cabbage, the leaves of four-week-old transgenic cabbage were carefully dewaxed by gently wiping with 0.1% Silwet L-77 solution to facilitate biotin penetration into leaf tissues, and then the leaves were immersed three times in a biotin solution at concentrations of 0 or 200 μ M for 10 minutes each time, at one-hour intervals. Two independent biological replicates were taken. For the biotin treatment of rice, the leaves of five-week-old transgenic rice were immersed three times in a biotin solution at concentrations of 0 or 200 μ M for 10 minutes each time, at one-hour intervals.

For other crops, the fundamental principle of biotin treatment is to ensure its absorption by the treated tissues. This method is primarily applied to leaves. For other tissues such as fruits, alternative approaches like direct injection can be attempted for treatment.

Biotinylated proteins purification

Nuclear protein extraction: Five-gram treated leaves were rinsed with ddH₂O for at least five times and subsequently collected for nuclear protein extraction⁴.

- 1) Ground 5 grams leaf to powder and mixture with 15 mL Buffer A (10 mM HEPES, 10 mM KCl, 10 mM MgCl₂, 5 mM EDTA, 250 mM sucrose, 0.5% Triton X-100, pH 7.8). Incubate on ice for 10 min to release cytoplasmic proteins, inverting the

tube occasionally.

- 2) Filter the lysate through Miracloth (475855, Merck-Millipore, Billerica, USA): first using a single layer, then using a double layer.
- 3) Centrifuge the filtrate at $3000\times g$ for 20 min at 4 °C. A green pellet should be visible.
- 4) Discard the supernatant. Gently resuspend the pellet in 5 mL of Buffer A by pipetting up and down. Transfer the suspension to a 10 mL tube.
- 5) Centrifuge at $2000\times g$ for 15 min at 4 °C.
- 6) Discard the supernatant. Gently resuspend the pellet in 1 mL of Buffer A by pipetting and transfer to a 1.5 mL tube.
- 7) Centrifuge at $2,000\times g$ for 10 min at 4 °C.
- 8) Discard the supernatant. the pellet was resuspended with a mixture of 180 μ L low-salt buffer (20 mM HEPES, 20 mM KCl, 1.5 mM $MgCl_2$, 0.2 mM EDTA and 25% glycerol, pH 7.8). This may be difficult.
- 9) Add 270 μ L high-salt buffer solution (20 mM HEPES, 1.6 M KCl, 1.5 mM $MgCl_2$, 0.2 mM EDTA and 25% glycerol, pH 7.8) and then inverted on the rotator for 1 hour at 4°C.
- 10) Centrifuge at $14000\times g$ for 20 min at 4 °C.
- 11) Carefully transfer the supernatant, which may appear cloudy, to a new tube. Centrifuge again at $14000\times g$ for 5 min at 4 °C to clarify.
- 12) Transfer the final supernatant to a clean 1.5 mL tube. Store at -20 °C or -70 °C.

All the protein extraction steps were conducted at 4°C.

Wipe out the free biotin: Then, the extracted nuclear protein solutions were subjected to buffer exchange to wipe out the free biotin using a PD-10 Desalting Column (17085101, Cytiva, Cardiff, UK) to replace the solvent with cell lysis buffer (SL1000, Coolaber, Beijing, China). Then, the protein was concentrated to 400 μ L by Ultra Centrifugal Filter (UFC8003, Millipore, Billerica, USA) for further analysis.

Streptavidin affinity: The concentrated nuclear protein solution (400 μ L) was incubated with 20 μ L magnetic streptavidin beads (5947S, Cell Signaling Technology,

Danvers, MA, USA) overnight at 4°C with rotation. Collect the pellet using a magnetic stand and wash the beads with 500 µL of cell lysis buffer by gently vortexing; repeat this wash five times. Resuspend the pellet with 40 µL 2× SDS sample buffer, heat the samples for five minutes at 95°C, then collect the supernatant for the SDS-PAGE.

LC-MS/MS study

The experiment: Load all the samples (40 µL) into the SDS-PAGE gel. To prevent potential cross-contamination, samples should be loaded intermittently with sufficient spacing between lanes. Gel excision should be performed once the samples have migrated approximately 0.5 cm into the separation gel. Following destaining, the gel bands containing the proteins were carefully cut out for in-gel digestion and identification by mass spectrometry. Briefly, proteins were disulfide reduced with 10 mM dithiothreitol (DTT) and alkylated with 40 mM iodoacetamide. In-gel digestion was performed using sequencing grade-modified trypsin in 25 mM ammonium bicarbonate at 37°C overnight. The peptides were extracted twice with 60% acetonitrile aqueous solution for 30 min. The peptide extracts were then centrifuged in a SpeedVac to reduce the volume.

For LC-MS/MS analysis, peptides were separated by a 100 min gradient elution at a flow rate 0.300 L/min with a Thermo NanoLC1000 HPLC system, which was directly interfaced with the Thermo Orbitrap Q Exactive plus mass spectrometer. The analytical column was a homemade fused silica capillary column (75 µm ID, 150 mm length) packed with 1.8 µm C-18 resin. Mobile phase A consisted of 0.1% formic acid, and mobile phase B consisted of 100% acetonitrile and 0.1% formic acid. The Orbitrap Q Exactive plus mass spectrometer was operated in the data-dependent acquisition mode using Xcalibur software and there is a single full-scan mass spectrum in the Orbitrap (300-1600 m/z, 70,000 resolution) followed by 110 ms data-dependent MS/MS scans in an Ion Routing Multipole at 27% normalized collision energy (HCD). The MS/MS spectra from each LC-MS/MS run were searched against the selected database using Proteome Discovery searching algorithm

(version 2.1).

Data analysis: Proteins captured by LC-MS/MS analysis under different experimental conditions were compared, and condition-specific proteins were then extracted. Subcellular localizations of these condition-specific proteins were predicted using DeepLoc2.1 (<https://services.healthtech.dtu.dk/services/DeepLoc-2.1/>), a deep learning-based tool, with "high-quality" model⁵. Transcription factors (TF) among these nuclear-localized proteins were then predicted using PlantTFDB (<https://planttfdb.gao-lab.org/>)⁶. For the remaining non-TF proteins, Gene Ontology (GO) enrichment analysis was performed using ClusterProfiler (v4.0.5) with default parameters.

References

1. He, F., Zhang, F., Sun, W., Ning, Y. & Wang, G. A Versatile Vector Toolkit for Functional Analysis of Rice Genes. *RICE* **11**, 27 (2018).
2. Zhang, X., Henriques, R., Lin, S., Niu, Q. & Chua, N. Agrobacterium-mediated transformation of *Arabidopsis thaliana* using the floral dip method. *NATURE PROTOCOLS* **1**, 641-646 (2006).
3. Gerszberg, A. Tissue culture and genetic transformation of cabbage (*Brassica oleracea* var. capitata): an overview. *PLANTA* **248**, 1037-1048 (2018).
4. Xu, Y., Chen, X. S. and Xiong, L. Z. (2018). Nuclear protein isolation protocol. *Bio-101* e1010122. Doi: 10.21769/BioProtoc.1010122. (in Chinese)
5. Odum, M. et al. DeepLoc 2.1: multi-label membrane protein type prediction using protein language models. *NUCLEIC ACIDS RESEARCH* **52**, W215-W220 (2024).
6. Jin, J. et al. PlantTFDB 4.0: toward a central hub for transcription factors and regulatory interactions in plants. *NUCLEIC ACIDS RESEARCH* **45**, D1040-D1045 (2017).

Supplementary Sequence 1 | The sequence of gRNA expression cassettes. The promoters, targets, gRNA, and terminators are highlighted in green, yellow, red, and blue, respectively.

dCas9-TD gRNA expression cassettes:

CGACTTGCCTTCCGCACAATACATCATTCTTCTTAGCTTTTTTTCTTCTTCTTCGT
TCATACAGTTTTTTTTGTTTATCAGCTTACATTTTCTTGAACCGTAGCTTTCGTTT
TCTTCTTTTAACTTTCCATTCCGAGTTTTTGTATCTTGTTCATAGTTTGTCCCAG
GATTAGAATGATTAGGCATCGAACCTTCAAGAATTTGATTGAATAAAACATCTTC
ATTCTTAAGATATGAAGATAATCTTCAAAAGGCCCTGGGAATCTGAAAGAAGA
GAAGCAGGCCCATTTATATGGGAAAGAACAATAGTATTTCTTATATAGGCCCAT
TAAGTTGAAAACAATCTTCAAAAGTCCCACATCGCTTAGATAAGAAAACGAAGC
TGAGTTTATATACAGCTAGAGTCGAAGTAGTGATTGNNNNNNNNNNNNNNNNNNNN
NGTTTTAGAGCTAGAAATAGCAAGTTAAATAAGGCTAGTCCGTTATCAACTTGA
AAAAGTGGCACCGAGTCGGTGCTTTTTTTTGCAAAATTTTCCAGATCGATTTCTTC
TTCCTCTGTTCTTCGGCGTTCAATTTCTGGGGTTTTCTCTTCGTTTTCTGTAACGA
AACCTAAAATTTGACCTAAAAAAAATCTCAAATAATATGATTCAGTGGTTTTGT
CTTTTCAGTTAGTTGAGTTTTGCAGTTCGGATGAGATAAACCAATATTAATCCAAA
CTACTGCAGCCTGACAGACAAATGAGGATGCAAACAATTTAAAGTTTATCTAAC
GCTAGCTGTTTTGTTTCTTCTCTGTTGCACCAACGACGGCGTTTTCTCAATCAT
AAAGAGGCTTGTTTTACTTAAGGCCAATAATGTTGATGGATCGAAAGAAGAGGG
CTTTTAATAAACGAGCCCGTTTAAGCTGTAAACGATGTCAAAAACATCCCACATC
GTTTCAGTTGAAAATAGAAGCTCTGTTTATATATTGGTAGAGTCGACTAAGAGATT
GNNNNNNNNNNNNNNNNNNNNNGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG
GCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTTTTTGCAA
AATTTTCCAGATCGATTTCTTCTTCTCTGTTCTTCGGCGTTCAATTTCTGGGGTTT
TCTCTTCGTTTTCTGTAACGTAAACCTAAAATTTGACCTAAAAAAAATCTCAAATA
ATATGATTCAGTGGTTTTGTACTTTTCAGTTAGTTGAGTTTTGCAGTTCGGATGAG
ATAAACCAATAAGCTTGCATGCCTGCAGGTCAAC

dCas9-TDmo gRNA expression cassette:

AAGAACGAACCTAAGCCGGACAAGAAAAGGAGCACATATACAAACCGTTTTATT
CATGAATGGTCACGATGGATGATGGGGCTCAGACTTGAGCTACGAGGCCGCAGG
CGAGAGAAGCCTAGTGTGCTCTCTGCTTGTTTGGGCGTAACGGAGGATACGGCC
GACGAGCGTGTACTACCGCGCGGGATGCCGCTGGGCGCTGCGGGGGCCGTTGGA
TGGGGATCGGTGGGTGCGGGGAGCGTTGAGGGGAGACAGGTTTAGTACCACCTC
GCCTACCGAACAATGAAGAACCCACCTTATAACCCCGCGCGCTGCCGCTTGTTGTT
NNNNNNNNNNNNNNNNNNNNNGTTTCAGAGCTATGCTGGAAACAGCATAGCAAG
TTGAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTT
TTTTTTGCAAAATTTTCCAGATCGATTTCTTCTTCTCTGTTCTTCGGCGTTCAATT
TCTGGGGTTTTCTCTTCGTTTTCTGTAACGTAAACCTAAAATTTGACCTAAAAAAA
ATCTCAAATAATATGATTCAGTGGTTTTGTACTTTTCAGTTAGTTGAGTTTTGCAG
TTCCGATGAGATAAACCAATA

Supplementary Sequence 2 | Complete coding sequences of dCas9-TD. The NLS and (GGGS)₃ Linker is highlighted in red and blue.

dCas9-TD:

ATGGAC**CCTAAGAAGAAACGTAAGGTG**ATGGATAAGAAGTACTCTATCGGA
CTCGCTATCGGAACTAACTCTGTGGGATGGGCTGTGATCACCGATGAGTAC
AAGGTGCCATCTAAGAAGTTCAAGGTTCTCGGAAACACCGATAGGCACTCT
ATCAAGAAAAACCTTATCGGTGCTCTCCTCTTCGATTCTGGTGAAACTGCT
GAGGCTACCAGACTCAAGAGAACCGCTAGAAGAAGGTACACCAGAAGAA
AGAACAGGATCTGCTACCTCCAAGAGATCTTCTCTAACGAGATGGCTAAAG
TGGATGATTCACTTCTCCACAGGCTCGAAGAGTCATTCCTCGTGGAAGAAG
ATAAGAAGCACGAGAGGACACCCTATCTTCGGAAACATCGTTGATGAGGTGG
CATACCACGAGAAGTACCCTACTATCTACCACCTCAGAAAGAAGCTCGTTG
ATTCTACTGATAAGGCTGATCTCAGGCTCATCTACCTCGCTCTCGCTCACAT
GATCAAGTTCAGAGGACACTTCCTCATCGAGGGTGATCTCAACCCTGATAA
CTCTGATGTGGATAAGTTGTTTCATCCAGCTCGTGCAGACCTACAACCAGCT
TTTCGAAGAGAACCCTATCAACGCTTCAGGTGTGGATGCTAAGGCTATCCT
CTCTGCTAGGCTCTCTAAGTCAAGAAGGCTTGAGAACCCTCATTGCTCAGCT
CCCTGGTGAGAAGAAGAACGGACTTTTCGGAAACTTGATCGCTCTCTCTCT
CGGACTCACCCCTAACTTCAAGTCTAACTTCGATCTCGCTGAGGATGCAAA
GCTCCAGCTCTCAAAGGATACCTACGATGATGATCTCGATAACCTCCTCGCT
CAGATCGGAGATCAGTACGCTGATTTGTTCCCTCGCTGCTAAGAACCTCTCT
GATGCTATCCTCCTCAGTGATATCCTCAGAGTGAACACCGAGATCACCAAG
GCTCCACTCTCAGCTTCTATGATCAAGAGATACGATGAGCACCACCAGGAT
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GGTGCATCTCAAGAAGAGTTCTACAAGTTCATCAAGCCTATCCTCGAGAAG
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AGAAAGCAGAGGACCTTCGATAACGGATCTATCCCTCATCAGATCCACCTC
GGAGAGTTGCACGCTATCCTTAGAAGGCAAGAGGATTCTACCCATTCTC
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TACGTGGGACCTCTCGCTAGAGGAAACTCAAGATTGCTTGGATGACCAGA
AAGTCTGAGGAAACCATCACCCCTTGGAACCTCGAAGAGGTGGTGGATAA
GGGTGCTAGTGCTCAGTCTTTCATCGAGAGGATGACCAACTTCGATAAGAA
CCTTCCAAACGAGAAGGTGCTCCCTAAGCACTCTTTGCTCTACGAGTACTT
CACCGTGTACAACGAGTTGACCAAGGTTAAGTACGTGACCGAGGGAATGA
GGAAGCCTGCTTTTTTGTGAGGTGAGCAAAAGAAGGCTATCGTTGATCTCT
TGTTCAAGACCAACAGAAAGGTGACCGTGAAGCAGCTCAAAGAGGATTAC
TTCAAGAAAATCGAGTGCTTCGATTGAGTTGAGATTTCTGGTGTTGAGGAT
AGGTTCAACGCATCTCTCGGAACCTACCACGATCTCCTCAAGATCATTAAG
GATAAGGATTTCTTGATAACGAGGAAAACGAGGATATCTTGAGGATATC
GTTCTTACCCTCACCTCTTTGAAGATAGAGAGATGATTGAAGAAAGGCTC
AAGACCTACGCTCATCTCTTCGATGATAAGGTGATGAAGCAGTTGAAGAGA
AGAAGATACACTGGTTGGGGAAGGCTCTCAAGAAAGCTCATTAACGGAAT

CAGGGATAAGCAGTCTGGAAAGACAATCCTTGATTTCTCAAGTCTGATGG
ATTCGCTAACAGAACTTCATGCAGCTCATCCACGATGATTCTCTCACCTTT
AAAGAGGATATCCAGAAGGCTCAGGTTTCAGGACAGGGTGATAGTCTCCAT
GAGCATATCGCTAACCTCGCTGGATCTCCTGCAATCAAGAAGGGAATCCTC
CAGACTGTGAAGGTTGTGGATGAGTTGGTGAAGGTGATGGGAAGGCATAA
GCCTGAGAACATCGTGATCGAAATGGCTAGAGAGAACCAGACCACTCAGA
AGGGACAGAAGAACTCTAGGGAAAGGATGAAGAGGATCGAGGAAGGTAT
CAAAGAGCTTGGATCTCAGATCCTCAAAGAGCACCTGTGAGAACACTC
AGCTCCAGAATGAGAAGCTCTACCTCTACTACCTCCAGAACGGAAGGGATA
TGTATGTGGATCAAGAGTTGGATATCAACAGGCTCTCTGATTACGATGTTGA
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CTCACCAGGTCTGATAAGAACAGGGGTAAGAGTGATAACGTGCCAAGTGA
AGAGGTTGTGAAGAAAATGAAGAACTATTGGAGGCAGCTCCTCAACGCTA
AGCTCATCACTCAGAGAAAGTTCGATAACTTGACTAAGGCTGAGAGGGGA
GGACTCTCTGAATTGGATAAGGCAGGATTCATCAAGAGGCAGCTTGTGGAA
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ACCAAGTACGATGAGAACGATAAGTTGATCAGGGAAGTGAAGGTTATCACC
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GATTATTGGTGATAAGGAGATTTTCGGTATCTCCAGGGGGATTGATAAACAG
GGAGCGCTCCTTCTGGAGCAGGATGGTGTTCATCAAGCCTTGGATGGGAGG
AGAGATAAGTCTCAGGTCAGCAGAGAAATCAAGGGCTGATCCTAAGAAGA
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dCas9-TDmo:

ATGGCACACTAAGAAGAAAAGGAAAGTCGGCATTTCATGGCGTTCCGGCAGC
CGACAAAAAGTATAGCATCGGCCTCGCTATTGGGACAACTCTGTGGGCTG
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TTTTCGACTCCGGAGAGACGGCGGAGGCGACGCGTCTCAAGCGTACCGCG
CGCCGCAGGTACACAAGAAGGAAGAATAGGATCTGCTACTTGCAGGAAAT
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TCACCTCCGTAAGAAGCTTGTCGATTCAACTGATAAGGCTGATCTCAGACT
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GAAAGGATGACCAATTTTGACAAAAATCTGCCTAACGAAAAGGTGCTTCC
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TGACAAGGTCATGAAACAACCTCAAGCGCCGGCGCTATACTGGCTGGGGCC
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CAATTTTGGAATTCCTCAAATCCGACGGATTCGCAAATAGGAATTTTATGCA
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AGTAAGTTTCTGCTTCTACCTTTGATATATATATAATAATTATCATTATTAGTA
GTAATATAATATTTCAAATATTTTTTTCAAATAAAAGAATGTAGTATATAGCA
ATTGCTTTTCTGTAGTTTATAAGTGTGTATATTTAATTTATAACTTTTCTAATA
TATGACCAAAATTTGTTGATGTGCAGACCGGTTGAGCGATTATGACGTTGA
CCATATTGTGCCCCAATCTTTCCTTAAAGACGACTCTATCGACAATAAAGTG
CTGACGCGCAGCGATAAAAAATCGCGGTAAGTCGGATAATGTCCCGTCGGAA
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GCTGATCACTCAGAGGAAATTCGACAATCTCACCAAGGCAGAAAGGGGTG
GACTTAGCGAGCTCGACAAGGCCGGTTTTATCAAAGACAGCTGGTGGAG
ACACGCCAAATACCAAACACGTTGCCCAGATCCTGGATTCGAGGATGAA
CACGAAGTATGACGAGAACGACAAGTTGATTAGGGAAGTCAAGGTCATCA
CTTTGAAGTCCAAGCTGGTGAGCGACTTTCGCAAAGACTTCCAGTTTACA
AAGTCAGGGAAATTAATACTACCACCACGCCCACGACGCCTACCTTAACG
CCGTGGTTGGCACAGCACTCATCAAGAAATACCCTAAGCTCGAATCTGAGT
TCGTCTATGGCGACTATAAGGTCTACGACGTTAGAAAAATGATCGCGAAATC
TGAGCAGGAAATAGGCAAGGCAACTGCCAAGTACTTCTTCTATTCCAATAT

CATGAACTTTTTTAAGACGGAGATTACCCTGGCGAATGGTGAGATCCGCAA
GCGCCCTTTGATTGAGACAAACGGAGAAACAGGAGAGATCGTATGGGACA
AAGGGCGGGACTTTGCTACTGTTAGGAAGGTGCTCTCTATGCCACAAGTTA
ACATTGTCAAAAAAACTGAAGTGCAGACAGGTGGGTTTAGCAAGGAATCT
ATCCTGCCGAAGAGGAACTCTGACAAGCTGATCGCCCGCAAGAAAGATTG
GGATCCGAAAAAGTACGGAGGATTCGACTCCCCACAGTTGCGTACTCCGT
GCTTGTCGTGGCCAAAGTGGAGAAGGGCAAGTCTAAGAAGCTCAAGAGC
GTCAAAGAGTTGTTGGGGATCACGATTATGGAGCGGTTCGTCTTTCGAAAAG
AATCCGATAGATTTTCTCGAGGCCAAGGGTTATAAAGAAGTCAAGAAGGAT
CTTATCATCAAGCTCCCTAAGTACTCCCTCTTTGAGCTTGAAAACGGACGG
AAAAGAATGCTGGCTTCAGCGGGTGAAGTTCAGAAGGGTAATGAACTCGC
TCTGCCCTCAAAATATGTGAATTTCTTTACCTGGCATCACACTATGAGAAG
CTTAAGGGGTCTCCAGAGGACAACGAGCAGAAGCAACTGTTCGTTGAACA
ACACAAGCACTACCTTGACGAGATTATCGAGCAAATCAGCGAGTTTAGCAA
GCGCGTTATACTGGCAGACGCAAATCTTGATAAGGTCCTTAGCGCCTACAA
CAAGCATAGAGACAAACCCATCCGGGAGCAGGCCGAGAACATTATTCATCT
CTTCACCTTGACGAATCTTGGGGCCCCGGCCGCGTTCAAGTACTTCGATACT
ACCATAGACAGAAAGCGCTATACATCGACAAAGGAAGTTCTTGACGCCAC
GCTGATCCACCAAAGTATAACAGGCCTCTATGAGACACGCATCGACCTTTC
GCAGTTGGGCGGTGACCGC**CCCAAAAAGAAGAGGAAAGTC**GGAGGT**GBA**
GGAGGAGGTTTCGGGTGGAGGTGGGAGCGGTGGTGGAGGTTCCAAGGATA
ACACAGTCCCTCTTAAGTTGATTGCCCTTCTCGCTAACGGCGAATTCACA
GTGGAGAGCAACTAGGTGAAACGCTCGGAATGTCAAGAGCTGCTATTAATA
AACATATCCAACTTTGAGAGATTGGGGTGTTGATGTCTTCACCGTACCCG
GAAAGGGTTACTCACTCCCAGAGCCAATCCCCCTACTGAATGCGAAGCAGA
TCTTGGGACAACCTCGATGGTGGATCCGTGGCAGTATTGCCTGTTGTGACA
GCACGAATCAGTACTTGCTCGACAGGATCGGTGAGTTGAAGTCTGGAGATG
CTTGCATCGCTGAGTACCAACAAGCAGGAAGAGGAAGCAGAGGTCGTAAG
TGGTTCTCCCCGTTTGGAGCCAACTTGACCTTTCAATGTTCTGGAGACTCA
AGCGTGGACCAGCGGCAATTGGTCTGGGCCAGTCATCGGCATCGTGATGG
CCGAGGCTTTGCGTAAGTTGGGAGCTGACAAGGTGAGAGTTAAGTGGCCT
AATGATCTGTACCTCCAAGATAGAAAACCTCGCGGGTATCCTTGTCGAACCT
GCTGGAATTACGGGCGACGCAGCTCAGATAGTCATCGGTGCTGGAATCAAT
GTGGCAATGAGGAGGGTCGAGGAGTCAGTGGTGAACCAAGGTTGGATCAC
TCTTCAAGAAGCCGGTATCAATTTGGATCGTAATACACTTGCTGCTACACTC
ATCCGTGAGCTGAGGGCCGCTCTAGAACTATTCGAACAAGAAGGACTGGC
GCCGTACTTGCCAAGGTGGGAAAAGTTGGATAATTTCATAAATCGTCCAGT
TAAATTGATTATTGGTGATAAGGAGATTTTCGGTATCTCCAGGGGGATTGAT
AAACAGGGAGCGCTCCTTCTGGAGCAGGATGGTGTCATCAAGCCTTGGAT
GGGAGGAGAGATAAGTCTCAGGTCAGCAGAGAAATCAAGGGCTGAT**CCTA**
AGAAGAAGAGGAAAGTTGA

Supplementary Table 1 | Ninety-nine predicted nucleus-localized proteins in Arabidopsis.

Protein_ID	Localization	Number of captured peptides	Description
AT2G47110.1	Nucleus	50	UBIQUITIN EXTENSION PROTEIN 6, Ubiquitin 6, Ribosomal Protein S27ab
AT3G46520.1	Cytoplasm Nucleus	28	Actin-12
AT5G22880.1	Nucleus	16	Histone B2, HISTONE H2B
AT3G58570.1	Cytoplasm Nucleus	14	Rna Helicase 52
AT2G37470.1	Nucleus	10	Histone Superfamily Protein
AT3G11510.1	Cytoplasm Nucleus	9	Ribosomal Protein S11 Family Protein
AT3G47620.1	Nucleus	9	"TEOSINTE BRANCHED, Cycloidea And PCF (TCP) 14"
AT3G49430.4	Nucleus	9	Serine/Arginine-Rich Protein Splicing Factor 34a, SER/ARG-Rich Protein 34A
AT1G02840.1	Nucleus	8	Serine/Arginine-Rich Protein Splicing Factor 34
AT2G31160.1	Nucleus	8	Light Sensitive Hypocotyls 3, Organ Boundary 1
AT5G27770.1	Cytoplasm Nucleus	7	Ribosomal L22e Protein Family
AT1G16610.3	Nucleus	6	Arginine/Serine-Rich 45
AT1G67680.1	Nucleus	6	SRP72 RNA-Binding Domain-Containing Protein
AT4G26630.2	Nucleus	6	DEK-Domain Containing Protein 3
AT5G35680.3	Cytoplasm Nucleus	6	Nucleic Acid-Binding, OB-Fold-Like Protein
AT1G72710.1	Cytoplasm Nucleus	5	Casein Kinase 1-Like Protein 2
AT2G45640.1	Cytoplasm Nucleus	5	SIN3 Associated Polypeptide P18, SIN3 ASSOCIATED POLYPEPTIDE 18
AT3G03340.2	Nucleus	5	LETHAL UNLESS CBC 7 A, Unfertilized Embryo Sac 6
AT3G60245.1	Cytoplasm Nucleus	5	Zinc-Binding Ribosomal Protein Family Protein
AT5G18620.2	Nucleus	5	Chromatin Remodeling Factor17
AT5G41770.1	Nucleus	5	Crooked Neck Protein, Putative / Cell Cycle Protein
AT2G03150.1	Nucleus	4	SHORT ROOT IN SALT MEDIUM 1, Embryo Defective 1579
AT5G47690.3	Nucleus	4	Binding Protein
AT5G67240.1	Cytoplasm Nucleus	4	Small RNA Degrading Nuclease 3
AT1G01140.3	Cytoplasm Nucleus	3	CBL-Interacting Protein Kinase 9, PROTEIN KINASE 6
AT1G17790.1	Nucleus	3	DNA-Binding Bromodomain-Containing Protein
AT1G33240.1	Nucleus	3	GT2-LIKE 1, GT-2-Like 1
AT1G76010.1	Cytoplasm Nucleus	3	Alba DNA/RNA-Binding Protein

AT2G13540.1	Cytoplasm Nucleus	3	Aba Hypersensitive 1, Ensalada, Cap-Binding Protein 80
AT2G25170.3	Nucleus	3	Hypersensitive To Red And Blue 2, Enhanced Photomorphogenic 1, PICKLE
AT2G27100.1	Nucleus	3	Serrate
AT2G40510.1	Cytoplasm Nucleus	3	Ribosomal Protein S26e Family Protein
AT2G41100.3	Cytoplasm Nucleus	3	Arabidopsis Thaliana Calmodulin Like 4, Calmodulin-Like 12, TOUCH 3
AT3G07030.4	Cytoplasm Nucleus	3	Alba DNA/RNA-Binding Protein
AT4G10710.2	Nucleus	3	Global Transcription Factor C
AT4G24270.2	Nucleus	3	Embryo Defective 140
AT5G27640.2	Cytoplasm Nucleus	3	Eukaryotic Translation Initiation Factor 3B1, Translation Initiation Factor 3B1
AT5G40490.1	Cytoplasm Nucleus	3	RNA-Binding Glycine-Rich Protein D5
AT1G04270.1	Cytoplasm Nucleus	2	Cytosolic Ribosomal Protein S15
AT1G48630.1	Cytoplasm Nucleus	2	Receptor For Activated C Kinase 1B
AT1G56110.1	Cytoplasm Nucleus	2	Homolog Of Nucleolar Protein NOP56
AT2G01710.2	Nucleus	2	SUVH1/3-Interacting DNAJ Domain-Containing Protein 2
AT2G20330.1	Nucleus	2	Overly Zinc Sensitive3
AT2G43770.1	Cytoplasm Nucleus	2	Transducin/WD40 Repeat-Like Superfamily Protein
AT2G45850.2	Nucleus	2	AT-Hook Motif Nuclear Localized Protein 9
AT2G47420.1	Cytoplasm Nucleus	2	Adenosine Dimethyl Transferase 1A
AT2G47640.4	Cytoplasm Nucleus	2	Small Nuclear Ribonucleoprotein Family Protein
AT3G18990.2	Nucleus	2	REPRODUCTIVE MERISTEM 39, REDUCED VERNALIZATION RESPONSE 1; AP2/B3-Like Transcriptional Factor Family Protein
AT3G44110.1	Cytoplasm Nucleus	2	DNAJ Homologue 3
AT3G61110.1	Nucleus	2	Ribosomal Protein S27
AT4G20980.2	Cytoplasm Nucleus	2	Eukaryotic Translation Initiation Factor 3 Subunit 7
AT4G22140.1	Nucleus	2	Early Bolting In Short Days
AT4G29910.2	Nucleus	2	EMBRYO DEFECTIVE 2798, Origin Recognition Complex Protein 5
AT4G31580.1	Nucleus	2	Serine/Arginine-Rich 22, RS-Containing Zinc Finger Protein 22, RS-CONTAINING ZINC FINGER PROTEIN 22
AT5G04280.1	Nucleus	2	RNA-Binding Glycine-Rich Protein B3, RZ-1c, Atrz-1c
AT5G22840.1	Cytoplasm Nucleus	2	Protein Kinase Superfamily Protein
AT5G25757.1	Cytoplasm Nucleus	2	RNA Polymerase I-Associated Factor PAF67
AT5G41520.1	Cytoplasm Nucleus	2	Ribosomal Protein S10e B
AT5G51280.1	Cytoplasm Nucleus	2	DEAD-Box Protein Abstrakt

AT5G55670.1	Nucleus	2	RNA-Binding (RRM/RBD/RNP Motifs) Family Protein
AT5G67630.1	Cytoplasm Nucleus	2	"Reptin, RVB2, Ruvbl2, Tip49b"
ATCG00750.1	Nucleus	2	Ribosomal Protein S11
AT1G10580.1	Nucleus	1	Transducin/WD40 Repeat-Like Superfamily Protein
AT1G10840.1	Cytoplasm Nucleus	1	Translation Initiation Factor 3 Subunit H1
AT1G20220.1	Cytoplasm Nucleus	1	Alba DNA/RNA-Binding Protein
AT1G28060.1	Nucleus	1	RNA-Directed DNA Methylation 16
AT1G54060.1	Nucleus	1	6B-Interacting Protein 1-Like 1
AT1G63160.1	Nucleus	1	Replication Factor C 2, EMBRYO DEFECTIVE 2811
AT1G73720.1	Cytoplasm Nucleus	1	Suppressors Of Mec-8 And Unc-52 1
AT1G79730.1	Nucleus	1	Early Flowering 7
AT2G21440.1	Nucleus	1	RNA-Binding (RRM/RBD/RNP Motifs) Family Protein
AT2G33620.3	Nucleus	1	AT-Hook Motif Nuclear Localized Protein 10
AT2G35940.3	Nucleus	1	BEL1-Like Homeodomain 1, Embryo Sac Development Arrest 29
AT2G44730.1	Nucleus	1	Alcohol Dehydrogenase Transcription Factor Myb/SANT-Like Family Protein
AT3G13200.1	Nucleus	1	Embryo Defective 2769
AT3G14180.1	Nucleus	1	Arabidopsis 6B-Interacting Protein 1-Like 2
AT3G18740.1	Cytoplasm Nucleus	1	Ribosomal Protein L7Ae/L30e/S12e/Gadd45 Family Protein
AT3G22170.2	Nucleus	1	Far-Red Elongated Hypocotyls 3, CHLOROPLAST DIVISION MUTANT 45
AT3G23390.1	Cytoplasm Nucleus	1	Rpl36a A
AT3G26560.1	Nucleus	1	ATP-Dependent RNA Helicase
AT3G43980.1	Cytoplasm Nucleus	1	Ribosomal Protein S14p/S29e Family Protein
AT3G55460.1	Nucleus	1	SC35-Like Splicing Factor 30
AT3G60830.1	Cytoplasm Nucleus	1	Actin-Related Protein 7
AT3G61310.1	Nucleus	1	AT-Hook Motif Nuclear Localized Protein 11
AT4G03430.3	Nucleus	1	Starik 1, Embryo Defective 2770, Stabilized 1
AT4G05410.1	Nucleus	1	Yaozhe
AT4G18465.1	Cytoplasm Nucleus	1	RNA Helicase Family Protein
AT4G19610.1	Nucleus	1	Nucleotide/Nucleic Acid Binding Protein
AT4G21110.2	Nucleus	1	G10 Family Protein
AT4G39520.1	Cytoplasm Nucleus	1	GTP-Binding Protein-Like Protein
AT5G05450.1	Nucleus	1	RNA Helicase 18
AT5G08450.2	Nucleus	1	Histone Deacetylation Complex 1, RXT3-Like

AT5G28040.2	Nucleus	1	Virf Interacting Protein 4
AT5G40200.1	Nucleus	1	Degradation Of Periplasmic Proteins 9, Degp Protease 9
AT5G42970.1	Cytoplasm Nucleus	1	Constitutive Photomorphogenic 14, Cop9 Signalosome Subunit 4, Fusca 4, Embryo Defective 134, Constitutive Photomorphogenic 8, Fusca 8
AT5G47930.1	Nucleus	1	Zinc-Binding Ribosomal Protein Family Protein
AT5G64200.2	Nucleus	1	Ortholog Of Human Splicing Factor SC35
AT5G65410.1	Nucleus	1	Zinc Finger Homeodomain 1

Note: Ten transcription factors being highlighted in red and four validated candidates in red and bold.

Supplementary Table 2 | Five hundred and one predicted nucleus-localized proteins in cabbage.

Protein_ID	Localization	PSMs	Description
BolC03g011650.2J	Nucleus	130	AT3G46030.1: Histone superfamily protein;(source:Araport11) HTB11
BolC05g059240.2J	Nucleus	98	AT3G06400.2: Encodes a SWI2/SNF2 chromatin remodeling protein belonging to the ISWI family. Involved in nuclear proliferation during megagametogenesis and cell expansion in the sporophyte. Constitutively expressed. RNAi induced loss of function in megagametogenesis results in female sterility.35S:RNAi plants have reduced stature. Double mutation in CHR17 and CHR11 results in the loss of the evenly spaced nucleosome pattern in gene bodies, but does not affect nucleosome density. CHR11; CHROMATIN-REMODELING PROTEIN 11
BolC08g058270.2J	Cytoplasm Nucleus	67	AT1G06220.1: Encodes a protein with similarity to splicing factor Snu114. Snu114 is thought to be involved in activation of the spliceosome. Loss of GFA1 function results in reduced female fertility. Approximately 50% of ovules abort due to defects in the female gametophyte. In mutant gametophytes antipodal cells express egg cell markers suggesting a defect in specification of cell fate.GFA1 is also required to restrict the expression of LIS. The mRNA is cell-to-cell mobile. CLO; CLOTHO; GAMETOPHYTE FACTOR 1; GFA1; MATERNAL EFFECT EMBRYO ARREST 5; MEE5
BolC06g030730.2J	Nucleus	66	AT4G40030.4: Histone superfamily protein;(source:Araport11) HTR4
BolC08g002230.2J	Cytoplasm Nucleus	65	AT1G06220.1: Encodes a protein with similarity to splicing factor Snu114. Snu114 is thought to be involved in activation of the spliceosome. Loss of GFA1 function results in reduced female fertility. Approximately 50% of ovules abort due to defects in the female gametophyte. In mutant gametophytes antipodal cells express egg cell markers suggesting a defect in specification of cell fate.GFA1 is also required to restrict the expression of LIS. The mRNA is cell-to-cell mobile. CLO; CLOTHO; GAMETOPHYTE FACTOR 1; GFA1; MATERNAL EFFECT EMBRYO ARREST 5; MEE5
BolC01g050800.2J	Nucleus	60	AT3G11964.1: Encodes a nucleolar protein that is a ribosome biogenesis co-factor. Mutants display aberrant RNA processing and female gametophyte development. RIBOSOMAL RNA PROCESSING 5; RRP5
BolC03g012250.2J	Cytoplasm Nucleus	57	AT5G59870.1: Encodes HTA6, a histone H2A protein. H2A.W.6; HISTONE H2A 6; HTA6
BolC09g053890.2J	Nucleus	57	AT5G18620.1: Encodes a member of the A. thaliana imitation switch (AtISWI) subfamily of chromatin remodeling factors. Double mutation in CHR17 and CHR11 results in the loss of the evenly spaced nucleosome pattern in gene bodies, but does not affect nucleosome density. CHR17; CHROMATIN REMODELING FACTOR17
BolC08g041180.2J	Nucleus	53	AT3G57300.2: Encodes the Arabidopsis INO80 ortholog of the SWI/SNF ATPase family that has been shown to interact with H2A.Z and facilitates the enrichment of H2A.Z at the ends of the flowering repressor genes FLC and MAF4/5. Functions as a positive regulator of DNA homologous recombination (HR) and plays a crucial role in genome stability maintenance. In INO80 mutants, the HR frequency is reduced to 15% of that in the wild-type. Plants mutated in INO80 display a pleiotropic phenotype including smaller plant and organ size, and late flowering

but are not more sensitive to genotoxic agents or less efficient at T-DNA integration. INO80 has also been shown to regulate a subset of the Arabidopsis transcriptome. INO80; INO80 ORTHOLOG

BolC01g042240.2J	Cytoplasm Nucleus	52	AT3G20670.1: Encodes HTA13, a histone H2A protein. HISTONE H2A 13; HTA13
BolC05g006640.2J	Cytoplasm Nucleus	48	AT1G08880.1: Encodes HTA5, a histone H2A protein. H2AX is a meiosis-specific isoform of histone H2A. Upon DSB formation, rapid accumulation of phosphorylated H2AX (γ-H2AX) occurs around the break site.
BolC06g010370.2J	Nucleus	47	AT1G56110.1: NOP56-like protein HOMOLOG OF NUCLEOLAR PROTEIN NOP56; NOP56
BolC09g005460.2J	Cytoplasm Nucleus	47	AT5G27670.1: Encodes HTA7, a histone H2A protein. H2A.W.7; HISTONE H2A 7; HTA7
BolC01g022110.2J	Cytoplasm Nucleus	46	AT4G27230.2: Encodes HTA2, a histone H2A protein. HISTONE H2A 2; HTA2
BolC06g019680.2J	Nucleus	44	AT5G41770.1: crooked neck protein, putative / cell cycle protein;(source:Araport11)
BolC08g038530.2J	Nucleus	42	AT3G54670.1: Encodes a member of the Arabidopsis cohesin complex that is essential for viability and sister chromatid alignment. ATSMC1; SMC1; STRUCTURAL MAINTENANCE OF CHROMOSOMES 1; TITAN8; TTN8
BolC01g054540.2J	Nucleus	38	AT3G06010.1: Encodes AtCHR12, a SNF2/Brahma-type chromatin-remodeling protein. AtCHR12 mediates temporary growth arrest in Arabidopsis upon perceiving environmental stress. ATCHR12; CHR12; CHROMATIN REMODELING 12
BolC02g040810.2J	Nucleus	37	AT3G57150.1: Encodes a putative pseudouridine synthase (NAP57). ATCBF5; ATNAP57; CBF5; HOMOLOGUE OF NAP57; NAP57
BolC03g054200.2J	Cytoplasm Nucleus	37	AT5G67630.1: P-loop containing nucleoside triphosphate hydrolases superfamily protein;(source:Araport11) ISE4; REPTIN, RVB2, RUVBL2, TIP49B
BolC08g001390.2J	Nucleus	33	AT1G50920.1: Putative GTPase involved in HA - and ABA-mediated signaling pathways, particularly during defense respnses to pathogens. Has paralog NOG1-2. NOG1-1
BolC04g059200.2J	Cytoplasm Nucleus	32	AT2G33340.1: Encodes MAC3B, a U-box proteins with homology to the yeast and human E3 ubiquitin ligase Prp19. Associated with the MOS4-Associated Complex (MAC). Involved in plant innate immunity. Regulator of flowering time. MAC3B; MOS4-ASSOCIATED COMPLEX 3B; PLANT U-BOX 60; PUB60
BolC04g067840.2J	Nucleus	31	AT2G46020.3: Encodes a SWI/SNF chromatin remodeling ATPase that upregulates transcription of all three CUC genes and is involved in the formation and/or maintenance of boundary cells during embryogenesis. Also mediates repression of expression of seed storage proteins in vegetative tissues. Interacts strongly with AtSWI3C, also with AtSWI3B, but not with AtSWI3A or AtSWI3D.
BolC05g004750.2J	Nucleus	31	AT1G06720.2: P-loop containing nucleoside triphosphate hydrolases superfamily protein;(source:Araport11)
BolC03g074540.2J	Nucleus	30	AT1G63810.2: nucleolar protein;(source:Araport11)

BolC05g002670.2J	Cytoplasm Nucleus	29	AT1G04510.2: Encodes MAC3A, a U-box proteins with homology to the yeast and human E3 ubiquitin ligase Prp19. Associated with the MOS4-Associated Complex (MAC). Involved in plant innate immunity. Regulator of flowering time. MAC3A; MOS4-ASSOCIATED COMPLEX 3A; PLANT U-BOX 59; PUB59
BolC02g007020.2J	Nucleus	28	AT5G15550.2: Transducin/WD40 repeat-like superfamily protein;(source:Araport11) ARABIDOPSIS THALIANA PESCADILLO ORTHOLOG; ATPEIP2; ATPEP2
BolC04g009200.2J	Cytoplasm Nucleus	28	AT2G38770.1: P-loop containing nucleoside triphosphate hydrolases superfamily protein;(source:Araport11) EMB2765; EMBRYO DEFECTIVE 2765; MAC7; MOS4-ASSOCIATED COMPLEX 7
BolC06g025940.2J	Cytoplasm Nucleus	28	AT3G60830.1: Encodes an actin-related protein required for normal embryogenesis, plant architecture and floral organ abscission. ACTIN-RELATED PROTEIN 7; ARP7; ATARP7
BolC06g032540.2J	Nucleus	28	AT1G73100.1: Encodes a SU(VAR)3-9 homolog, a SET domain protein. Known SET domain proteins are involved in epigenetic control of gene expression and act as histone methyltransferases. There are 10 SUVH genes in Arabidopsis and members of this subfamily of the SET proteins have an additional conserved SRA domain. SDG19; SET DOMAIN PROTEIN 19; SU(VAR)3-9 HOMOLOG 3; SUVH3
BolC09g010240.2J	Nucleus	28	AT5G67320.1: Encodes a WD-40 protein involved in histone deacetylation in response to abiotic stress. Identified in a screen for mutations with altered expression of stress induced genes. Functions as a repressor of cold tolerance induced genes. Loss of function mutants are hypersensitive to freezing. Part of a PWR-HOS15-HD2C complex to regulate expression of COR genes involved in cold tolerance via histone modification. HIGH EXPRESSION OF OSMOTICALLY RESPONSIVE GENES 15; HOS15; OLI1; OLIGOCELLULA1
BolC02g011550.2J	Cytoplasm Nucleus	27	AT5G22330.1: P-loop containing nucleoside triphosphate hydrolases superfamily protein;(source:Araport11) ATTIP49A; PONTIN, RUVBL1; RESISTANCE TO PSEUDOMONAS SYRINGAE PV MACULICOLA INTERACTOR 1; RIN1; RVB1
BolC03g064190.2J	Nucleus	27	AT3G44530.3: Encodes a nuclear localized WD-repeat containing protein involved in negative regulation of knox gene expression via epigenetic mechanism of chromatin re-organization. It is a part of the HISTONE REGULATOR complex that deposits histones in a DNA synthesis-independent manner and affects both nucleosome occupancy and the maintenance of transcriptional silencing. Interacts physically and genetically with AS1. Expressed in meristem and leaf primordia. Homozygous mutants are embryo lethal. Phenotype of cosuppressed lines is variable but show effects on leaf development similar to as1/as2.
BolC04g000680.2J	Nucleus	27	AT2G47620.1: Homologous to yeast SWI3 and a member of the Arabidopsis SWI3 gene family. Protein physically interacts with ATSWI3B and ATSWI3C, the other two members of the SWI3 family. ATSWI3A; CHB1; SWI3A; SWITCH/SUCROSE NONFERMENTING 3A
BolC09g057650.2J	Nucleus	27	AT5G15550.2: Transducin/WD40 repeat-like superfamily protein;(source:Araport11) ARABIDOPSIS THALIANA PESCADILLO ORTHOLOG; ATPEIP2; ATPEP2

BolC03g007660.2J	Nucleus	26	AT5G15550.2: Transducin/WD40 repeat-like superfamily protein;(source:Araport11) ARABIDOPSIS THALIANA PESCADILLO ORTHOLOG; ATPEIP2; ATPEP2
BolC03g019160.2J	Nucleus	26	AT2G31970.1: Encodes the Arabidopsis RAD50 homologue. It is involved in double strand break repair. Component of the meiotic recombination complex that processes meiotic double-strand-breaks to produce single-stranded DNA ends, which act in the homology search and recombination. Accumulates in the nucleus during meiotic prophase, a process regulated by PHS1. ATRAD50; RAD50
BolC08g022030.2J	Nucleus	26	AT1G10490.2: GNAT acetyltransferase (DUF699);(source:Araport11)
BolC01g028910.2J	Cytoplasm Nucleus	25	AT3G50000.1: Encodes the casein kinase II (CK2) catalytic subunit (alpha). CASEIN KINASE II, ALPHA CHAIN 2; ATCKA2; CKA2
BolC03g054350.2J	Nucleus	25	AT5G65770.3: Encodes a protein that localizes to the nuclear periphery and affects nuclear morphology. Member of a small gene family in Arabidopsis containing 4 proteins (LNC1-4 or CRWN 1-4) with redundant functions in protection from oxidative damage, control of nuclear morphology and degradation of ABI5. CROWDED NUCLEI 4; CRWN4; LINC4; LITTLE NUCLEI4
BolC04g038500.2J	Cytoplasm Nucleus	25	AT2G37620.3: Member of the actin gene family. Expressed in mature pollen.
BolC05g058480.2J	Nucleus	25	AT3G07220.1: Forkhead domain protein that is a subunit of ISWI chromatin remodeling complex.Interacts with histones and regulates the expression of genes involved in stamen filament elongation. ATFHA2; FHA2; FORKHEAD-ASSOCIATED 2
BolC08g041900.2J	Nucleus	25	AT3G57940.1: GNAT acetyltransferase (DUF699);(source:Araport11)
BolC08g046860.2J	Nucleus	25	AT2G25170.3: Encodes a SWI/SWF nuclear-localized chromatin remodeling factor of the CHD3 group. Involved in post-germination repression of embryonic development. Acts with GA to establish repression of embryonic genes upon germination. Protein preferentially accumulates in differentiating tissues. Loss of function alleles are associated with expression of embryonic traits in adult plants and derepression of embryonic genes such as PHEROS1. Is an extragenic suppressor of slr2 (SSL2). Mutations in PKL (SSL2) restores lateral root formation in the slr2 mutant slr-1. It was proposed that PKL/SSL2-mediated chromatin remodeling negatively regulates auxin-mediated LR formation in Arabidopsis.The mRNA is cell-to-cell mobile. Regulates plant responses to cold and salt stress. CHD3; CHR6; CKH2; CYTOKININ-HYPERSENSITIVE 2; ENHANCED PHOTOMORPHOGENIC 1; EPP1; GYM; GYMNOS; HRB2; HYPERSENSITIVE TO RED AND BLUE 2; PICKLE; PKL; SSL2; SUPPRESSOR OF SLR 2
BolC02g056590.2J	Nucleus	24	AT5G28740.1: Tetratricopeptide repeat (TPR)-like superfamily protein;(source:Araport11)
BolC03g008170.2J	Cytoplasm Nucleus	24	AT5G16310.1: Peptidase C12, ubiquitin carboxyl-terminal hydrolase 1;(source:Araport11) UCH1
BolC03g056400.2J	Nucleus	24	AT5G64420.1: DNA polymerase V family;(source:Araport11)
BolC05g054710.2J	Nucleus	24	AT3G11964.1: Encodes a nucleolar protein that is a ribosome biogenesis co-factor. Mutants display aberrant RNA processing and female gametophyte development. RIBOSOMAL RNA PROCESSING 5; RRP5

BolC09g004580.2J	Nucleus	24	AT3G07220.1: Forkhead domain protein that is a subunit of ISWI chromatin remodeling complex. Interacts with histones and regulates the expression of genes involved in stamen filament elongation. ATFHA2; FHA2; FORKHEAD-ASSOCIATED 2
BolC04g002360.2J	Nucleus	23	AT4G21710.1: Encodes the unique second-largest subunit of DNA-dependent RNA polymerase II; the ortholog of budding yeast RPB2 and a homolog of the E. coli RNA polymerase beta subunit. EMB1989; EMBRYO DEFECTIVE 1989; NRPB2; RPB2
BolC04g063320.2J	Cytoplasm Nucleus	23	AT2G38770.1: P-loop containing nucleoside triphosphate hydrolases superfamily protein;(source:Araport11) EMB2765; EMBRYO DEFECTIVE 2765; MAC7; MOS4-ASSOCIATED COMPLEX 7
BolC03g038750.2J	Nucleus	22	AT3G07050.1: Arabidopsis NSN1 encodes a nucleolar GTP-binding protein and is required for maintenance of inflorescence meristem identity and floral organ development. NSN1; NUCLEOSTEMIN-LIKE 1
BolC03g070280.2J	Nucleus	22	AT1G28420.1: homeobox-1;(source:Araport11) HB-1; HOMEODOMAIN-BOX 1; RINGLET 1; RLT1
BolC05g002860.2J	Nucleus	22	AT1G50920.1: Putative GTPase involved in HA - and ABA-mediated signaling pathways, particularly during defense responses to pathogens. Has paralog NOG1-2. NOG1-1
BolC06g012730.2J	Cytoplasm Nucleus	22	AT1G33140.1: Encodes ribosomal protein L9. Identified in a screen for enhancers of as1. as1/pgy double mutants show defects in leaf vascular patterning and adaxial cell fate. Double mutant analysis indicates pyg genes function in the same pathway as REV, KAN1 and KAN2. The mRNA is cell-to-cell mobile. PGY2; PIGGYBACK2
BolC03g042950.2J	Nucleus	21	AT3G14180.1: sequence-specific DNA binding transcription factor;(source:Araport11) ARABIDOPSIS 6B-INTERACTING PROTEIN 1-LIKE 2; ASIL2
BolC08g041670.2J	Nucleus	21	AT3G57660.2: Encodes a subunit of RNA polymerase I (aka RNA polymerase A). The mRNA is cell-to-cell mobile.
BolC01g019310.2J	Nucleus	20	AT3G62870.1: Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein;(source:Araport11)
BolC03g053900.2J	Nucleus	20	AT2G18750.3: Calmodulin-binding protein;(source:Araport11)
BolC05g031060.2J	Cytoplasm Nucleus	20	AT1G32730.1: electron carrier/iron ion-binding protein;(source:Araport11)
BolC09g013400.2J	Nucleus	20	AT2G18750.3: Calmodulin-binding protein;(source:Araport11)
BolC02g012830.2J	Nucleus	19	AT5G60040.1: Encodes a subunit of RNA polymerase III (aka RNA polymerase C). NRPC1; NUCLEAR RNA POLYMERASE C1
BolC03g024220.2J	Nucleus	19	AT2G40030.1: Encodes the unique largest subunit of nuclear DNA-dependent RNA polymerase V; homologous to budding yeast RPB1 and the E. coli RNA polymerase beta prime subunit. Required for normal RNA-directed DNA methylation at non-CG methylation sites and transgene silencing. The nrpe1 mutant is more resistant to biotrophic pathogens and is primed to activate salicylic acid-dependent defence genes. ATNRPD1B; DEFECTIVE IN MERISTEM SILENCING 5; DMS5; DRD3; NRPD1B; NRPE1; NUCLEAR RNA POLYMERASE D1B
BolC04g059470.2J	Nucleus	19	AT2G33610.1: Homologous to yeast SWI3 & RSC8, components of the SWI/SNF and RSC chromatin remodeling complexes. Interacts with BSH, AtSWI3A, SWI3C and FCA. Expressed ubiquitously. ATSWI3B; CHB2; CHROMATIN REMODELING COMPLEX SUBUNIT B; SWI3B; SWITCH SUBUNIT 3

BolC08g054270.2J	Nucleus	19	AT1G13030.1: Encodes a plant coilin, a protein that in other organisms is a major structural scaffolding protein necessary for Cajal body formation, composition and activity. It has been shown to bind both U1 and U1 snRNAs in vitro. ATCOILIN; COILIN
BolC01g026000.2J	Nucleus	18	AT3G21540.1: transducin family protein / WD-40 repeat family protein;(source:Araport11)
BolC04g012800.2J	Cytoplasm Nucleus	18	AT2G36130.1: Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein;(source:Araport11) CYCLOPHILIN
BolC04g064900.2J	Cytoplasm Nucleus	18	AT2G40930.1: Encodes ubiquitin-specific protease with nuclear localization signals that is likely to be involved in ubiquitin-mediated protein degradation. ATUBP5; PDE323; PIGMENT DEFECTIVE EMBRYO 323; UBIQUITIN-SPECIFIC PROTEASE 5; UBP5
BolC09g012780.2J	Nucleus	18	AT2G17930.1: Component of the SPT module of the SAGA complex. TRA1A
BolC09g061500.2J	Nucleus	18	AT5G11240.1: GHS40 encodes a WD40 protein, that is localized in the nucleus and nucleolus. In the presence of high glucose it negatively regulates the expression of abscisic acid degradation and signaling genes. ATGHS40; GHS40; GLUCOSE HYPERSENSITIVE 40; NUCLEAR GLUCOSE-RESPONSIVE WD40 PROTEIN1; NUGWD1
BolC03g033230.2J	Nucleus	17	AT4G04940.2: transducin family protein / WD-40 repeat family protein;(source:Araport11)
BolC03g053460.2J	Nucleus	17	AT2G17930.1: Component of the SPT module of the SAGA complex. TRA1A
BolC04g025470.2J	Nucleus	17	AT1G29940.1: Encodes a subunit of RNA polymerase 1 (aka RNA polymerase A). NRPA2; NUCLEAR RNA POLYMERASE A2
BolC06g048230.2J	Nucleus	17	AT1G76880.1: DF1 is a putative transcription factor required for the synthesis of seed mucilage polysaccharides. The df1 seeds produce almost 50% less mucilage than wild-type, but show less severe defects than the myb5 and ttg2 mutants. DF1
BolC07g007990.2J	Cytoplasm Nucleus	17	AT2G15430.3: Encodes a non-catalytic subunit of nuclear DNA-dependent RNA polymerases II, IV and V; homologous to budding yeast RPB3 and the E. coli RNA polymerase alpha subunit. A closely related paralog, encoded by At2g15400, can substitute for At2g15430 in the context of Pol V.
BolC09g017880.2J	Nucleus	17	AT1G62970.2: SDJ3 functions partially redundantly with SDJ1 and SDJ2 and interacts with SUVH1 and SUVH3 to form a SUVH-SDJ complex. The complex binds promoters with DNA methylation and mediates transcriptional activation of promoter methylated genes. SDJ3; SUVH1/3-INTERACTING DNAJ DOMAIN-CONTAINING PROTEIN 3
BolC01g044330.2J	Nucleus	16	AT3G18600.1: P-loop containing nucleoside triphosphate hydrolases superfamily protein;(source:Araport11)
BolC02g035890.2J	Cytoplasm Nucleus	15	AT1G80670.1: This gene is predicted to encode a protein with a DWD motif. It can bind to DDB1a in Y2H assays, and may be involved in the formation of a CUL4-based E3 ubiquitin ligase RAE1; RNA EXPORT FACTOR 1
BolC03g050350.2J	Nucleus	15	AT2G05120.1: Nucleoporin, Nup133/Nup155-like protein;(source:Araport11) NUP133
BolC03g070630.2J	Nucleus	15	AT1G29320.1: Transducin/WD40 repeat-like superfamily protein;(source:Araport11)

BolC06g047330.2J	Nucleus	15	AT1G76110.1: HMG (high mobility group) box protein with ARID/BRIGHT DNA-binding domain-containing protein;(source:Araport11)
BolC07g013890.2J	Nucleus	15	AT3G23620.1: BRIX domain containing protein, similar to RNA biogenesis factors in yeast. Binds rRNA and likely also functions in RNA biogenesis in Arabidopsis. Essential gene, mutants are embryo lethal and does not transmit well through the gametophyte. ARABIDOPSIS HOMOLOG OF YEAST RPF2; ARPF2
BolC09g007910.2J	Nucleus	15	AT5G62190.1: DEAD/DEAH box RNA helicase PRH75 ATRH7; PRH75
BolC01g042990.2J	Cytoplasm Nucleus	14	AT3G19895.1: RING/U-box superfamily protein;(source:Araport11)
BolC01g048820.2J	Cytoplasm Nucleus	14	AT3G13920.1: eukaryotic translation initiation factor 4A-1 EIF4A1; EUKARYOTIC TRANSLATION INITIATION FACTOR 4A1; RH4; TIF4A1
BolC04g049460.2J	Nucleus	14	AT2G22300.1: Encodes a putative CAM binding transcription factor. Loss of function mutations show enhanced resistance to fungal and bacterial pathogens suggesting that CAMTA functions to suppress defense responses.It acts in the cold response pathway, it can bind to and activate the expression of DREB1 genes. CALMODULIN-BINDING TRANSCRIPTION ACTIVATOR 3; CAMTA3; SIGNAL RESPONSIVE 1; SR1
BolC05g042480.2J	Nucleus	14	AT3G20780.1: Encodes putative eukaryotic homolog of archaeobacterial topoisomerase VI subunit B, TOP6B. Is essential for endoreduplication and is involved in cell expansion and cell proliferation. The hlq (harlequin) dwarf mutant has fewer root hair and leaf trichome. It has abnormal epidermal cell and accumulates callose. ATTOP6B; BIN3; BRASSINOSTEROID INSENSITIVE 3; ELONGATED HYPOCOTYL 6; HARLEQUIN; HLQ; HYP6; RHL3; ROOT HAIRLESS 3; TOP6B; TOPOISOMERASE 6 SUBUNIT B
BolC05g049350.2J	Nucleus	14	AT3G16940.3: calmodulin-binding transcription activator;(source:Araport11) CALMODULIN-BINDING TRANSCRIPTION ACTIVATOR 6; CAMTA6
BolC05g053280.2J	Nucleus	14	AT3G13350.1: HMG (high mobility group) box protein with ARID/BRIGHT DNA-binding domain-containing protein;(source:Araport11)
BolC08g027130.2J	Nucleus	14	AT1G18610.2: Galactose oxidase/kelch repeat superfamily protein, induced by calcium.
BolC09g055730.2J	Nucleus	14	AT5G17510.2: mediator of RNA polymerase II transcription subunit-like protein;(source:Araport11) BRAHMA-INTERACTING PROTEIN 2; BRIP2
BolC01g005690.2J	Nucleus	13	AT4G32910.1: SBB1 is a putative nucleoporin that is localized to the nuclear envelope. SBB1 was identified in a screen for supressors of BAK1, BKK1 mediated cell death. NUCLEOPORIN 85; NUP85; SBB1; SUPPRESSOR OF BAK1 BKK1
BolC01g038620.2J	Nucleus	13	AT3G23620.1: BRIX domain containing protein, similar to RNA biogenesis factors in yeast. Binds rRNA and likely also functions in RNA biogenesis in Arabidopsis. Essential gene, mutants are embryo lethal and does not transmit well through the gametophyte. ARABIDOPSIS HOMOLOG OF YEAST RPF2; ARPF2
BolC02g007140.2J	Nucleus	13	AT5G15750.1: Alpha-L RNA-binding motif/Ribosomal protein S4 family protein;(source:Araport11)
BolC02g035510.2J	Nucleus	13	AT1G80930.1: MIF4G domain-containing protein / MA3 domain-containing protein;(source:Araport11)

BolC02g060880.2J	Nucleus	13	AT5G62190.1: DEAD/DEAH box RNA helicase PRH75 ATRH7; PRH75
BolC03g083850.2J	Nucleus	13	AT1G51720.4: Amino acid dehydrogenase family protein;(source:Araport11)
BolC05g039240.2J	Nucleus	13	AT3G22990.1: Armadillo-repeat containing protein. Involved in leaf and flower development. Located in nucleus. Broadly expressed throughout vegetative and floral tissues. LFR is functionally associated with AS2 to mediate leaf development. LEAF AND FLOWER RELATED; LFR
BolC06g050210.2J	Cytoplasm Nucleus	13	AT1G79280.3: Encodes a 237-kDA protein with similarity to vertebrate Tpr, a long coiled-coil proteins of nuclear pore inner basket filaments. It is localized to the inner surface of the nuclear envelope and is a component of the nuclear pore-associated steps of sumoylation and mRNA export in plants. Mutations affect flowering time regulation and other developmental processes. Probably acts in the same pathway as ESD4 in affecting flowering time, vegetative and inflorescence development. NUA; NUCLEAR PORE ANCHOR
BolC06g050590.2J	Nucleus	13	AT1G80930.1: MIF4G domain-containing protein / MA3 domain-containing protein;(source:Araport11)
BolC08g020690.2J	Nucleus	13	AT1G09060.2: JMJ24 is a nuclear localized JmjC domain containing protein. It has been shown to bind to transcribed regions AtSN1 and solo LTR and the promoter of SDC. JMJ24 appears to regulate basal levels of transcription of silenced loci in part by controlling methylation in heterochromatic regions. JMJ24
BolC01g018630.2J	Nucleus	12	AT4G24270.4: A locus involved in embryogenesis. Mutations in this locus result in embryo lethality. EMB140; EMBRYO DEFECTIVE 140
BolC01g051550.2J	Nucleus	12	AT3G11100.1: SANT and trihelix-domain protein. Interacts with agrobacterium virulence protein VirF. It also plays a role in regulation of histone acetylation during ethylene signaling. It binds EIN2 and EIN3 and histone H3. EIN2 NUCLEAR ASSOCIATED PROTEIN 1; ENAP1; VFP3
BolC05g020070.2J	Nucleus	12	AT1G21700.1: a member of the Arabidopsis SWI3 gene family. Protein physically interacts with ATSWI3B and ATSWI3A, the other two members of the SWI3 family. Homologous to yeast SWI3 & RSC8, components of the SWI/SNF and RSC chromatin remodeling complexes. Referred to as CHB3 in Zhou et al (2003). ATSWI3C; CHB4; SWI3C; SWITCH/SUCROSE NONFERMENTING 3C
BolC05g060850.2J	Nucleus	12	AT3G04740.1: encodes a protein with similarities to subunits of the Mediator complex, required for RNA polymerase II recruitment at target promoters in response to specific activators. Lines carrying loss of function mutations in the gene have reduced cell numbers in aerial organs. On the other hand, lines overexpressing the gene have increased number of small cells in clusters, suggesting cell division is more unsynchronized in the overexpressors. Required for expression of CBF-controlled cold-responsive genes. Required for recruitment of the Mediator complex and RNA polymerase II to CBF-controlled cold-responsive genes. Required for expression of some dark-upregulated genes. ARABIDOPSIS MEDIATOR COMPONENTS 14; ATMED14; MED14; MEDIATOR COMPONENTS 14; STRUWWELPETER; SWP
BolC09g019770.2J	Cytoplasm Nucleus	12	AT1G60850.1: DNA-directed RNA polymerase family protein;(source:Araport11) AAC42; ATRPAC42
BolC01g040730.2J	Nucleus	11	AT3G21810.2: Zinc finger C-x8-C-x5-C-x3-H type family protein;(source:Araport11)

BolC01g044750.2J	Cytoplasm Nucleus	11	AT3G18165.1: Encodes MOS4 (Modifier of snc1, 4), a nuclear protein homologous to human Breast Cancer-Amplified Sequence (BCAS2). MOS4 interacts with AtCDC5 and PRL1. All three proteins are essential for plant innate immunity. MODIFIER OF SNC1,4; MOS4
BolC02g017090.2J	Nucleus	11	AT5G55300.1: Encodes a type-I DNA topoisomerase I. Disruptions in this gene affect phyllotaxis and plant architecture suggesting that the gene plays a critical role in the maintenance of a regular pattern of organ initiation. Isolated as a protein oxidized during seed germination; proteomics approach revealed differences in de novo synthesis levels of this protein in condition with vs. without salicylic acid in the period from 0 to 40 hrs. following seed imbibition. Functions in stem cell maintenance at all stages of shoot and floral meristems and in the regulation of gene silencing. DNA TOPOISOMERASE I ALPHA; FAS5; FASCIATA5; MGO1; MGOUN 1; TOP1; TOP1ALPHA; TOPOISOMERASE 1
BolC03g007890.2J	Nucleus	11	AT5G15750.1: Alpha-L RNA-binding motif/Ribosomal protein S4 family protein;(source:Araport11)
BolC03g010480.2J	Cytoplasm Nucleus	11	AT5G19990.2: 26S proteasome AAA-ATPase subunitThe mRNA is cell-to-cell mobile.
BolC03g045920.2J	Nucleus	11	AT3G18990.1: Required for vernalization. Essential for the complete repression of FLC in vernalized plants. Required for the methylation of histone H3 REDUCED VERNALIZATION RESPONSE 1; REM39; REPRODUCTIVE MERISTEM 39; VRN1
BolC03g060270.2J	Nucleus	11	AT3G49000.1: RNA polymerase III subunit RPC82 family protein;(source:Araport11)
BolC03g085490.2J	Nucleus	11	AT1G54060.1: Member of the trihelix DNA binding protein family. Nuclear localized. Involved in repressing seed maturation genes during seed germination and seedling development. 6B-INTERACTING PROTEIN 1-LIKE 1; ASIL1
BolC05g009970.2J	Nucleus	11	AT1G13030.1: Encodes a plant coilin, a protein that in other organisms is a major structural scaffolding protein necessary for Cajal body formation, composition and activity. It has been shown to bind both U1 and U1 snRNAs in vitro. ATCOILIN; COILIN
BolC06g018640.2J	Nucleus	11	AT5G40480.1: embryo defective 3012;(source:Araport11) EMB3012; EMBRYO DEFECTIVE 3012
BolC08g010870.2J	Nucleus	11	AT1G33240.2: Encodes a plant transcriptional activator that contains two separate, but similar, trihelix DNA-binding domains, similar to GT-2. Gene is expressed in all aerial parts of the plant, with higher level of expression in siliques. At-GTL2 was thought to be a duplicated copy of this gene but is likely to be a cloning artefact, the result of a chimeric clone. Regulates ploidy-dependent cell growth in trichome.
BolC08g029620.2J	Nucleus	11	AT1G21700.1: a member of the Arabidopsis SWI3 gene family. Protein physically interacts with ATSWI3B and ATSWI3A, the other two members of the SWI3 family. Homologous to yeast SWI3 & RSC8, components of the SWI/SNF and RSC chromatin remodeling complexes. Referred to as CHB3 in Zhou et al (2003). ATSWI3C; CHB4; SWI3C; SWITCH/SUCROSE NONFERMENTING 3C
BolC01g000700.2J	Nucleus	10	AT4G39680.1: SAP domain-containing protein;(source:Araport11)
BolC01g022940.2J	Cytoplasm Nucleus	10	AT4G27740.1: Yippee family putative zinc-binding protein;(source:Araport11)

BolC01g024040.2J	Nucleus	10	AT4G17060.1: Encodes one of the FRI interacting proteins: FRIGIDA INTERACTING PROTEIN 1 (FIP1)/At2g06005, FIP2/ At4g17060. FRI (At4G00650) is a major determinant of natural variation in Arabidopsis flowering time. FIP2; FRIGIDA INTERACTING PROTEIN 2
BolC01g025870.2J	Nucleus	10	AT4G15570.1: Similar to yeast Sen1 (splicing endonuclease 1)helicase protein. Involved in female gametophyte development. The mRNA is cell-to-cell mobile. MAA3; MAGATAMA 3
BolC01g030070.2J	Nucleus	10	AT3G48800.1: Sterile alpha motif (SAM) domain-containing protein;(source:Araport11)
BolC01g049090.2J	Nucleus	10	AT3G13670.1: MUT9-like protein kinase. Contributes to phosphorylation of photoexcited CRY2. Interaction with CRY2 occurs via the non catalytic PPKC domain.MLK4 phosphorylates the conserved H2A serine 95 residue. Synthetic mutants that cannot phosphorylate H2AS95 fail to complement the late flowering phenotype suggesting that MLK4 promotes long day flowering via phosphorylation.MLK4 is required for H2A295 phosphorylation of GI. AEL2; ARABIDOPSIS EL1-LIKE 2; MLK4; MUT9P-LIKE-KINASE 4; PHOTOREGULATORY PROTEIN KINASE 1; PPK1
BolC03g002130.2J	Nucleus	10	AT5G04940.1: Encodes a SU(VAR)3-9 homolog, a SET domain protein. Known SET domain proteins are involved in epigenetic control of gene expression and act as histone methyltransferases. There are 10 SUVH genes in Arabidopsis and members of this subfamily of the SET proteins have an additional conserved SRA domain. SUVH1 has been shown to have a preference for binding methylated DNA. SU(VAR)3-9 HOMOLOG 1; SUVH1
BolC03g035720.2J	Nucleus	10	AT3G01610.1: AAA-type ATPase - Over 90% homologous to CDC48a CDC48C; CELL DIVISION CYCLE 48C; EMB1354; EMBRYO DEFECTIVE 1354
BolC03g040340.2J	Nucleus	10	AT3G10650.1: Encodes a nucleoporin involved in mRNA export from the nucleus. It is also involved in the regulation of nuclear morphology. ATNUP1; NUP1
BolC03g065560.2J	Nucleus	10	AT3G45830.1: nuclear factor kappa-B-binding-like protein;(source:Araport11)
BolC03g075230.2J	Nucleus	10	AT4G35800.1: Encodes the unique largest subunit of nuclear DNA-dependent RNA polymerase II; the ortholog of budding yeast RPB1 and a homolog of the E. coli RNA polymerase beta prime subunit. NRPB1; RNA POLYMERASE II LARGE SUBUNIT; RNA_POL_II_LS; RNA_POL_II_LSRNA_POL_II_LS; RPB1
BolC04g050970.2J	Nucleus	10	AT2G23740.6: Encodes a SET-domain protein SUVR5 that mediates H3K9me2 deposition and silencing at stimulus response genes in a DNA methylation-independent manner.
BolC05g004570.2J	Nucleus	10	AT1G06460.1: ACD32.1 encodes an alpha-crystallin domain containing protein with homology to small heat shock proteins. ACD31.2; ACD32.1; ALPHA-CRYSTALLIN DOMAIN 31.2; ALPHA-CRYSTALLIN DOMAIN 32.1
BolC05g018900.2J	Nucleus	10	AT1G20910.1: ARID/BRIGHT DNA-binding domain-containing protein;(source:Araport11) ARID3; AT RICH INTERACTION DOMAIN 3

BolC05g050770.2J	Nucleus	10	AT1G52930.1: Encodes one of two Arabidopsis orthologs of yeast BRX1, a protein involved in maturation of the large ribosomal subunit. The proteins are mainly localized in nucleolus. Mutant plants are affected in pre-rRNA processing. ARABIDOPSIS HOMOLOGUE OF YEAST BRX1 2; ATBRX1-2
BolC05g056070.2J	Nucleus	10	AT3G10480.1: Encodes a NAC transcription factor that physically associates with the histone H3K4 demethylase JMJ14 and through that association is involved in transcriptional repression and flowering time control. It binds the NAC-binding site, the Mitochondrial Dysfunction Motif. ANAC050; NAC DOMAIN CONTAINING PROTEIN 50; NAC050; NAC50
BolC06g023580.2J	Nucleus	10	AT3G57660.2: Encodes a subunit of RNA polymerase I (aka RNA polymerase A).The mRNA is cell-to-cell mobile.
BolC06g024540.2J	Nucleus	10	AT3G58660.1: Ribosomal protein L1p/L10e family;(source:Araport11)
BolC06g028110.2J	Nucleus	10	AT1G80680.1: Mutant has early-flowering phenotype, encodes a putative nucleoporin. Required for the activation of downstream defense pathways by the snc1 mutation. Involved in basal resistance against bacterial pathogens. MODIFIER OF SNC1,3; MOS3; NUP96; PRE; PRECOCIOUS; SAR3; SUPPRESSOR OF AUXIN RESISTANCE 3
BolC06g048250.2J	Nucleus	10	AT1G76890.2: encodes a plant trihelix DNA-binding protein AT-GT2; GT2
BolC07g027390.2J	Nucleus	10	AT5G45140.1: Encodes a subunit of RNA polymerase III (aka RNA polymerase C). NRPC2; NUCLEAR RNA POLYMERASE C2
BolC09g001140.2J	Nucleus	10	AT4G01560.1: Ribosomal RNA processing Brix domain protein;(source:Araport11) MATERNAL EFFECT EMBRYO ARREST 49; MEE49
BolC09g017660.2J	Nucleus	10	AT4G00930.3: Encodes COP1-interacting protein CIP4.1.
BolC09g053900.2J	Nucleus	10	AT5G18620.1: Encodes a member of the A. thaliana imitation switch (AtISWI) subfamily of chromatin remodeling factors. Double mutation in CHR17 and CHR11 results in the loss of the evenly spaced nucleosome pattern in gene bodies, but does not affect nucleosome density. CHR17; CHROMATIN REMODELING FACTOR17
BolC09g056440.2J	Nucleus	10	AT5G16750.1: Encodes a nucleolar localized WD-40 repeat protein that is preferentially expressed in dividing cells and is required for regulated division planes and embryo development. TORMOZEMBRYO DEFECTIVE; TOZ
BolC01g019780.2J	Nucleus	9	AT4G25340.2: Encodes a member of the FKBP-type immunophilin family that functions as a histone chaparone. Binds to 18S rDNA and represses its expression. The N-terminal nucleoplasmin domain interacts with H2A/H2B and H3/H4 histone oligomers, individually, as well as simultaneously, suggesting two different binding sites for H2A/H2B and H3/H4. FK506 BINDING PROTEIN 53; FKBP53
BolC01g036020.2J	Cytoplasm Nucleus	9	AT1G60850.1: DNA-directed RNA polymerase family protein;(source:Araport11) AAC42; ATRPAC42

BolC01g047970.2J	Nucleus	9	AT3G42170.1: transposase-like gene with conserved domains from the family of hAT transposases that includes hobo from <i>Drosophila melanogaster</i> , Activator (Ac) from maize, and Tam3 from snapdragon but lacks several amino acids known to be essential for Ac transposition ⁵ . The DAYSLEEPER gene lacks 8 bp duplications and TIRs (a common feature of transcriptionally silent hAT transposases), however, DAYSLEEPER expression was detected, and several expressed sequence tags are available. The expression seems to be under the control of factors determining the circadian rhythm. DAYSLEEPER was isolated as a factor binding to a motif (Kubox1) present in the upstream region of the Arabidopsis DNA repair gene Ku70. Mutant plants lacking DAYSLEEPER or strongly overexpressing this gene do not develop in a normal manner. DAYSLEEPER
BolC01g048800.2J	Nucleus	9	AT3G13940.1: DNA binding / DNA-directed RNA polymerase;(source:Araport11)
BolC01g056040.2J	Cytoplasm Nucleus	9	AT3G03920.1: H/ACA ribonucleoprotein complex, subunit Gar1/Naf1 protein;(source:Araport11)
BolC02g010440.2J	Nucleus	9	AT5G20200.1: nucleoporin-like protein;(source:Araport11)
BolC03g005950.2J	Nucleus	9	AT5G12220.2: las1-like family protein;(source:Araport11)
BolC03g023630.2J	Nucleus	9	AT2G28290.1: Encodes a SWI2/SNF2-like protein in the SNF2 subclass. Homozygous plants with null mutations exhibit premature termination of the meristem and carpelloid structures from the inflorescence meristem. Co-activator of floral homeotic gene expression. Acts with LFY to regulate shoot apical meristem identity. Required for meristem maintenance. Regulates flowering under a non-inductive photoperiod. It promotes the expression of CUC2 during cotyledon boundary formation. Affects reproductive shoot apical meristem function by regulating the expression of WUS. In ChIP experiments SYD binds to WUS promoter. Present as two forms in the nucleus, full-length and truncated, with the latter apparently lacking the C-terminal domain. The ratio of the two forms differs in juvenile and in adult tissues. The C-terminal domain is not required for activity. The mRNA is cell-to-cell mobile. CHR3; CHROMATIN REMODELING COMPLEX SUBUNIT R 3; SPLAYED; SYD
BolC03g047990.2J	Cytoplasm Nucleus	9	AT3G22320.1: Non-catalytic subunit common to DNA-dependent RNA polymerases I, II, III and IV; homologous to budding yeast RPB5. ATRPABC24.3; NRPB5; NRPD5; RNA POLYMERASE II FIFTH LARGEST SUBUNIT, A; RPB5A
BolC03g049250.2J	Nucleus	9	AT3G24490.1: Alcohol dehydrogenase transcription factor Myb/SANT-like family protein;(source:Araport11)
BolC05g000490.2J	Nucleus	9	AT1G01510.1: Encodes a homolog of human CtBP. Mutant has longer and thicker leaves than wild type. Involved in controlling polar cell expansion in the leaf width direction. It has been shown to localize to cytosolic stress granules and is involved in their formation. AN; ANGUSTIFOLIA; DETORQUEO; DOQ
BolC05g009820.2J	Nucleus	9	AT1G13220.3: Encodes a nuclear coiled-coil protein related to the carrot peripheral nuclear protein NMCP1 that is involved in the determination of plant nuclear structure. Member of a small gene family in Arabidopsis containing 4 proteins (LNC1-4 or CRWN 1-4) with redundant functions in protection from oxidative damage, control of nuclear morphology and degradation of ABI5.
BolC05g045940.2J	Nucleus	9	AT3G18790.1: pre-mRNA-splicing factor ISY1-like protein;(source:Araport11)

BolC06g029930.2J	Nucleus	9	AT1G77030.1: Required for functional maturation of male and female gametophytes. DEAD-BOX RNA HELICASE 29; RH29
BolC06g045140.2J	Nucleus	9	AT1G73720.1: Encodes SMU1, a protein involved in RNA splicing. SMU1; SUPPRESSORS OF MEC-8 AND UNC-52 1
BolC08g015680.2J	Nucleus	9	AT4G16630.1: DEA(D/H)-box RNA helicase family protein;(source:Araport11)
BolC08g017910.2J	Cytoplasm Nucleus	9	AT4G25550.1: Cleavage/polyadenylation specificity factor, 25kDa subunit;(source:Araport11) INVOLVED IN RRNA PROCESSING 9; IRP9
BolC09g024700.2J	Nucleus	9	AT5G44800.1: Interacts with transcription factors involved in floral meristem identity and affects the expression of key floral regulators. Affects H3K27me3 and H3K4me3 levels at a subset of loci in the genome. CHR4; CHROMATIN REMODELING 4; PICKLE RELATED 1; PKR1
BolC09g042390.2J	Nucleus	9	AT5G54910.1: DEA(D/H)-box RNA helicase family protein;(source:Araport11)
BolC09g067000.2J	Nucleus	9	AT5G04940.1: Encodes a SU(VAR)3-9 homolog, a SET domain protein. Known SET domain proteins are involved in epigenetic control of gene expression and act as histone methyltransferases. There are 10 SUVH genes in Arabidopsis and members of this subfamily of the SET proteins have an additional conserved SRA domain. SUVH1 has been shown to have a preference for binding methylated DNA. SU(VAR)3-9 HOMOLOG 1; SUVH1
BolC01g013200.2J	Nucleus	8	AT4G19610.1: nucleotide/nucleic acid binding protein;(source:Araport11)
BolC01g014330.2J	Nucleus	8	AT4G21110.2: G10 family protein;(source:Araport11)
BolC01g045980.2J	Nucleus	8	AT3G16840.1: P-loop containing nucleoside triphosphate hydrolases superfamily protein;(source:Araport11)
BolC01g049740.2J	Nucleus	8	AT3G13200.1: Associates with core components of the Arabidopsis NineTeen complex (NTC) and its loss leads to inefficient splicing. CWC15; EMB2769; EMBRYO DEFECTIVE 2769
BolC01g052560.2J	Cytoplasm Nucleus	8	AT3G09840.1: Encodes a cell division cycle protein, a member of AAA-type ATPases gene family. Expressed throughout the plant in regions of cell division. Within the cell, sub-cellular localization varies depending on the stage of the cell cycle. Mutants in which the expression of CDC48A is altered show defects in cytokinesis, cell expansion and cell differentiation. The mRNA is cell-to-cell mobile. ATCDC48; ATCDC48A; CDC48; CDC48A; CELL DIVISION CYCLE 48
BolC02g060250.2J	Nucleus	8	AT5G61150.1: Encodes highly hydrophilic protein involved in positively regulating FLC expression. Mutants are early flowering and show a loss of FLC expression in the absence of cold. Member of PAF-C complex. VERNALIZATION INDEPENDENCE 4; VIP4
BolC02g062130.2J	Nucleus	8	AT5G64360.5: EIP9 interacts with EMF1 to regulate flowering. It functions partially redundantly with SDJ2 and SDJ3 and interacts with SUVH1 and SUVH3 to form a SUVH-SDJ complex. The complex binds promoters with DNA methylation and mediates transcriptional activation of promoter methylated genes. DNAJ1; SDJ1; SUVH1/3-INTERACTING DNAJ DOMAIN-CONTAINING PROTEIN 1

BolC03g026570.2J	Nucleus	8	AT2G43650.1: SAS10/C1D family protein. Loss of function mutants are embryo lethal. Ubiquitously expressed, with preference for tissues undergoing rapid cellular growth and differentiation. EMB2777; EMB2796; EMBRYO DEFECTIVE 2777; THAL; THALLO
BolC04g000500.2J	Nucleus	8	AT2G47980.1: Essential to the monopolar orientation of the kinetochores during meiosis. ATSCC3; SCC3; SISTER-CHROMATID COHESION PROTEIN 3
BolC04g018470.2J	Nucleus	8	AT2G31320.1: Encodes a poly(ADP-ribose) polymerase. PARP1; POLY(ADP-RIBOSE) POLYMERASE 1
BolC05g048010.2J	Nucleus	8	AT5G25470.3: AP2/B3-like transcriptional factor family protein;(source:Araport11)
BolC05g061190.2J	Cytoplasm Nucleus	8	AT5G18380.1: Ribosomal protein S5 domain 2-like superfamily protein;(source:Araport11)
BolC06g007980.2J	Nucleus	8	AT1G52980.1: Encodes a GTPase that belongs to the subfamily of YlqF/YawG GTPases. Functions in Pre-60S ribosomal subunit maturation. The mRNA is cell-to-cell mobile. ATNUG2; NUCLEAR/NUCLEOLAR GTPASE 2; NUG2
BolC06g029820.2J	Nucleus	8	AT1G77310.2: wound-responsive family protein;(source:Araport11)
BolC06g033990.2J	Nucleus	8	AT3G63500.1: Encodes a PHD-finger protein that, with TTA2, is redundantly required for MP-dependent embryonic root meristem initiation. OBE4; TITANIA 2; TTA2
BolC06g044030.2J	Nucleus	8	AT1G72440.1: Encodes SLOW WALKER2 (SWA2), a NOC1/Mak21 homologue. Essential for coordinated cell cycle progression during female gametophyte development. EDA25; EMBRYO SAC DEVELOPMENT ARREST 25; SLOW WALKER2; SWA2
BolC07g010930.2J	Nucleus	8	AT1G17450.3: B-block binding subunit of TFIIC;(source:Araport11)
BolC09g012420.2J	Nucleus	8	AT2G17250.1: Encodes a nucleolar protein that is a ribosome biogenesis co-factor. Mutants display aberrant RNA processing and homozygous embryos arrest in the globular stage of development. EMB2762; EMBRYO DEFECTIVE 2762; NOC4; NUCLEOLAR COMPLEX ASSOCIATED 4
BolC09g037330.2J	Nucleus	8	AT4G06634.3: Encodes an ABA responsive C2H2-type zinc finger transcription factor with both transcriptional repression and activation domains, that binds a G-rich, 11-bp DNA-binding motif. YY1 binds to the promoter of ABR1 and disruption represses ABA- and salt-induced ABR1 expression. ATYY1; YIN YANG 1; YY1
BolC09g043650.2J	Nucleus	8	AT5G55660.1: DEK domain-containing chromatin associated protein;(source:Araport11)
BolC09g050410.2J	Nucleus	8	AT5G22650.1: Encodes a member of a plant-specific class of histone deacetylases. Controls the development of adaxial/abaxial leaf polarity. Its mRNA is widely expressed in stems, leaves, flowers and young siliques. Plant lines expressing RNAi constructs directed against this gene showed a marked reduction in agrobacterium-mediated root transformation. ARABIDOPSIS HISTONE DEACETYLASE 2; ATHD2; ATHD2B; HD2; HD2B; HDA4; HDT02; HDT2; HISTONE DEACETYLASE 2; HISTONE DEACETYLASE 2B
BolC01g012100.2J	Cytoplasm Nucleus	7	AT4G18465.1: RNA helicase family protein;(source:Araport11)
BolC01g034330.2J	Nucleus	7	AT1G58025.6: DNA-binding bromodomain-containing protein;(source:Araport11)
BolC02g004880.2J	Nucleus	7	AT5G11600.1: hypothetical protein;(source:Araport11)

BolC02g025570.2J	Nucleus	7	AT1G69070.1: nucleolar-like protein;(source:Araport11)
BolC02g038170.2J	Nucleus	7	AT4G02550.2: Myb/SANT-like DNA-binding domain protein;(source:Araport11)
BolC03g030720.2J	Nucleus	7	AT4G07410.1: Encodes a WD-40 protein expressed both during embryo development and postembryonically in the SAM and RAM that functions in the auxin pathway, integrating auxin signaling in the organization and maintenance of the SAM and RAM. PCN; POPCORN
BolC03g081660.2J	Nucleus	7	AT4G31430.1: Encodes a plant-specific protein that physically interacts with CRWN1 and its homolog CRWN4 and localizes at the inner nuclear membrane. KAKU4 deforms the nuclear envelope in a dose-dependent manner, in association with nuclear membrane invagination and stack formation. (JAPANESE FOR NUCLEUS) 4; KAKU4
BolC04g006660.2J	Nucleus	7	AT2G40360.2: Encodes BOP1, an ortholog of Block of cell proliferation (BOP) protein. A T-DNA null allele of the BOP1 gene is lethal, and a 50% decrease in transcript accumulation is sufficient to cause severe developmental defects linked to defective cell division.
BolC04g013000.2J	Nucleus	7	AT2G35940.1: Encodes a member of the BEL-like homeodomain protein family. Ecotopic expression in the embryo sac leads to defects in nuclear migration and cellularization and embryo sacs with multiple egg cells. Loss of function alleles have no female gametophyte defects. The ecotopic expression phenotype requires KNAT3 because it can be suppressed by loss of KNAT3 function alleles. Localized to the nucleus but interaction with OFP1 relocates it to the cytoplasm. BEL1-LIKE HOMEODOMAIN 1; BLH1; EDA29; EMBRYO SAC DEVELOPMENT ARREST 29
BolC04g036410.2J	Cytoplasm Nucleus	7	AT3G55620.1: Translation initiation factor IF6;(source:Araport11) EIF6A; EMB1624; EMBRYO DEFECTIVE 1624; EUKARYOTIC INITIATION FACOR 6A
BolC05g013100.2J	Nucleus	7	AT1G15440.2: Encodes a nucleolar protein that is a ribosome biogenesis co-factor. Mutants display aberrant RNA processing and female gametophyte development. ATPWP2; PERIODIC TRYPTOPHAN PROTEIN 2; PWP2
BolC05g047300.2J	Nucleus	7	AT3G23780.1: This gene encodes the second largest, catalytic subunit of the nuclear DNA-dependent RNA polymerase IV (aka RNA polymerase D). The NRPD2 protein is found at nuclear foci that overlap or are adjacent to chromocentromeres but are not fully coincident with chromocentromeres. The loss of NRPD2 leads to the loss of cytosine methylation at pericentromeric 5S genes and AtSN1 retroelements but has no discernible effect on centromere repeat methylation. This suggests that Pol IV primarily affects facultative heterochromatin rather than constitutive heterochromatin. DEFECTIVE IN MERISTEM SILENCING 2; DMS2; DRD2; NRPD2; NRPD2A; NRPE2; NUCLEAR RNA POLYMERASE D2A; OCP1; OVEREXPRESSOR OF CATIONIC PEROXIDASE 1
BolC06g034270.2J	Nucleus	7	AT1G23280.1: MAK16 protein-like protein;(source:Araport11)
BolC06g050680.2J	Nucleus	7	AT1G80810.5: One of 5 PO76/PDS5 cohesion cofactor orthologs of Arabidopsis.
BolC07g021960.2J	Nucleus	7	AT1G20910.1: ARID/BRIGHT DNA-binding domain-containing protein;(source:Araport11) ARID3; AT RICH INTERACTION DOMAIN 3

BolC08g011420.2J	Nucleus	7	AT1G32750.1: This gene is predicted to encode a histone acetyltransferase. Five lines with RNAi constructs directed against HAF1 grow normally and can produce root calli, but have defects in agrobacterium-mediated transformation. GTD1; HAC13; HAF01; HAF1; HISTONE ACETYLTRANSFERASE OF THE CBP FAMILY 13; HISTONE ACETYLTRANSFERASE OF THE TAFII250 FAMILY 1; TAF1; TBP-ASSOCIATED FACTOR 1
BolC08g012230.2J	Nucleus	7	AT5G35330.2: Protein containing methyl-CpG-binding domain.Has sequence similarity to human MBD proteins. MBD02; MBD2; METHYL-CPG-BINDING DOMAIN PROTEIN 02; METHYL-CPG-BINDING DOMAIN PROTEIN 2
BolC08g019060.2J	Nucleus	7	AT4G28200.1: U3 small nucleolar RNA-associated-like protein;(source:Araport11)
BolC08g027370.2J	Nucleus	7	AT1G18950.3: DDT domain superfamily;(source:Araport11) DDR4; DDT-RELATED PROTEIN4
BolC08g052200.2J	Nucleus	7	AT1G15940.1: One of 5 PO76/PDS5 cohesion cofactor orthologs of Arabidopsis. ATPDS5E; PDS5E
BolC09g007560.2J	Nucleus	7	AT5G61150.1: Encodes highly hydrophilic protein involved in positively regulating FLC expression. Mutants are early flowering and show a loss of FLC expression in the absence of cold. Member of PAF-C complex. VERNALIZATION INDEPENDENCE 4; VIP4
BolC09g042840.2J	Nucleus	7	AT5G55310.1: Encodes one of two Arabidopsis type-I DNA topoisomerase I genes. Reducing the level of expression of this gene in a toplalpha (At5g55300) mutant background causes seedling lethality. DNA TOPOISOMERASE 1 BETA; TOP1; TOP1BETA; TOPOISOMERASE 1
BolC09g046130.2J	Nucleus	7	AT5G57580.1: Calmodulin-binding protein;(source:Araport11)
BolC09g056890.2J	Nucleus	7	AT5G16270.1: Encodes a SCC1/REC8 ortholog that may be involved in mitosis and may represent a mitotic cohesin. Plays a role in somatic DNA double strand break damage repair. The mRNA is cell-to-cell mobile. ARABIDOPSIS HOMOLOG OF RAD21 3; ATRAD21.3; SISTER CHROMATID COHESION 1 PROTEIN 4; SYN4
BolC09g059120.2J	Nucleus	7	AT5G13950.3: nuclear factor kappa-B-binding protein;(source:Araport11)
BolC01g048620.2J	Nucleus	6	AT3G14120.1: nuclear pore complex protein;(source:Araport11) NUP107
BolC01g055440.2J	Nucleus	6	AT3G04590.2: AHL proteins contain two conserved structural units, the AT-hook motif and DUF296 domain. AHL14; AT-HOOK MOTIF NUCLEAR LOCALIZED PROTEIN 14
BolC02g010210.2J	Nucleus	6	AT5G19960.1: RNA-binding (RRM/RBD/RNP motifs) family protein;(source:Araport11)
BolC02g015090.2J	Nucleus	6	AT5G57580.1: Calmodulin-binding protein;(source:Araport11)
BolC02g023250.2J	Nucleus	6	AT1G67230.1: Encodes a nuclear coiled-coil protein related to the carrot peripheral nuclear protein NMCP1 that is involved in the determination of plant nuclear structure. Member of a small gene family in Arabidopsis containing 4 proteins (LNC1-4 or CRWN 1-4) with redundant functions in protection from oxidative damage, control of nuclear morphology and degradation of ABI5. (JAPANESE FOR NUCLEUS) 2; ATLINC1; CROWDED NUCLEI 1; CRWN1; KAKU2; LINC1; LITTLE NUCLEI1

BolC02g035880.2J	Nucleus	6	AT1G80680.1: Mutant has early-flowering phenotype, encodes a putative nucleoporin. Required for the activation of downstream defense pathways by the snc1 mutation. Involved in basal resistance against bacterial pathogens. MODIFIER OF SNC1,3; MOS3; NUP96; PRE; PRECOCIOUS; SAR3; SUPPRESSOR OF AUXIN RESISTANCE 3
BolC02g045370.2J	Nucleus	6	AT5G45140.1: Encodes a subunit of RNA polymerase III (aka RNA polymerase C). NRPC2; NUCLEAR RNA POLYMERASE C2
BolC02g054050.2J	Nucleus	6	AT3G28730.1: encodes a component of the FAcilitates Chromatin Transcription (FACT) complex, SSRP1. Along with STP16 binds to the promoter of FLC. ATHMG; HIGH MOBILITY GROUP; HMG; NFD; NUCLEOSOME/CHROMATIN ASSEMBLY FACTOR D; SSRP1
BolC03g008140.2J	Nucleus	6	AT5G16270.1: Encodes a SCC1/REC8 ortholog that may be involved in mitosis and may represent a mitotic cohesin. Plays a role in somatic DNA double strand break damage repair. The mRNA is cell-to-cell mobile. ARABIDOPSIS HOMOLOG OF RAD21 3; ATRAD21.3; SISTER CHROMATID COHESION 1 PROTEIN 4; SYN4
BolC03g010450.2J	Nucleus	6	AT5G19960.1: RNA-binding (RRM/RBD/RNP motifs) family protein;(source:Araport11)
BolC03g011230.2J	Cytoplasm Nucleus	6	AT5G22040.3: ubiquitin carboxyl-terminal hydrolase;(source:Araport11)
BolC03g056460.2J	Nucleus	6	AT5G64360.5: EIP9 interacts with EMF1 to regulate flowering. It functions partially redundantly with SDJ2 and SDJ3 and interacts with SUVH1 and SUVH3 to form a SUVH-SDJ complex. The complex binds promoters with DNA methylation and mediates transcriptional activation of promoter methylated genes. DNAJ1; SDJ1; SUVH1/3-INTERACTING DNAJ DOMAIN-CONTAINING PROTEIN 1
BolC03g059810.2J	Nucleus	6	AT5G61770.3: A single-copy gene encoding a 346 aa protein with a single Brix domain. Similar to yeast ribosome biogenesis proteins Ssf1/2. PETER PAN-LIKE PROTEIN; PPAN; SNAIL1
BolC03g086300.2J	Nucleus	6	AT1G55540.2: Nuclear pore complex protein;(source:Araport11) EMB1011; EMBRYO DEFECTIVE 1011; LNO1; LONO 1
BolC04g001170.2J	Nucleus	6	AT2G47210.3: myb-like transcription factor family protein;(source:Araport11) ATSWC4; SWC4; SWR1 COMPLEX 4
BolC04g044220.2J	Nucleus	6	AT5G38720.2: RRP7 shares limited sequence similarity to human and yeast RRP7. In Arabidopsis RRP7 functions in 18S ribosomal RNA maturation. RIBOSOMAL RNA PROCESSING7 I; RRP7
BolC04g046000.2J	Cytoplasm Nucleus	6	AT2G44860.2: cytosolic ribosomal protein gene, part of eL24 family RIBOSOMAL PROTEIN L24C; RPL24C
BolC05g003050.2J	Nucleus	6	AT1G04950.2: Encodes one of two Arabidopsis proteins with significant similarity to the histone fold TBP-associated factor TAF6. Mutants are embryo lethal and transmission of the mutant allele through the male gametophyte is significantly reduced. This is due to reduced pollen tube growth of the mutant. ATTA6; EMB2781; EMBRYO DEFECTIVE 2781; TAF6; TAFII59; TATA BOX ASSOCIATED FACTOR II 59; TBP-ASSOCIATED FACTOR 6

BolC05g004180.2J	Nucleus	6	AT1G05910.1: Encodes an acetylated histone-binding protein BRAT1. BRAT1 forms a complex with BRP1 to prevent transcriptional silencing. BRAT1; BROMODOMAIN AND ATPASE DOMAIN-CONTAINING PROTEIN 1
BolC05g016520.2J	Nucleus	6	AT1G18850.1: PCP2 encodes a novel plant specific protein that is co-expressed with components of pre-rRNA processing complex. Co-localizes with NuGWD1 and SWA1. LANT-SPECIFIC COMPONENT OF THE PRE-RRNA PROCESSING COMPLEX2; PCP2
BolC05g021280.2J	Nucleus	6	AT1G22950.1: Belongs to the 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily proteins and contains an oxoglutarate/iron-dependent oxygenase domain (InterPro:IPR005123) of the prolyl 4-hydroxylase, alpha subunit subtype (P4Hc; InterPro:IPR006620), participates in epigenetic repression of flowering genes, works redundantly with CP2 to repress several members of the MADS-box transcription factors family, during vegetative development via histone modification. ICU11; INCURVATA11
BolC05g048480.2J	Nucleus	6	AT3G17590.2: Encodes the Arabidopsis homologue of yeast SNF5 and represents a conserved subunit of plant SWI/SNF complexes. BSH; BUSHY GROWTH; CHE1
BolC05g052410.2J	Nucleus	6	AT3G14120.1: nuclear pore complex protein;(source:Araport11) NUP107
BolC06g023940.2J	Nucleus	6	AT3G58110.2: Encodes an adaptor protein that connects JAZ repressors with the TPR2 co-repressor to suppress jasmonate-responsive anthocyanin accumulation. EAR MOTIF-CONTAINING ADAPTOR PROTEIN; ECAP
BolC06g036670.2J	Nucleus	6	AT1G67310.1: Calmodulin-binding transcription activator protein with CG-1 and Ankyrin domain;(source:Araport11)
BolC06g050050.2J	Nucleus	6	AT1G79150.1: binding protein;(source:Araport11) ATNOC3; NOC3; NUCLEOLAR COMPLEX ASSOCIATED 3
BolC07g043160.2J	Nucleus	6	AT5G60990.1: DEA(D/H)-box RNA helicase family protein;(source:Araport11) RH10; RNA HELICASE10
BolC08g058470.2J	Nucleus	6	AT1G05910.1: Encodes an acetylated histone-binding protein BRAT1. BRAT1 forms a complex with BRP1 to prevent transcriptional silencing. BRAT1; BROMODOMAIN AND ATPASE DOMAIN-CONTAINING PROTEIN 1
BolC09g030910.2J	Cytoplasm Nucleus	6	AT4G22380.1: Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein;(source:Araport11)
BolC09g065330.2J	Nucleus	6	AT5G06350.2: ARM repeat superfamily protein;(source:Araport11)
BolC01g006200.2J	Nucleus	5	AT4G32820.2: Tetratricopeptide repeat (TPR)-like superfamily protein;(source:Araport11) CABIN1; CALCINEURIN BINDING PROTEIN 1
BolC01g006450.2J	Nucleus	5	AT4G32620.2: Polycomb related protein that is part of a protein complex involved in histone deacetylation and heterochromatin silencing. EPCR1
BolC02g004540.2J	Nucleus	5	AT5G11060.1: A member of Class II KN1-like homeodomain transcription factors (together with KNAT3 and KNAT5), with greatest homology to the maize knox1 homeobox protein. Expression regulated by light. Detected in all tissues examined, but most prominent in leaves and young siliques. Transient expression of GFP translational fusion protein suggests bipartite localization in nucleus and cytoplasm. KNAT4 promoter activity showed cell-type

specific pattern along longitudinal root axis; GUS expression pattern started at the elongation zone, predominantly in the phloem and pericycle cells, extending to endodermis toward the base of the root. KNAT4; KNOTTED1-LIKE HOMEBOX GENE 4

BolC03g007390.2J	Nucleus	5	AT5G15020.2: Encodes a homolog of the transcriptional repressor SIN3 (AT1G24190). SIN3-LIKE 2; SNL2
BolC03g013300.2J	Cytoplasm Nucleus	5	AT5G58230.1: Encodes a WD-40 repeat containing protein that functions in chromatin assembly as part of the CAF1 and FIE complex. Mutants exhibit parthenogenetic development that includes proliferation of unfertilized endosperm and embryos. In heterozygous plants 50% of embryos abort. Of the aborted embryos the early aborted class are homozygous and the later aborting class are heterozygotes in which the defective allele is maternally transmitted. Other phenotypes include defects in ovule morphogenesis and organ initiation, as well as increased levels of heterochromatic DNA. MSI1 is needed for the transition to flowering. In Arabidopsis, the three CAF-1 subunits are encoded by FAS1, FAS2 and, most likely, MSI1, respectively. Mutations in FAS1 or FAS2 lead to increased frequency of homologous recombination and T-DNA integration in Arabidopsis. In the ovule, the MSI1 transcripts are accumulated at their highest level before fertilization and gradually decrease after fertilization. MSI1 is biallelically expressed, the paternal allele is expressed in the endosperm and embryo and is not imprinted. MSI1 forms a complex with RBR1 that is required for activation of the imprinted genes FIS2 and FWA. This activation is mediated by MSI1/RBR1 mediated repression of MET1. ARABIDOPSIS MULTICOPY SUPPRESSOR OF IRA1; ATMSI1; MATERNAL EFFECT EMBRYO ARREST 70; MEE70; MSI1; MULTICOPY SUPPRESSOR OF IRA1
BolC03g082940.2J	Nucleus	5	AT1G49950.3: Encodes a telomeric DNA binding protein and Single Myb Histone (SMH) gene family member. In vitro, an N-terminal Myb domain enables it to interact with double-stranded telomeric repeats. Mutations in TRB1 and TRB3 enhance the lhp1 mutant phenotype. Triple mutants are more strongly affected than the respective double mutants with lhp1. TRB1 binds non-H3K27me3 target genes predominantly at the transcription start sites and its presence increases the expression of several of these targets, enriched for functions of primary metabolism. At H3K27me3 target genes, TRB1 binding is more distributed across gene bodies and at extended promoter regions, corresponding to an enrichment of putative binding sites "RMCCTAR". At these genes, TRB1 participates in the repression because several direct targets are further upregulated in trb1 lhp1 double mutants as compared to lhp1 mutants. ATTRB1; TELOMERE REPEAT BINDING FACTOR 1; TRB1

BolC04g037650.2J	Nucleus	5	AT3G54610.1: Encodes a histone acetyltransferase that plays a role in the determination of the embryonic root-shoot axis. It is also required to regulate the floral meristem activity by modulating the extent of expression of WUS and AG. In addition, it is involved in stem cuticular wax accumulation by modulating CER3 expression via H3K9/14 acetylation. In other eukaryotes, this protein is recruited to specific promoters by DNA binding transcription factors and is thought to promote transcription by acetylating the N-terminal tail of histone H3. The enzyme has indeed been shown to catalyse primarily the acetylation of H3 histone with only traces of H4 and H2A/B being acetylated. Non-acetylated H3 peptide or an H3 peptide that had been previously acetylated on K9 both serve as excellent substrates for HAG1-catalyzed acetylation. However, prior acetylation of H3 lysine 14 blocks radioactive acetylation of the peptide by HAG1. HAG1 is specific for histone H3 lysine 14. BGT; BIG TOP; GCN5; GENERAL CONTROL NONDEREPRESSIBLE 5; HAC3; HAG01; HAG1; HAT1; HISTONE ACETYLTRANSFERASE 1; HISTONE ACETYLTRANSFERASE OF THE GNAT FAMILY 1
BolC04g040220.2J	Cytoplasm Nucleus	5	AT3G52140.3: Involved in regulating mitochondrial quality control. Regulates mitochondrial association time and thereby is involved in mitochondrial fusion. Mutants show unregulated autophagy and display transcriptomic markers of mitochondrial stress. Its activity can be modulated by Lys acetylation. FMT; FRIENDLY; FRIENDLY MITOCHONDRIA; NON RESPONDING TO OXYLIPINS 38; NOXY38
BolC04g042260.2J	Nucleus	5	AT1G54390.1: ING2 encodes a member of the Inhibitor of Growth family of nuclear-localized Phd domain containing homeodomain proteins. Binds to H3K4 di or trimethylated DNA. ING2; INHIBITOR OF GROWTH 2
BolC05g053870.2J	Nucleus	5	AT3G12810.1: Encodes a protein similar to ATP-dependent, chromatin-remodeling proteins of the ISWI and SWI2/SNF2 family. Genetic analyses suggest that this gene is involved in multiple flowering pathways. Mutations in PIE1 results in suppression of FLC-mediated delay of flowering and causes early flowering in noninductive photoperiods independently of FLC. PIE1 is required for expression of FLC in the shoot apex but not in the root. Along with ARP6 forms a complex to deposit modified histone H2A.Z at several loci within the genome. This modification alters the expression of the target genes (i.e. FLC, MAF4, MAF6). The mRNA is cell-to-cell mobile. CHR13; PHOTOPERIOD-INDEPENDENT EARLY FLOWERING 1; PIE1; SRCAP
BolC05g056020.2J	Nucleus	5	AT3G10530.1: Transducin/WD40 repeat-like superfamily protein;(source:Araport11)
BolC06g015670.2J	Cytoplasm Nucleus	5	AT1G55170.1: DNA double-strand break repair protein;(source:Araport11) FLL3; FLX-LIKE 3
BolC06g024490.2J	Nucleus	5	AT3G58630.2: sequence-specific DNA binding transcription factor;(source:Araport11)
BolC07g003380.2J	Cytoplasm Nucleus	5	AT2G18900.1: Transducin/WD40 repeat-like superfamily protein;(source:Araport11)
BolC07g055720.2J	Nucleus	5	AT4G30990.2: ARM repeat superfamily protein;(source:Araport11)
BolC08g013300.2J	Nucleus	5	AT1G31360.5: Encodes a (d)NTP-dependent 3 Prime->5 Prime DNA helicase. This protein can also disrupt D loop structures and may mediate branch migration of Holliday junctions when tested in vitro. The unwinding activity of the enzyme depends on the presence of divalent cations (Mg2+, Mn2+, or Ca2+, but not Zn2+).(d)NTPs are also required with ATP and dATP supporting the greatest amount of DNA unwinding in vitro.

BolC08g030380.2J	Nucleus	5	AT1G22950.1: Belongs to the 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily proteins and contains an oxoglutarate/iron-dependent oxygenase domain (InterPro:IPR005123) of the prolyl 4-hydroxylase, alpha subunit subtype (P4Hc; InterPro:IPR006620), participates in epigenetic repression of flowering genes, works redundantly with CP2 to repress several members of the MADS-box transcription factors family, during vegetative development via histone modification. ICU11; INCURVATA11
BolC08g039660.2J	Cytoplasm Nucleus	5	AT3G55620.1: Translation initiation factor IF6;(source:Araport11) EIF6A; EMB1624; EMBRYO DEFECTIVE 1624; EUKARYOTIC INITIATION FACOR 6A
BolC08g041010.2J	Cytoplasm Nucleus	5	AT3G57080.1: Non-catalytic subunit unique to Nuclear DNA-dependent RNA polymerase V; homologous to budding yeast RPB5. DEFECTIVE IN MERISTEM SILENCING 12; DMS12; NRPE5; RNA POLYMERASE II FIFTH LARGEST SUBUNIT, B; RPB5B
BolC09g004380.2J	Nucleus	5	AT5G48240.1: Rrp15p protein;(source:Araport11)
BolC09g011470.2J	Nucleus	5	AT2G13370.2: chromatin remodeling 5;(source:Araport11)
BolC09g012480.2J	Nucleus	5	AT2G17410.2: AT Rich domain protein. ARID2; AT RICH INTERACTION DOMAIN 2
BolC09g027940.2J	Nucleus	5	AT2G03070.1: Encodes a subunit of the Mediator complex. Regulates plant defense and flowering. MED8; MEDIATOR SUBUNIT 8
BolC09g042400.2J	Nucleus	5	AT5G54930.2: AT hook motif-containing protein;(source:Araport11) METABOLIC NETWORK MODULATOR 1; MNM1
BolC09g046570.2J	Nucleus	5	AT5G58040.2: Encodes a subunit of the polyadenylation apparatus that interacts with and stimulates the activity of poly(A) polymerase. Additionally , it interacts with several polyadenylation factor subunits and is an RNA-binding protein. It is suggested that this protein coordinates a number of polyadenylation factor subunits with PAP and with RNA.The mRNA is cell-to-cell mobile. Important for plant development and root responses to abiotic stresses. FIP1
BolC09g060040.2J	Nucleus	5	AT5G13020.2: Agenet domain containing nucleosome binding protein. Binds H3K36 sites.
BolC09g066360.2J	Nucleus	5	AT5G05550.2: Encodes trihelix-domain transcription factor VFP5. Interacts with agrobacterium virulence protein VirF. EIN2 NUCLEAR ASSOCIATED PROTEIN 2; ENAP2; VFP5
BolC09g066740.2J	Nucleus	5	AT5G05230.1: RING/U-box superfamily protein;(source:Araport11)
BolC01g003920.2J	Nucleus	4	AT4G34910.1: P-loop containing nucleoside triphosphate hydrolases superfamily protein;(source:Araport11)
BolC01g020710.2J	Cytoplasm Nucleus	4	AT5G56950.1: Encodes a member of a small gene family of proteins with similarity to nucleosome assembly proteins.May function in nucleotide excision repair. Loss of function mutations have no obvious visible phenotypes but do seem to affect transcription of NER related genes. Plants mutated in three ubiquitously expressed NAP1 genes (NAP1;1~NAP1;3) and organ-specifically expressed NAP1;4 gene show hypersensitivity to genotoxic stresses including UV and DSB-inducing agent Bleomycin. The NAP1 genes act synergistically with NRP genes in promoting somatic homologous recombination. NAP1;3; NFA03; NFA3; NUCLEOSOME ASSEMBLY PROTEIN

1;3; NUCLEOSOME/CHROMATIN ASSEMBLY FACTOR GROUP A 03; NUCLEOSOME/CHROMATIN ASSEMBLY FACTOR GROUP A3

BolC01g040140.2J	Nucleus	4	AT3G22660.1: rRNA processing protein-like protein;(source:Araport11) EBP2
BolC01g045410.2J	Nucleus	4	AT3G17460.1: PHD finger family protein;(source:Araport11)
BolC01g053370.2J	Nucleus	4	AT3G08020.1: PHD finger family protein;(source:Araport11)
BolC02g003880.2J	Nucleus	4	AT5G09860.2: Encodes a component of the putative Arabidopsis THO/TREX complex: THO1 or HPR1 (At5g09860), THO2 (At1g24706), THO3 or TEX1 (At5g56130), THO5 (At5g42920, At1g45233), THO6 (At2g19430), and THO7 (At5g16790, At3g02950). THO/TREX complexes in animals have been implicated in the transport of mRNA precursors. Mutants of THO3/TEX1, THO1, THO6 accumulate reduced amount of small interfering (si)RNA, suggesting a role of the putative Arabidopsis THO/TREX in siRNA biosynthesis. One of the pathways affected by THO1 is the miRNA399-PHO2 pathway that regulates root APase activity. THO1
BolC02g011350.2J	Nucleus	4	AT5G22010.2: Encodes RFC1, the largest subunit of replication factor C. Mediates genomic stability and transcriptional gene silencing.
BolC03g037830.2J	Nucleus	4	AT3G05680.2: Encodes a splicing/methylation factor that is a homologue to the mammalian VIRILIZER, is member of a core set of mRNA m6A writer proteins and is required for N6-adenosine methylation of mRNA. Analysis of transcriptional profiles of the vir-1 mutant suggests that VIR is likely involved in regulation of gene expression, but the function of VIR is rather general than specific and knock-down of VIR does not affect overall splicing rates. EMB2016; EMBRYO DEFECTIVE 2016; VIR; VIRILIZER
BolC04g006480.2J	Nucleus	4	AT2G45000.1: Encodes a nucleoporin, a component of the nuclear pore complex, that appears to be a major negative regulator of auxin signalling. Loss of function mutants are embryo lethal. ATNUP62; EMB2766; EMBRYO DEFECTIVE 2766; NUCLEOPORIN 62; NUP62
BolC04g010530.2J	Cytoplasm Nucleus	4	AT2G37770.1: Encodes an NADPH-dependent aldo-keto reductase that can act on a wide variety of substrates in vitro including saturated and unsaturated aldehydes, steroids, and sugars. GFP-tagged AKR4C9 localizes to the chloroplast where it may play a role in detoxifying reactive carbonyl compounds that threaten to impair the photosynthetic process. Transcript levels for this gene are up-regulated in response to cold, salt, and drought stress. AKR4C9; ALDO-KETO REDUCTASE FAMILY 4 MEMBER C9; CHLAKR; CHLOROPLASTIC ALDO-KETO REDUCTASE
BolC04g020480.2J	Cytoplasm Nucleus	4	AT2G29540.2: RNA polymerase I(A) and III(C) 14 kDa subunit ATRPAC14; ATRPC14; RNAPOLYMERASE 14 KDA SUBUNIT; RPC14
BolC04g033710.2J	Nucleus	4	AT3G58660.1: Ribosomal protein L1p/L10e family;(source:Araport11)

BolC04g037310.2J	Nucleus	4	AT1G50240.3: The FUSED (FU) gene belongs to Ser/Thr protein kinase family and has a key role in the hedgehog signaling pathway known to control cell proliferation and patterning in fruit flies and humans . Arabidopsis thaliana genome has a single Fu gene that is involved in male meiosis cytokinesis. Cytokinesis-defective mutants, named two-in-one (tio), result from mutations in Arabidopsis Fu. Phenotypic analysis of tio mutants reveals an essential role for TIO in conventional modes of cytokinesis in plant meristems and during male gametogenesis. TIO is tightly localized to the midline of the nascent phragmoplast and remains associated with the expanding phragmoplast ring. This gene was previously annotated as two gene models, AT1G50230.1 and AT1G50240.1, however the experimental evidence exists (Oh et al, Current Biology, 2005) showing that these two models are in fact single gene, named FUSED. TIO; TWO IN ONE
BolC04g044870.2J	Cytoplasm Nucleus	4	AT3G29075.1: glycine-rich protein;(source:Araport11)
BolC04g062780.2J	Nucleus	4	AT2G37990.1: ribosome biogenesis regulatory protein (RRS1) family protein;(source:Araport11) ARABIDOPSIS HOMOLOG OF YEAST RRS1; ARRS1
BolC05g011130.2J	Nucleus	4	AT1G13690.1: AtE1 - stimulates the ATPase activity of DnaK/DnaJ ATE1; ATPASE E1
BolC05g014280.2J	Nucleus	4	AT1G16610.7: Encodes SR45, a member of the highly conserved family of serine/arginine-rich (SR) proteins, which play key roles in pre-mRNA splicing and other aspects of RNA metabolism. SR45 is a spliceosome protein, interacts with SR33 and the U1-70K protein of the U1 snRNP. Also involved in plant sugar response. sr45-1 mutation confers hypersensitivity to glucose during early seedling growth.
BolC05g019320.2J	Nucleus	4	AT1G21200.1: sequence-specific DNA binding transcription factor;(source:Araport11)
BolC05g023600.2J	Cytoplasm Nucleus	4	AT1G26370.1: RNA helicase family protein;(source:Araport11) RID1; ROOT INITIATION DEFECTIVE 1
BolC05g036770.2J	Cytoplasm Nucleus	4	AT1G35160.2: GF14 protein phi chain member of 14-3-3 protein family. This protein is reported to interact with the BZR1 transcription factor involved in brassinosteroid signaling and may affect the nucleocytoplasmic shuttling of BZR1 The mRNA is cell-to-cell mobile. GF14 PHI; GF14 PROTEIN PHI CHAIN
BolC05g040380.2J	Nucleus	4	AT3G22220.1: hAT transposon superfamily;(source:Araport11)
BolC06g003930.2J	Nucleus	4	AT3G42170.1: transposase-like gene with conserved domains from the family of hAT transposases that includes hobo from Drosophila melanogaster, Activator (Ac) from maize, and Tam3 from snapdragon but lacks several amino acids known to be essential for Ac transposition5. The DAYSLEEPER gene lacks 8 bp duplications and TIRs (a common feature of transcriptionally silent hAT transposases), however, DAYSLEEPER expression was detected, and several expressed sequence tags are available. The expression seems to be under the control of factors determining the circadian rhythm. DAYSLEEPER was isolated as a factor binding to a motif (Kubox1) present in the upstream region of the Arabidopsis DNA repair gene Ku70. Mutant plants lacking DAYSLEEPER or strongly overexpressing this gene do not develop in a normal manner. DAYSLEEPER
BolC06g044610.2J	Nucleus	4	AT1G73240.1: nucleoporin protein Ndc1-Nup protein;(source:Araport11)
BolC06g049950.2J	Nucleus	4	AT1G79020.1: Enhancer of polycomb-like transcription factor protein;(source:Araport11)

BolC07g002280.2J	Cytoplasm Nucleus	4	AT2G19480.3: This gene is predicted to encode a nucleosome assembly protein. Plant lines expressing an RNAi construct directed against this gene show a reduction in agrobacterium-mediated root transformation. The mRNA is cell-to-cell mobile. Plants mutated in three ubiquitously expressed NAP1 genes (NAP1;1~NAP1;3) and organ-specifically expressed NAP1;4 gene show hypersensitivity to genotoxic stresses including UV and DSB-inducing agent Bleomycin. The NAP1 genes act synergistically with NRP genes in promoting somatic homologous recombination. NAP1;2; NUCLEOSOME ASSEMBLY PROTEIN 1;2
BolC07g023510.2J	Cytoplasm Nucleus	4	AT5G67240.2: small RNA degrading nuclease 3;(source:Araport11) SDN3; SMALL RNA DEGRADING NUCLEASE 3
BolC07g029430.2J	Nucleus	4	AT5G46840.2: RNA-binding (RRM/RBD/RNP motifs) family protein;(source:Araport11)
BolC07g044520.2J	Nucleus	4	AT3G51120.1: zinc finger CCCH domain-containing protein 44;(source:Araport11)
BolC07g046040.2J	Cytoplasm Nucleus	4	AT4G16143.2: Protein interacts with Agrobacterium proteins VirD2 and VirE2. Is not individually essential for Agrobacterium-mediated root transformation, but when overexpressed can rescue the impa-4 decreased transformation susceptibility phenotype. IMPA-2; IMPORTIN ALPHA ISOFORM 2
BolC07g052020.2J	Nucleus	4	AT4G25340.2: Encodes a member of the FKBP-type immunophilin family that functions as a histone chaparone. Binds to 18S rDNA and represses its expression. The N-terminal nucleoplasmin domain interacts with H2A/H2B and H3/H4 histone oligomers, individually, as well as simultaneously, suggesting two different binding sites for H2A/H2B and H3/H4. FK506 BINDING PROTEIN 53; FKBP53
BolC08g002470.2J	Nucleus	4	AT1G06790.1: Encodes a subunit of RNA polymerase III involved in maintaining global RNA homeostasis, not just that of genes transcribed by RNA pol III. NRPC7; NUCLEAR RNA POLYMERASE C, SUBUNIT 7
BolC08g005160.2J	Nucleus	4	AT1G48380.1: Encodes a novel nuclear protein required for root hair initiation and ploidy-dependent cell growth. Its sequence has similarity to the C-terminal domain of mammalian DNA topo IIalpha. Shows in vitro DNA binding activity and is likely to be part of the topo VI complex by binding to subunit A. HYP7; HYPOCOTYL 7; RHL1; ROOT HAIRLESS 1
BolC08g028770.2J	Nucleus	4	AT1G20670.1: DNA-binding bromodomain-containing protein;(source:Araport11)
BolC08g033270.2J	Cytoplasm Nucleus	4	AT3G49180.1: Transducin/WD40 repeat-like superfamily protein;(source:Araport11) RID3; ROOT INITIATION DEFECTIVE 3
BolC08g039540.2J	Nucleus	4	AT3G55510.1: Encodes a regulator of floral determinacy in that interacts with both nucleolar and nucleoplasmic proteins. RBL; REBELOTE
BolC08g045730.2J	Nucleus	4	AT3G62820.1: Plant invertase/pectin methylesterase inhibitor superfamily protein;(source:Araport11)
BolC08g052040.2J	Nucleus	4	AT1G16280.1: Encodes a putative DEAD-box RNA helicase. Essential for female gametogenesis. ARABIDOPSIS THALIANA RNA HELICASE 36; ATRH36; RH36; RNA HELICASE 36; SLOW WALKER 3; SWA3
BolC09g016680.2J	Cytoplasm Nucleus	4	AT1G64350.1: seh1-like protein SEH1H

BolC09g027980.2J	Nucleus	4	AT2G03150.2: Encodes a nuclear-localized calcium-binding protein RSA1 (SHORT ROOT IN SALT MEDIUM 1), which is required for salt tolerance. EMB1579; EMBRYO DEFECTIVE 1579; RSA1; SHORT ROOT IN SALT MEDIUM 1
BolC09g032870.2J	Nucleus	4	AT4G10760.1: Encodes a member of a core set of mRNA m6A writer proteins and is required for N6-adenosine methylation of mRNA. EMB1706; EMBRYO DEFECTIVE 1706; MRNAADENOSINE METHYLASE; MTA
BolC09g051910.2J	Nucleus	4	AT5G20600.1: ribosomal RNA processing-like protein;(source:Araport11)
BolC09g063170.2J	Nucleus	4	AT5G09540.1: Chaperone DnaJ-domain superfamily protein;(source:Araport11)
BolC09g066300.2J	Nucleus	4	AT5G05680.1: Encodes MOS7 (Modifier of snc1,7), homologous to human and Drosophila melanogaster nucleoporin Nup88. Resides at the nuclear envelope. Modulates the nuclear concentrations of certain defense proteins regulates defense outputs. EMB2789; EMBRYO DEFECTIVE 2789; MODIFIER OF SNC1,7; MOS7
BolC01g032890.2J	Nucleus	3	AT5G35210.1: Encodes a chloroplast envelope-bound plant homeodomain (PHD) transcription factor with transmembrane domains that functions in multiple retrograde signal pathways. The proteolytic cleavage of PTM occurs in response to retrograde signals and amino-terminal PTM accumulates in the nucleus, where it activates ABI4 transcription in a PHD-dependent manner associated with histone modifications. DDP1; DDT-PHD PROTEIN1; PHD TYPE TRANSCRIPTION FACTOR WITH TRANSMEMBRANE DOMAINS; PTM
BolC01g040540.2J	Nucleus	3	AT3G22170.1: A component of the PHYA signaling network, mediates the FR-HIR response to far-red light in concert with FAR1. Expression is induced by age; involved in negative regulation of leaf senescence. CHLOROPLAST DIVISION MUTANT 45; CPD45; FAR-RED ELONGATED HYPOCOTYLS 3; FHY3
BolC01g053580.2J	Nucleus	3	AT3G07780.3: Encodes a nuclear PHD finger protein that is functionally redundant with OBE2 and plays an important role in the maintenance and/or establishment of the root and shoot apical meristems.The mRNA is cell-to-cell mobile.
BolC01g055420.2J	Cytoplasm Nucleus	3	AT4G38130.2: Encodes a histone deacetylase that enhances AtERF7-mediated transcriptional repression. Binds SIM3 and ERF7. Expressed in the nucleus in most tissues examined and throughout the life of the plant. Involved in jasmonic acid and ethylene dependent pathogen resistance. The sequence in GenBank has 17 AG dinucleotide repeats missing, which is also missing in Ler shotgun sequence from Cereon. Although it is annotated to be in Columbia, the GB sequence is probably not of Columbia origin. Plays a role in embryogenesis as mutants grown at higher temperatures display abnormalities in the organization of the root and shoot. Plant lines expressing an RNAi construct targeted against HDA19 shows some resistance to agrobacterium-mediated root transformation. HDA19 acts in a WOX5 mediated pathway to maintain columella stem cell fate by repressing CDF4. Class I RPD3-like family HDAC member which controls positive responses to salinity stress. ARABIDOPSIS HISTONE DEACETYLASE 1; ATHD1; HD1; HDA1; HDA19; HDAC19; HISTONE DEACETYLASE 1; HISTONE DEACETYLASE 19; RPD3A

BolC01g056450.2J	Nucleus	3	AT3G03140.1: Encodes a chromatin-associated protein that interacts with plant nuclear lamin-like components to regulate nuclear size. PRO-TRP-PRO-TRP PROTEIN 1; PWO1; PWWP-DOMAIN INTERACTOR OF POLYCOMBS1; PWWP1
BolC02g039770.2J	Nucleus	3	AT4G12390.1: pectin methylesterase inhibitor 1;(source:Araport11) PECTIN METHYLESTERASE INHIBITOR 1; PME1
BolC03g002340.2J	Nucleus	3	AT5G05210.1: Surfeit locus protein 6;(source:Araport11)
BolC03g004970.2J	Nucleus	3	AT5G10550.1: This gene is predicted to encode a bromodomain-containing protein. A plant line expressing RNAi constructs targeted against GTE7 shows some resistance to agrobacterium-mediated root transformation. GLOBAL TRANSCRIPTION FACTOR GROUP E2; GTE2
BolC03g009310.2J	Cytoplasm Nucleus	3	AT3G03920.1: H/ACA ribonucleoprotein complex, subunit Gar1/Naf1 protein;(source:Araport11)
BolC03g011520.2J	Nucleus	3	AT5G22650.1: Encodes a member of a plant-specific class of histone deacetylases. Controls the development of adaxial/abaxial leaf polarity. Its mRNA is widely expressed in stems, leaves, flowers and young siliques. Plant lines expressing RNAi constructs directed against this gene showed a marked reduction in agrobacterium-mediated root transformation. ARABIDOPSIS HISTONE DEACETYLASE 2; ATHD2; ATHD2B; HD2; HD2B; HDA4; HDT02; HDT2; HISTONE DEACETYLASE 2; HISTONE DEACETYLASE 2B
BolC03g015210.2J	Nucleus	3	AT5G55210.1: Involved in hygromycin resistance through facilitating hygromycin phosphotransferase transportation from cytosol to chloroplast. HS1; HYGROMYCIN-SENSITIVE 1
BolC03g017880.2J	Cytoplasm Nucleus	3	AT3G01340.2: Transducin/WD40 repeat-like superfamily protein;(source:Araport11)
BolC03g055970.2J	Cytoplasm Nucleus	3	AT5G64730.1: Transducin/WD40 repeat-like superfamily protein;(source:Araport11)
BolC03g064650.2J	Cytoplasm Nucleus	3	AT3G44680.1: Encodes HDA9 (a RPD3-like histone deacetylase). Functions in promoting the onset of leaf senescence.The hda9 mutant shows enhanced H3K9 acetylation levels,based on immunodetection using H3K9ac antibodies. Negatively controls gene expression in concert with interacting proteins POWERDRESS (PWR), HIGH EXPRESSION OF OSMOTICALLY RESPONSIVE GENES 15 (HOS15), WRKY53, ELONGATED HYPOCOTYL 5 (HY5), ABA INSENSITIVE 4 (ABI4) and EARLY FLOWERING 3 (ELF3). Involved in mutual negative feedback regulation with WRKY53. Mutations lead to a mild early flowering phenotype under SD. ATHDA9; ATHDAC9; HDA09; HDA9; HDAC9; HISTONE DEACETYLASE 9
BolC04g000940.2J	Cytoplasm Nucleus	3	AT2G47420.1: Encodes a putative rRNA dimethyltransferase. ADENOSINE DIMETHYL TRANSFERASE 1A; DIM1A
BolC04g019260.2J	Nucleus	3	AT2G30580.1: Encodes a C3HC4 RING-domain-containing ubiquitin E3 ligase capable of interacting with DREB2A. DRIP2 seems to be involved in regulating stress-related transcriptional changes and drought tolerance. ATDRIP2; BMI1A; DREB2A-INTERACTING PROTEIN 2; DRIP2
BolC04g026980.2J	Nucleus	3	AT1G61040.2: Encodes a yeast Paf1C subunit homolog required for the expression of the MADS box gene FLC and other members of the FLC/MAF MADS-box gene family. Member of PAF-C complex.

BolC04g030240.2J	Nucleus	3	AT3G63030.1: Protein containing methyl-CpG-binding domain.Has sequence similarity to human MBD proteins. MBD4; METHYL-CPG-BINDING DOMAIN 4
BolC04g047560.2J	Nucleus	3	AT3G12340.3: FKBP-like peptidyl-prolyl cis-trans isomerase family protein;(source:Araport11)
BolC05g015250.2J	Nucleus	3	AT1G17680.1: tetratricopeptide repeat (TPR)-containing protein;(source:Araport11)
BolC05g032540.2J	Nucleus	3	AT1G50620.1: RING/FYVE/PHD zinc finger superfamily protein;(source:Araport11)
BolC05g040210.2J	Nucleus	3	AT3G22380.3: Encodes a nucleus-acting plant-specific clock regulator working close to the central oscillator and affecting the circadian gating of light responses. Circadian gating is the alteration of circadian phase according to the photoperiod of the entraining day/light cycle and the rhythmic antagonism of light responses in the early subjective night. TIC differentially regulates CCA1 and PRR9 from LHY, with LHY expression as a dominant genetic target of TIC action. Also shown to be involved in the maintenance of Arabidopsis thaliana metabolic homeostasis.
BolC05g046210.2J	Nucleus	3	AT3G18610.2: Encodes ATNUC-L2 (NUCLEOLIN LIKE 2).
BolC05g063120.2J	Cytoplasm Nucleus	3	AT3G02950.2: Encodes a component of the putative Arabidopsis THO/TREX complex: THO1 or HPR1 (At5g09860), THO2 (At1g24706), THO3 or TEX1 (At5g56130), THO5 (At5g42920, At1g45233), THO6 (At2g19430), and THO7 (At5g16790, At3g02950). THO/TREX complexes in animals have been implicated in the transport of mRNA precursors. Mutants of THO3/TEX1, THO1, THO6 accumulate reduced amount of small interfering (si)RNA, suggesting a role of the putative Arabidopsis THO/TREX in siRNA biosynthesis.
BolC05g063460.2J	Nucleus	3	AT3G03300.4: Encodes a Dicer-like protein that functions in the antiviral silencing response in turnip-crinkle virus-infected plants but not in TMV or CMV-strain-Y-infected plants. Involved in the production of ta-siRNAs. Partially antagonizes the production of miRNAs by DCL1. Substitutes for DCL4 to produce viral siRNA when DCL4 is missing or inhibited. Able to produce siRNAs but not miRNAs.
BolC06g004080.2J	Cytoplasm Nucleus	3	AT1G22090.1: hypothetical protein;(source:Araport11) EMB2204; EMBRYO DEFECTIVE 2204
BolC06g009540.2J	Nucleus	3	AT1G55300.1: TBP-associated factor 7;(source:Araport11) TAF7; TBP-ASSOCIATED FACTOR 7
BolC06g048580.2J	Nucleus	3	AT1G77310.2: wound-responsive family protein;(source:Araport11)
BolC07g002220.2J	Nucleus	3	AT2G19520.1: Controls flowering. ACG1; ATMSI4; FVE; MSI4; MULTICOPY SUPPRESSOR OF IRA1 4; NFC04; NFC4
BolC07g011510.2J	Nucleus	3	AT3G24860.1: Trihelix transcription factor induced by osmotic and salt stress. Binds to a conserved AGAG-box sequence in the promoter of genes it regulates. Regulates the expression of stress tolerance genes, resulting in reduced reactive oxygen species, Na ⁺ accumulation, stomatal apertures, lipid peroxidation, cell death and water loss rate, and increased proline content and reactive oxygen species scavenging capability. ARABIDOPSIS SIP1 CLADE TRIHELIX1; AST1

BolC07g013940.2J	Cytoplasm Nucleus	3	AT3G23590.1: Encodes a protein shown to physically associate with the conserved transcriptional coregulatory complex, Mediator, and is involved in the regulation of phenylpropanoid homeostasis. Acts redundantly with REF4/MED5b (At2g48110). Required for expression of some dark-upregulated genes. RFR1 is the MED5a subunit of the mediator complex. MED33A; MED5A; REF4-RELATED 1; RFR1
BolC07g041570.2J	Nucleus	3	AT5G24630.8: This gene is predicted to encode a protein that forms part of the topoisomerase VI complex. BIN4 is a nuclear-localized protein that can bind DNA. bin4 mutants are brassinolide-insensitive dwarves with severely reduced cell size in leaves, roots, and hypocotyls. Proper development of root hairs and trichomes is also disrupted in bin4 mutants and they have elevated levels of double strand breaks in their cotyledon cells.
BolC07g042450.2J	Cytoplasm Nucleus	3	AT1G12910.1: Encodes LIGHT-REGULATED WD1 (LWD1), a clock proteins regulating circadian period length and photoperiodic flowering. ANTHOCYANIN11; ATAN11; LIGHT-REGULATED WD 1; LWD1
BolC07g053920.2J	Nucleus	3	AT4G28450.1: This gene is predicted to encode a protein with a DWD motif. It can bind to DDB1a in Y2H assays and may be involved in the formation of a CUL4-based E3 ubiquitin ligase
BolC08g033660.2J	Nucleus	3	AT3G49601.1: pre-mRNA-splicing factor;(source:Araport11)
BolC08g040780.2J	Nucleus	3	AT3G56900.1: Encodes ALADIN, a component of the nuclear pore complex. ALADIN
BolC08g051900.2J	Nucleus	3	AT1G16610.7: Encodes SR45, a member of the highly conserved family of serine/arginine-rich (SR) proteins, which play key roles in pre-mRNA splicing and other aspects of RNA metabolism. SR45 is a spliceosome protein, interacts with SR33 and the U1-70K protein of the U1 snRNP. Also involved in plant sugar response. sr45-1 mutation confers hypersensitivity to glucose during early seedling growth.
BolC08g060730.2J	Nucleus	3	AT1G01750.1: actin depolymerizing factor 11;(source:Araport11) ACTIN DEPOLYMERIZING FACTOR 11; ADF11
BolC09g000370.2J	Nucleus	3	AT4G00450.2: Encodes the Arabidopsis homolog of the transcriptional regulator MED12, is dynamically expressed during embryogenesis and regulates both developmental timing and the radial pattern formation. Involved in flowering time. The mutant enhances the expression of the flowering time (FT) gene. A knockout mutant of this gene showed late-flowering phenotype. CCT; CENTER CITY; CRP; CRYPTIC PRECOCIOUS; MED12; MEDIATOR 12
BolC09g001460.2J	Nucleus	3	AT4G02020.4: Encodes a polycomb group protein EZA1. Also known as SWINGER (SWN). Forms part of a large protein complex that can include VRN2 (VERNALIZATION 2), VIN3 (VERNALIZATION INSENSITIVE 3) and polycomb group proteins FERTILIZATION INDEPENDENT ENDOSPERM (FIE) and CURLY LEAF (CLF). The complex has a role in establishing FLC (FLOWERING LOCUS C) repression during vernalization. Performs a partially redundant role to MEA in controlling seed initiation by helping to suppress central cell nucleusendosperm proliferation within the FG.
BolC09g002380.2J	Nucleus	3	AT4G03090.2: AtNDX negatively regulates ABI4 expression during ABA signaling. ATNDX; NDX; NODULIN HOMEBOX

BolC09g005080.2J	Nucleus	3	AT5G30495.1: Fcf2 pre-rRNA processing protein;(source:Araport11)
BolC09g006530.2J	Nucleus	3	AT5G25150.1: Encodes a putative TATA-binding-protein associated factor TAF5. TAFs are subunits of the general transcription factor IID (TFIID). TAF5; TBP-ASSOCIATED FACTOR 5
BolC09g008860.2J	Nucleus	3	AT5G63610.1: significant sequence similarity to plant and animal cyclin-dependent protein kinases, and was classified as an E-type CDK with a SPTAIRE cyclin binding motif in the kinase domain. ATCDK8; CDKE1; CDKE;1; CYCLIN-DEPENDENT KINASE E1; CYCLIN-DEPENDENT KINASE E;1; HEN3; HUA ENHANCER 3
BolC09g041540.2J	Nucleus	3	AT5G54260.2: DNA repair and meiotic recombination protein, component of MRE11 complex with RAD50 and NBS1
BolC09g044260.2J	Cytoplasm Nucleus	3	AT5G56130.1: Encodes a component of the putative Arabidopsis THO/TREX complex: THO1 or HPR1 (At5g09860), THO2 (At1g24706), THO3 or TEX1 (At5g56130), THO5 (At5g42920, At1g45233), THO6 (At2g19430), and THO7 (At5g16790, At3g02950). THO/TREX complexes in animals have been implicated in the transport of mRNA precursors. Mutants of THO3/TEX1, THO1, THO6 accumulate reduced amount of small interfering (si)RNA, suggesting a role of the putative Arabidopsis THO/TREX in siRNA biosynthesis. ATTEX1; TEX1; THO3
BolC09g046850.2J	Cytoplasm Nucleus	3	AT5G58350.1: Encodes a member of the WNK family (9 members in all) of protein kinases, the structural design of which is clearly distinct from those of other known protein kinases, such as receptor-like kinases and mitogen-activated protein kinases. Its transcription is under the control of circadian rhythms. WITH NO LYSINE (K) KINASE 4; WNK4; ZIK2
BolC09g053780.2J	Nucleus	3	AT5G18750.1: DNAJ heat shock N-terminal domain-containing protein;(source:Araport11)
BolC09g059030.2J	Nucleus	3	AT5G14050.1: Transducin/WD40 repeat-like superfamily protein;(source:Araport11)
BolC09g063700.2J	Nucleus	3	AT5G08420.1: RNA-binding KH domain-containing protein;(source:Araport11)
BolC09g069440.2J	Cytoplasm Nucleus	3	AT5G01160.2: Encodes a member of a core set of mRNA m6A writer proteins and is required for N6-adenosine methylation of mRNA. HAKAI
BolC01g004300.2J	Nucleus	2	AT4G34430.4: Member of a small family of SWI3-like genes in Arabidopsis. Referred to as CHB4 in Zhou et al. (2002). ATSWI3D; CHB3; SWITCH/SUCROSE NONFERMENTING 3D
BolC01g013880.2J	Nucleus	2	AT4G20400.1: Encodes a histone H3K4 demethylase repressing floral transition.Coordinates and structure features have been deposited in the RCSB Protein Data Bank with the accession codes 5YKN (JMJ14CD) and 5YKO(JMJ14CD-NOG-H3K4em3 complex). Glu285 and Glu516 contribute to the recognition of H3R2. Asp312 contributes to the recognition of H3Q5. Phe171 and Val363 contribute to the recognition of H3A7. Ser290, Trp296, and Tyr298 contribute to the recognition of H3K4me3 (PMID:29233856). JMJ14; JUMONJI 14; PKDM7B
BolC01g017490.2J	Nucleus	2	AT4G23540.1: ARM repeat superfamily protein;(source:Araport11)
BolC01g021850.2J	Nucleus	2	AT4G27010.1: ribosome 60S biogenesis amino-terminal protein;(source:Araport11) EMB2788; EMBRYO

DEFECTIVE 2788

BolC01g029410.2J	Nucleus	2	AT5G24450.1: Transcription factor IIIC, subunit 5;(source:Araport11)
BolC01g029700.2J	Cytoplasm Nucleus	2	AT3G49180.1: Transducin/WD40 repeat-like superfamily protein;(source:Araport11) RID3; ROOT INITIATION DEFECTIVE 3
BolC01g033890.2J	Nucleus	2	AT1G56460.2: HIT zinc finger and PAPA-1-like domain-containing protein;(source:Araport11)
BolC01g054810.2J	Nucleus	2	AT4G31985.1: Ribosomal protein L39 family protein;(source:Araport11)
BolC02g003210.2J	Nucleus	2	AT5G07940.2: dentin sialophosphoprotein-like protein;(source:Araport11)
BolC02g003350.2J	Nucleus	2	AT5G08330.1: Circadian oscillator protein which interacts with bZIP63 and regulates a response of the circadian oscillator to sugar. Is not required for the sugar-induced circadian phase advance in the morning; regulates a response of CCA1 to sugars. ATTCP21; CCA1 HIKING EXPEDITION; CHE; TCP DOMAIN PROTEIN 21; TCP21
BolC02g008610.2J	Cytoplasm Nucleus	2	AT3G03920.1: H/ACA ribonucleoprotein complex, subunit Gar1/Naf1 protein;(source:Araport11)
BolC02g033080.2J	Nucleus	2	AT2G24020.2: STIC2 was identified in a screen for suppressors of chloroplast protein import defect in tic40. STIC2; SUPPRESSOR OF TIC40 2
BolC02g033770.2J	Nucleus	2	AT1G77600.1: One of 5 PO76/PDS5 cohesion cofactor orthologs of Arabidopsis. ATPDS5B; PDS5B
BolC02g037740.2J	Nucleus	2	AT4G02400.1: U3 ribonucleoprotein (Utp) family protein;(source:Araport11)
BolC02g060240.2J	Nucleus	2	AT5G61140.1: Encodes a predicted protein with 30% identity with MER3/RCK. Similar to yast Brr2p DEAD/DExH box ATP-dependent RNA helicase. BRR2C
BolC02g062290.2J	Nucleus	2	AT5G64680.1: mediator-associated protein;(source:Araport11)
BolC03g006060.2J	Nucleus	2	AT5G12400.1: PHD-finger and DNA binding domain-containing protein;(source:Araport11) DDP3; DDT-PHD PROTEIN3
BolC03g006720.2J	Nucleus	2	AT5G13950.3: nuclear factor kappa-B-binding protein;(source:Araport11)
BolC03g029630.2J	Cytoplasm Nucleus	2	AT2G25420.4: transducin family protein / WD-40 repeat family protein;(source:Araport11)
BolC03g030220.2J	Nucleus	2	AT5G49700.1: Putative AT-hook DNA-binding family protein;(source:Araport11) AHL17; AT-HOOK MOTIF NUCLEAR LOCALIZED PROTEIN 17
BolC03g039910.2J	Nucleus	2	AT3G09180.2: mediator of RNA polymerase II transcription subunit;(source:Araport11) MED3; MEDIATOR 3
BolC03g050380.2J	Nucleus	2	AT2G05250.1: DNAJ heat shock N-terminal domain-containing protein;(source:Araport11)
BolC03g054160.2J	Nucleus	2	AT5G67580.1: Encodes a telomeric DNA binding protein and Single Myb Histone (SMH) gene family member. In vitro, the protein preferentially binds double-stranded telomeric repeats, but it can also bind to the single G-rich telomeric strand. ATTPB3; ATTRB2; TBP3; TELOMERE REPEAT BINDING FACTOR 2; TELOMERE-BINDING PROTEIN 3; TRB2
BolC03g054940.2J	Nucleus	2	AT5G65540.1: transcription initiation factor TFIID subunit;(source:Araport11)
BolC03g066800.2J	Nucleus	2	AT3G47120.1: GDS1 is a member of the C3H-type zinc finger family of proteins. Mutants display growth defects due to reduced cell number and size. GDS1; GROWTH, DEVELOPMENT AND SPLICING 1

BolC03g068550.2J	Cytoplasm Nucleus	2	AT1G25260.1: Involved in male gamete development. Trans-acting factor in the assembly of the pre-60S particle. RDP; RDP1; REDUCED POLLEN NUMBER; REDUCED POLLEN NUMBER 1
BolC03g073860.2J	Nucleus	2	AT4G37440.2: hypothetical protein;(source:Araport11)
BolC03g086090.2J	Nucleus	2	AT2G28600.1: P-loop containing nucleoside triphosphate hydrolases superfamily protein;(source:Araport11)
BolC04g016280.2J	Nucleus	2	AT2G32950.1: Represses photomorphogenesis and induces skotomorphogenesis in the dark. Contains a ring finger zinc-binding motif, a coiled-coil domain, and several WD-40 repeats, similar to G-beta proteins. The C-terminus has homology to TAFII80, a subunit of the TFIID component of the RNA polymerase II of Drosophila. Nuclear localization in the dark and cytoplasmic in the light. The mRNA is cell-to-cell mobile. ARABIDOPSIS THALIANA CONSTITUTIVE PHOTOMORPHOGENIC 1; ATCOP1; CONSTITUTIVE PHOTOMORPHOGENIC 1; COP1; DEETIOLATED MUTANT 340; DET340; EMB168; EMBRYO DEFECTIVE 168; FUS1; FUSCA 1
BolC04g040280.2J	Cytoplasm Nucleus	2	AT3G52090.2: Non-catalytic subunit common to nuclear DNA-dependent RNA polymerases II, IV and V; homologous to budding yeast RPB11 and the E. coli RNA polymerase alpha subunit. NRPB11
BolC04g040940.2J	Nucleus	2	AT2G47300.4: Encodes a protein involved in rRNA but not tRNA maturation.
BolC04g050990.2J	Nucleus	2	AT2G23760.1: Encodes a member of the BEL family of homeodomain proteins. Plants doubly mutant for saw1/saw2 (blh2/blh4) have serrated leaves. BP is expressed in the serrated leaves, therefore saw2 and saw1 may act redundantly to repress BP in leaves. Regulates together with BLH2 demethylesterification of homogalacturonan in seed mucilage. BEL1-LIKE HOMEODOMAIN 4; BLH4; SAW2; SAWTOOTH 2
BolC04g053060.2J	Nucleus	2	AT2G25560.1: DNAJ heat shock N-terminal domain-containing protein;(source:Araport11)
BolC04g054510.2J	Nucleus	2	AT2G27840.3: Belongs to the plant specific HD2 type proteins; similar to nucleolar Zea mays histone deacetylase; HD2-p39
BolC05g007010.2J	Nucleus	2	AT1G09230.3: Encodes a U12-type spliceosomal protein that is an indispensable component of the minor spliceosome and plays a crucial role in U12 intron splicing and plant development.
BolC05g018570.2J	Nucleus	2	AT1G20670.1: DNA-binding bromodomain-containing protein;(source:Araport11)
BolC05g027960.2J	Nucleus	2	AT1G30240.1: proline-, glutamic acid/leucine-rich protein;(source:Araport11)
BolC05g054340.2J	Nucleus	2	AT3G12250.4: basic leucine zipper transcription factor involved in the activation of SA-responsive genes. BZIP45; TGA6; TGACG MOTIF-BINDING FACTOR 6
BolC05g063020.2J	Cytoplasm Nucleus	2	AT3G02830.1: Encodes a zinc finger protein that binds to PORA mRNA in vivo and recruits the Pfr form of phytochrome to the 5'-UTR of PORA mRNA to regulate translation of the mRNA. PENTA 1; PNT1; ZFN1; ZINC FINGER PROTEIN 1
BolC06g000970.2J	Nucleus	2	AT1G44910.2: Binds the carboxyl-terminal domain (CTD) of the largest subunit of RNA polymerase II and functions as a scaffold for RNA processing machineries. ATPRP40A; PRE-MRNA-PROCESSING PROTEIN 40A; PRP40A
BolC06g002870.2J	Nucleus	2	AT1G48560.1: hypothetical protein;(source:Araport11)

BolC06g017930.2J	Nucleus	2	AT5G38600.2: Proline-rich spliceosome-associated (PSP) family protein / zinc knuckle (CCHC-type) family protein;(source:Araport11) ZCCHC8A
BolC06g030420.2J	Cytoplasm Nucleus	2	AT1G76440.1: HSP20-like chaperones superfamily protein;(source:Araport11)
BolC06g036920.2J	Nucleus	2	AT1G65440.1: Related to yeast Spt6 protein, which functions as part of a protein complex in transcription initiation and also plays a role in chromatin structure / assembly. It encodes a putative WG/GW-repeat protein involved in the regulation of apical-basal polarity of embryo ARABIDOPSIS SUPPRESSOR OF TY INSERTION 6-LIKE; GLOBAL TRANSCRIPTION FACTOR GROUP B1; GTB1; SPT6L
BolC06g038640.2J	Nucleus	2	AT1G65030.1: This gene is predicted to encode a protein with a DWD motif. It can bind to DDB1a in Y2H assays, and DDB1b in co-IP assays, and may be involved in the formation of a CUL4-based E3 ubiquitin ligase
BolC06g047830.2J	Nucleus	2	AT1G76380.2: DNA-binding bromodomain-containing protein;(source:Araport11)
BolC07g014640.2J	Nucleus	2	AT1G31660.1: Encodes a protein that is a ribosome biogenesis co-factor. Mutants display aberrant RNA processing and male and female gametophyte development. ATENP1; ENP1; ESSENTIAL NUCLEAR PROTEIN 1
BolC07g032130.2J	Nucleus	2	AT2G02070.2: RAVEN is part of the network regulated by BLJUEJAY, JACKDAW, SACRECROW and SHORT-ROOT to regulate root tissue patterning through cell lineage specification and asymmetric cell division. RAVEN is directly activated by SHORT-ROOT and directly repressed by JACKDAW.
BolC07g040450.2J	Nucleus	2	AT5G26210.1: Encodes a member of the Alfin1-like family of nuclear-localized PHD (plant homeodomain) domain containing proteins. All AL proteins except AL3 bind to di- or trimethylated histone H3 (H3K4me3/2). Members of this family include: AT5G05610 (AL1), AT3G11200 (AL2), AT3G42790 (AL3), AT5G26210 (AL4), AT5G20510 (AL5), AT2G02470 (AL6), AT1G14510 (AL7). AL4; ALFIN-LIKE 4
BolC07g045180.2J	Nucleus	2	AT3G52280.1: Bromodomain containing nuclear-localized protein involved in leaf development. GTE6 binds to the promoter and intron of AS1 and regulates its expression via histone acetylation. GENERAL TRANSCRIPTION FACTOR GROUP E6; GTE6
BolC07g047030.2J	Cytoplasm Nucleus	2	AT4G17640.1: Encodes casein kinase II beta (regulatory) subunit. CASEIN KINASE II BETA CHAIN 2; CKB2
BolC07g055630.2J	Nucleus	2	AT4G30840.1: Transducin/WD40 repeat-like superfamily protein;(source:Araport11) NUP43
BolC08g032530.2J	Nucleus	2	AT3G48430.1: Relative of Early Flowering 6 (REF6) encodes a Jumonji N/C and zinc finger domain-containing protein that acts as a positive regulator of flowering in an FLC-dependent pathway. REF6 mutants have hyperacetylation of histone H4 at the FLC locus. REF6 interacts with BES1 in a Y2H assay and in vitro. REF6 may play a role in brassinosteroid signaling by affecting histone methylation in the promoters of BR-responsive genes. It is most closely related to the JHDM3 subfamily of JmjN/C proteins. The mRNA is cell-to-cell mobile. EIN6; ETHYLENE INSENSITIVE 6; JMJ12; JUMONJI DOMAIN-CONTAINING PROTEIN 12; REF6; RELATIVE OF EARLY FLOWERING 6
BolC08g039260.2J	Nucleus	2	AT3G55340.1: Plant-specific protein. Interacts with phragmoplastin, Rop1 and Rop2. Involved in cell plate formation. PHIP1; PHRAGMOPLASTIN INTERACTING PROTEIN 1

BolC08g040910.2J	Nucleus	2	AT3G56990.3: embryo sac development arrest 7;(source:Araport11)
BolC08g042960.2J	Cytoplasm Nucleus	2	AT3G59600.1: One of two highly similar proteins that can serve as non-catalytic subunits of Nuclear RNA polymerases II, IV and V; homologous to budding yeast RPB8. Probably redundant with At1g54250. NRPB8B; NRPD8B; NRPE8B
BolC08g043580.2J	Nucleus	2	AT5G42520.1: Encodes a member of the BASIC PENTACYSTEINE (BPC) proteins. BPC proteins are plant-specific transcription factors present throughout land plants. BPC transcription factor family is integral for a wide range of processes that support normal growth and development. ARABIDOPSIS THALIANA BASIC PENTACYSTEINE 6; ATBPC6; BASIC PENTACYSTEINE 6; BBR/BPC6; BPC6
BolC08g049170.2J	Nucleus	2	AT2G21440.1: RNA-binding (RRM/RBD/RNP motifs) family protein;(source:Araport11)
BolC09g005450.2J	Nucleus	2	AT5G27650.1: PWWP domain protein involved in regulation of FLC and flowering time. PDP1; PWWP DOMAIN PROTEIN 1
BolC09g006030.2J	Nucleus	2	AT5G26210.1: Encodes a member of the Alfin1-like family of nuclear-localized PHD (plant homeodomain) domain containing proteins. All AL proteins except AL3 bind to di- or trimethylated histone H3 (H3K4me3/2). Members of this family include: AT5G05610 (AL1), AT3G11200 (AL2), AT3G42790 (AL3), AT5G26210 (AL4), AT5G20510 (AL5), AT2G02470 (AL6), AT1G14510 (AL7). AL4; ALFIN-LIKE 4
BolC09g010900.2J	Nucleus	2	AT5G66540.1: U3 small nucleolar ribonucleoprotein;(source:Araport11)
BolC09g040350.2J	Nucleus	2	AT5G53430.1: Homology Subgroup III; Orthology Group 2 - A putative histone methyltransferase (predicted to methylate H3K4) related to the Drosophila trithorax group proteins TRX and TRR and the yeast gene SET1. A plant line expressing an RNAi construct directed against this gene has reduced agrobacterium-mediated tumor formation. ARABIDOPSIS TRITHORAX5; ATX5; SDG29; SET DOMAIN GROUP 29; SET29
BolC09g040760.2J	Nucleus	2	AT5G53770.1: Nucleotidyltransferase family protein;(source:Araport11) TRF4/5-LIKE; TRL
BolC09g046820.2J	Cytoplasm Nucleus	2	AT5G58290.1: 26S proteasome AAA-ATPase subunit RPT3 (RPT3) mRNA, REGULATORY PARTICLE TRIPLE-A ATPASE 3; RPT3
BolC09g055560.2J	Nucleus	2	AT5G17690.3: Regulates the meristem response to light signals and the maintenance of inflorescence meristem identity. Influences developmental processes controlled by APETALA1. TFL2 silences specific genes within euchromatin but not genes positioned in heterochromatin. TFL2 protein localized preferentially to euchromatic regions and not to heterochromatic chromocenters. Involved in euchromatin organization. Required for epigenetic maintenance of the vernalized state.
BolC09g068820.2J	Nucleus	2	AT5G02820.1: Involved in the patterning and shape of leaf trichomes. Encodes the DNA topoisomerase VI SPO11-3, involved in endoreduplication BIN5; BRASSINOSTEROID INSENSITIVE 5; RHL2; ROOT HAIRLESS 2
BolC01g033320.2J	Cytoplasm Nucleus	1	AT1G54850.1: HSP20-like chaperones superfamily protein;(source:Araport11)

BolC01g035650.2J	Nucleus	1	AT1G60200.1: RMB25 is an alternative splicing factor involved in mediation of abiotic stress response and ABA response. Its expression is modulated by a variety of stressors and it in turn appears to affect the ratio of splice variants of stress responsive genes such as HAB1.2/HAB1.1. RBM25; RNA-BINDING PROTEIN 25
BolC01g042200.2J	Cytoplasm Nucleus	1	AT3G20740.1: Encodes a protein similar to the transcriptional regular of the animal Polycomb group and is involved in regulation of establishment of anterior-posterior polar axis in the endosperm and repression of flowering during vegetative phase. Mutation leads endosperm to develop in the absence of fertilization and flowers to form in seedlings and non-reproductive organs. Also exhibits maternal effect gametophytic lethal phenotype, which is suppressed by hypomethylation. Forms part of a large protein complex that can include VRN2 (VERNALIZATION 2), VIN3 (VERNALIZATION INSENSITIVE 3) and polycomb group proteins FERTILIZATION INDEPENDENT ENDOSPERM (FIE), CURLY LEAF (CLF) and SWINGER (SWN or EZA1). The complex has a role in establishing FLC (FLOWERING LOCUS C) repression during vernalization. In the ovule, the FIE transcript levels increase transiently just after fertilization. FERTILIZATION-INDEPENDENT ENDOSPERM; FERTILIZATION-INDEPENDENT ENDOSPERM 1; FIE; FIE1; FIS3
BolC01g049440.2J	Cytoplasm Nucleus	1	AT3G13460.1: Physically interacts with CIPK1. ECT2 regulates the mRNA levels of the proteasome regulator PTRE1 and of several 20S proteasome subunits, resulting in enhanced 26S proteasome activity. YTHDF protein which together with ECT3 and ECT4 is involved in cell proliferation during plant organogenesis. ECT2; EVOLUTIONARILY CONSERVED C-TERMINAL REGION 2
BolC01g050580.2J	Nucleus	1	AT3G12280.1: Encodes a retinoblastoma homologue RETINOBLASTOMA-RELATED protein (RBR or RBR1). RBR controls nuclear proliferation in the female gametophyte. Also required for correct differentiation of male gametophytic cell types. Regulates stem cell maintenance in Arabidopsis roots. Involved in the determination of cell cycle arrest in G1 phase after sucrose starvation. RBR1 is also involved in regulation of imprinted genes. Together with MSI1 it represses the expression of MET1. This in turn activates expression of the imprinted genes FIS2 and FWA. Functions as a positive regulator of the developmental switch from embryonic heterotrophic growth to autotrophic growth. ChIP studies indicate that one class of targets of RBR1 are transposable elements. ATRBR1; RB; RB1; RBR; RBR1; RETINOBLASTOMA 1; RETINOBLASTOMA-RELATED; RETINOBLASTOMA-RELATED 1; RETINOBLASTOMA-RELATED PROTEIN 1
BolC01g050680.2J	Nucleus	1	AT3G12140.2: Agenet domain containing nucleosome binding protein. Binds H3K36 sites. ATEML1; EML1; EMSY-LIKE 1
BolC02g012900.2J	Nucleus	1	AT5G59980.3: Encodes a predicted protein subunit of RNases P/MRP that plays a role in female gametophyte development and male competence.
BolC02g013660.2J	Nucleus	1	AT5G59180.1: Non-catalytic subunit specific to DNA-directed RNA polymerase II; the ortholog of budding yeast RPB7 NRPB7
BolC02g020660.2J	Nucleus	1	AT5G51660.3: cleavage and polyadenylation specificity factor 160;(source:Araport11)

BolC02g021010.2J	Nucleus	1	AT5G51230.3: Polycomb group protein with zinc finger domain involved in negative regulation of reproductive development. Forms a complex with FIE, CLF, and MSI1. This complex modulates the expression of target genes including AG, PI and AP3. ATEMF2; CYR1; CYTOKININ RESISTANT 1; EMBRYONIC FLOWER 2; EMF2; VEF2
BolC02g032080.2J	Nucleus	1	AT1G75670.3: DNA-directed RNA polymerase;(source:Araport11)
BolC02g037530.2J	Cytoplasm Nucleus	1	AT4G01590.2: DNA-directed RNA polymerase III subunit;(source:Araport11)
BolC03g018860.2J	Nucleus	1	AT2G31410.1: coiled-coil protein;(source:Araport11)
BolC03g020260.2J	Nucleus	1	AT2G34357.1: ARM repeat superfamily protein;(source:Araport11)
BolC03g029320.2J	Nucleus	1	AT2G27110.1: FAR1-related sequence 3;(source:Araport11) FAR1-RELATED SEQUENCE 3; FRS3
BolC03g035440.2J	Nucleus	1	AT4G00450.2: Encodes the Arabidopsis homolog of the transcriptional regulator MED12, is dynamically expressed during embryogenesis and regulates both developmental timing and the radial pattern formation. Involved in flowering time. The mutant enhances the expression of the flowering time (FT) gene. A knockout mutant of this gene showed late-flowering phenotype. CCT; CENTER CITY; CRP; CRYPTIC PRECOCIOUS; MED12; MEDIATOR 12
BolC03g038680.2J	Nucleus	1	AT3G05850.1: Encodes a member of a domesticated transposable element gene family MUSTANG. Members of this family are derived from transposable elements genes but gained function in plant fitness and flower development. Known members include: AT3G04605 (MUG1), AT2G30640 (MUG2), AT1G06740 (MUG3), AT5G16505 (MUG4), AT3G06940 (MUG5), AT5G48965 (MUG6), AT3G05850 (MUG7) and AT5G34853 (MUG8). MUG7; MUSTANG 7
BolC03g039690.2J	Nucleus	1	AT3G09360.2: Cyclin/Brf1-like TBP-binding protein. Double mutants with BRF1 show defects in pollen development. Controls FES1A regulated thermosensitivity. BRF2
BolC03g044880.2J	Nucleus	1	AT3G42170.1: transposase-like gene with conserved domains from the family of hAT transposases that includes hobo from Drosophila melanogaster, Activator (Ac) from maize, and Tam3 from snapdragon but lacks several amino acids known to be essential for Ac transposition ⁵ . The DAYSLEEPER gene lacks 8 bp duplications and TIRs (a common feature of transcriptionally silent hAT transposases), however, DAYSLEEPER expression was detected, and several expressed sequence tags are available. The expression seems to be under the control of factors determining the circadian rhythm. DAYSLEEPER was isolated as a factor binding to a motif (Kubox1) present in the upstream region of the Arabidopsis DNA repair gene Ku70. Mutant plants lacking DAYSLEEPER or strongly overexpressing this gene do not develop in a normal manner. DAYSLEEPER
BolC03g050290.2J	Nucleus	1	AT2G04865.1: Encodes a nuclear localized aminotransferase-like protein containing a plant mobile domain. The mRNA is cell-to-cell mobile. MAIL2; MAIN-LIKE 2
BolC03g054240.2J	Nucleus	1	AT5G65900.1: DEA(D/H)-box RNA helicase family protein;(source:Araport11)

BolC03g057940.2J	Cytoplasm Nucleus	1	AT5G63110.1: RPD3-like histone deacetylase. HDA6 mutations specifically increase the expression of auxin-responsive transgenes, suggesting a role in transgene silencing. ATHDA6; AXE1; HDA6; HDAC6; HISTONE DEACETYLASE 6; RNA-MEDIATED TRANSCRIPTIONAL SILENCING 1; RPD3B; RTS1; SIL1
BolC03g067200.2J	Cytoplasm Nucleus	1	AT3G47610.1: transcription regulator/ zinc ion binding protein;(source:Araport11)
BolC03g086250.2J	Nucleus	1	AT1G55520.2: TATA-box binding protein. Required for basal transcription. Acts facilitating the recruitment of TFIID to the promoter, which together with the RNA polymerase form the preinitiation complex. A. THALIANA TATA BINDING PROTEIN 2; ATTBP2; TATA BINDING PROTEIN 2; TBP2
BolC04g002740.2J	Nucleus	1	AT2G40700.1: DEAD-box helicase family protein. Overexpression confers tolerance to salt stress. RH17; RNA HELICASE 17
BolC04g007240.2J	Nucleus	1	AT2G45880.1: Encodes a beta-amylase-like protein present in the nucleus rather than targeted to the chloroplast. Contains BRASSINAZOLE RESISTANT1 (BZR1)-type DNA binding domains. Activates gene expression in protoplast transactivation assays. BAM7; BETA-AMYLASE 4; BETA-AMYLASE 7; BMY4
BolC04g014350.2J	Nucleus	1	AT2G34640.1: Present in transcriptionally active plastid chromosomes. Involved in plastid gene expression. HEMERA; HMR; PAP5; PLASTID TRANSCRIPTIONALLY ACTIVE 12; PTAC12; TAC12
BolC04g037200.2J	Nucleus	1	AT3G54760.2: dentin sialophosphoprotein-like protein;(source:Araport11)
BolC04g053720.2J	Cytoplasm Nucleus	1	AT2G26740.1: Encodes a soluble epoxide hydrolase whose expression is induced by auxin and water stress. ATSEH; SEH; SOLUBLE EPOXIDE HYDROLASE
BolC04g063740.2J	Nucleus	1	AT2G39580.2: zinc finger C3H1 domain protein;(source:Araport11)
BolC04g064260.2J	Cytoplasm Nucleus	1	AT2G40290.2: Encodes an eIF2alpha homolog that can be phosphorylated by GCN2 in vitro.
BolC04g064430.2J	Nucleus	1	AT2G40430.1: Encodes a homolog of yeast NOP53 that is an important regulator of cell division during organ growth. SMALL ORGAN 4; SMO4
BolC05g003030.2J	Nucleus	1	AT1G04930.3: hydroxyproline-rich glycoprotein family protein;(source:Araport11)
BolC05g003610.2J	Nucleus	1	AT1G05380.3: Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein;(source:Araport11)
BolC05g005850.2J	Nucleus	1	AT1G08060.2: Encodes a transcriptional silencer that is required for proper expression of PRR/NLR immune receptor genes. MAINTENANCE OF METHYLATION; MOM; MOM1; MORPHEUS MOLECULE; MORPHEUS MOLECULE 1
BolC05g006200.2J	Cytoplasm Nucleus	1	AT1G22090.1: hypothetical protein;(source:Araport11) EMB2204; EMBRYO DEFECTIVE 2204
BolC05g007270.2J	Nucleus	1	AT1G09520.1: hypothetical protein;(source:Araport11)
BolC05g010940.2J	Nucleus	1	AT1G13450.2: Encodes GT-1, a plant transcription factor that binds to one of the cis-acting elements, BoxII, which resides within the upstream promoter region of light-responsive genes. GT-1 was assumed to act as a molecular switch modulated through Ca(2+)-dependent phosphorylation/dephosphorylation in response to light signals. GT-1
BolC05g011950.2J	Nucleus	1	AT1G14460.1: AAA-type ATPase family protein;(source:Araport11)
BolC05g013850.2J	Nucleus	1	AT4G12670.2: Homeodomain-like superfamily protein;(source:Araport11)

BolC05g023830.2J	Cytoplasm Nucleus	1	AT1G25540.1: Encodes a nuclear protein that acts in a phyB pathway (but downstream of phyB) and induces flowering in response to suboptimal light conditions. PFT1 promotes flowering in CO dependent and independent pathways and integrates several environmental stimuli, such as light quality and JA-dependent defenses. Mutants are hypo-responsive to far-red and hyper-responsive to red light and flower late under long day conditions. Also shown to be a Mediator subunit regulating jasmonate-dependent defense. MED25; MEDIATOR 25; PFT1; PHYTOCHROME AND FLOWERING TIME 1
BolC05g030650.2J	Nucleus	1	AT1G32360.1: Zinc finger (CCCH-type) family protein;(source:Araport11)
BolC05g041310.2J	Nucleus	1	AT3G21350.2: RNA polymerase transcriptional regulation mediator-like protein;(source:Araport11) MED6
BolC05g041400.2J	Nucleus	1	AT3G21290.2: Nuclear-localized intrinsically disordered protein involved in promoting miRNA activity. CARP9; CONSTITUTIVE ALTERATIONS IN THE SMALL RNAS PATHWAYS9
BolC05g049470.2J	Nucleus	1	AT3G16810.1: Encodes a member of the Arabidopsis Pumilio (APUM) proteins containing PUF domain (eight repeats of approximately 36 amino acids each). PUF proteins regulate both mRNA stability and translation through sequence-specific binding to the 3' UTR of target mRNA transcripts. APUM24; PUM24; PUMILIO 24
BolC05g062180.2J	Nucleus	1	AT3G01460.1: Encodes a protein with a methyl-CpG-binding domain. Has sequence similarity to human MBD proteins. Involved in the modification of the FLC chromatin acetylation state to affect FLC expression. Mutants show an early flowering, and enhanced shoot branching phenotypes. ATMBD9; MBD9; METHYL-CPG-BINDING DOMAIN 9
BolC06g005600.2J	Nucleus	1	AT1G50910.2: hypothetical protein;(source:Araport11)
BolC06g009550.2J	Nucleus	1	AT3G13570.1: encodes an SC35-like splicing factor of 30 kD that is localized to the nuclear specks. Barta et al (2010) have proposed a nomenclature for Serine/Arginine-Rich Protein Splicing Factors (SR proteins): Plant Cell. 2010, 22:2926. AT-SCL30A; SC35-LIKE SPLICING FACTOR 30A; SCL30A
BolC06g021450.2J	Nucleus	1	AT3G54350.5: Forkhead-associated (FHA) domain-containing protein;(source:Araport11) EMB1967; EMBRYO DEFECTIVE 1967
BolC06g026120.2J	Nucleus	1	AT3G61240.1: DEA(D/H)-box RNA helicase family protein;(source:Araport11) RH12; RNA HELICASE 12
BolC06g036070.2J	Nucleus	1	AT1G67900.1: Phototropic-responsive NPH3 family protein;(source:Araport11)
BolC06g046610.2J	Nucleus	1	AT1G75340.2: Zinc finger C-x8-C-x5-C-x3-H type family protein;(source:Araport11)
BolC06g046830.2J	Nucleus	1	AT1G75560.2: zinc knuckle (CCHC-type) family protein;(source:Araport11)
BolC07g002070.2J	Cytoplasm Nucleus	1	AT2G19560.1: encodes a protein with a PAM domain involved in ethylene signaling. eer5 mutants show ethylene hypersensitivity in relation to hypocotyl elongation. EER5 interacts with EIN2 and with COP9 in Y2H assays. EIN3 protein levels are the same in WT and eer5-1 mutants. EER5 may be involved in promoting a dampening of the ethylene response. ATTHP1; ECTOPIC EXPRESSION OF SEED STORAGE PROTEINS 1; EER5; ENHANCED ETHYLENE RESPONSE 5; ESSP1; THP1
BolC07g006410.2J	Cytoplasm Nucleus	1	AT2G16860.1: GCIP-interacting family protein;(source:Araport11) ATSYF2

BolC07g028250.2J	Cytoplasm Nucleus	1	AT5G45600.2: The GSA41 human homolog is expressed in nuclei and binds NuMA, a component of the nuclear matrix in interphase nuclei. It negatively regulates flowering by controlling the H4 acetylation levels in the FLC and FT chromatin. GAS41; GLIOMAS 41; HOMOLOG OF YEAST YAF9 A; YAF9A
BolC07g038440.2J	Nucleus	1	AT5G49430.1: WD40/YVTN repeat and Bromo-WDR9-I-like domain-containing protein;(source:Araport11)
BolC07g038910.2J	Nucleus	1	AT5G28490.1: Encodes a nuclear protein that mediates light regulation of seedling development in a phytochrome-dependent manner. LIGHT-DEPENDENT SHORT HYPOCOTYLS 1; LSH1; OBO2; ORGAN BOUNDARY 2
BolC07g056230.2J	Nucleus	1	AT4G31880.2: One of 5 PO76/PDS5 cohesion cofactor orthologs of Arabidopsis. ATPDS5C; PDS5C
BolC08g015390.2J	Nucleus	1	AT4G16265.1: One of two highly similar, non-catalytic subunits common to nuclear DNA-directed RNA polymerases II, IV and V; homologous to budding yeast RPB9. Appears to be redundant with At3g16980 DEFECTIVE IN MERISTEM SILENCING 13; DMS13; NRPB9B; NRPD9B; NRPE9B
BolC08g017950.2J	Nucleus	1	AT5G52530.2: dentin sialophosphoprotein-like protein;(source:Araport11)
BolC08g031240.2J	Nucleus	1	AT1G23490.1: Gene encoding ADP-ribosylation factor and similar to other ARFs and ARF-like proteins. A member of ARF GTPase family. Arabidopsis has 21 known members, known to be essential for vesicle coating and uncoating and functions in GTP-binding. The gene is shown to play a role in cell division, cell expansion and cellulose production using antisense construct. ADP-RIBOSYLATION FACTOR; ADP-RIBOSYLATION FACTOR 1; ADP-RIBOSYLATION FACTOR 1A; ARF1; ATARF; ATARF1; ATARFA1A
BolC08g036300.2J	Nucleus	1	AT3G52100.1: RING/FYVE/PHD zinc finger-containing protein. Part of endomembrane trafficking system.
BolC08g040920.2J	Nucleus	1	AT3G57000.1: nucleolar essential protein-like protein;(source:Araport11)
BolC08g045370.2J	Nucleus	1	AT3G62330.1: Zinc knuckle (CCHC-type) family protein;(source:Araport11)
BolC08g045990.2J	Cytoplasm Nucleus	1	AT3G63130.1: Encodes a RAN GTPase activating protein involved in nuclear import, cell plate formation and mitotic spindle formation. Associates with nuclear envelope membranes. ATRANGAP1; RAN GTPASE ACTIVATING PROTEIN 1; RAN GTPASE-ACTIVATING PROTEIN 1; RANGAP1
BolC08g057950.2J	Nucleus	1	AT1G06910.1: Arabidopsis thaliana myb family transcription factor (At1g06910) TRF-LIKE 7; TRFL7
BolC08g059570.2J	Nucleus	1	AT1G03910.1: Encodes the Arabidopsis homolog of a conserved eukaryotic protein without known functional domains. The protein that localizes to nuclear speckles and colocalizes with known splicing proteins. CACTIN; CTN
BolC09g007370.2J	Nucleus	1	AT5G23080.1: Interacts with TATA-box binding protein 2. Contains domains with strong similarity to G-patch and SWAP domains, characteristic of RNA binding and processing proteins. Colocalizes with the splicing regulator SRp34 to subnuclear particles. It is an important component of miRNA and siRNA biogenesis. Mutants display developmental defects, including reduced plant height, polycotily, and reduced vascularization. Strong genetic interaction between TGH and AMP1. TGH; TOUGH
BolC09g016990.2J	Nucleus	1	AT1G64050.2: hypothetical protein;(source:Araport11)

BolC09g023200.2J	Nucleus	1	AT5G42820.1: U2 auxiliary factor small subunit. The atU2AF35b protein and its homolog, atU2AF35a, contain most of the conserved domains of hsU2AF35, including the psiRRM, one RS domain, two zinc fingers, and the two regions for interacting with U2AF large subunit. Both proteins lack the stretch of glycines present in human U2AF35. The sequences are overall 83% identical, and each Arabidopsis homolog shows approximately 70% similarity to hsU2AF35. U2AF(35) homologs were also identified from maize, rice and other plants with large-scale EST projects. Both genes are expressed in all major tissues, with atU2AF(35)a expressed at a higher level than atU2AF(35)b in most tissues. The expression patterns were different in roots: atU2AF(35)b expressed strongly in whole young roots and root tips and atU2AF(35)a limited to root vascular regions. ATU2AF35B; U2AF35B
BolC09g024340.2J	Nucleus	1	AT5G44280.3: Encodes a nuclear localized protein with similarity to animal polycomb repressive core complex1 (PRC1) core component RING. Appears to function redundantly with ATRING1b, a close paralog. Both interact physically with CLF and LHP1 and appear to function together to repress class I KNOX gene expression.
BolC09g027790.2J	Nucleus	1	AT2G02470.2: Encodes a member of the Alfin1-like family of nuclear-localized PHD (plant homeodomain) domain containing proteins that acts as a novel upstream regulator of root hair formation during Pi starvation. All AL proteins except AL3 bind to di- or trimethylated histone H3 (H3K4me3/2). Members of this family include: AT5G05610 (AL1), AT3G11200 (AL2), AT3G42790 (AL3), AT5G26210 (AL4), AT5G20510 (AL5), AT2G02470 (AL6), AT1G14510 (AL7). AL6; ALFIN-LIKE 6
BolC09g029860.2J	Nucleus	1	AT4G04920.2: Encodes a nuclear targeted protein that plays a role in the CBF pathway -downstream of CBF translation. Mutants have impaired cold responses, reduced levels of cold induced RNA transcripts, are sensitive to osmotic stress. Required for expression of CBF-controlled cold-upregulated genes and some, but not all, other cold up-regulated genes. Required for recruitment of the Mediator complex and RNA polymerase II to CBF-controlled cold-responsive genes. Required for expression of some dark-upregulated genes. SFR6 was isolated as a suppressor of cell wall defects in cob6 mutant background. AT5FR6; GLASSY HAIR 2; GLH2; IEN1; INSENSITIVE TO EXOGENOUS NAD ⁺ 1; MED16; MEDIATOR 16; SENSITIVE TO FREEZING 6; SFR6; YELLOW AND SENSITIVE TO IRON-DEFICIENCY 1; YID1
BolC09g057730.2J	Nucleus	1	AT5G15540.1: Encodes Adherin SCC2. Essential for viability. Required for normal seed development. Plays a role in the establishment of sister-chromatid cohesion and chromosome organization during meiosis. ARABIDOPSIS THALIANA SISTER-CHROMATID COHESION 2; ATSCC2; EMB2773; EMBRYO DEFECTIVE 2773; SCC2; SISTER-CHROMATID COHESION 2

Note: Transcription factors being highlighted in red and validated candidates in red and bold.

Supplementary Table 3 | Twenty-two predicted nucleus-localized proteins in rice.

Protein_ID	Localization	PSMs	Description
A2WKP3	Nucleus	556	Histone H2B.3 OS=Oryza sativa subsp. indica OX=39946 GN=H2B.3 PE=3 SV=1
A2ZL69	Cytoplasm Nucleus	121	Probable histone H2AXb OS=Oryza sativa subsp. indica OX=39946 GN=OsI_037312 PE=3 SV=1
A2Y533	Nucleus	100	Histone H3.2 OS=Oryza sativa subsp. indica OX=39946 GN=OsI_019426 PE=1 SV=1
B8ADZ3	Nucleus	13	PHD finger protein ALFIN-LIKE 7 OS=Oryza sativa subsp. indica OX=39946 GN=OsI_07694 PE=3 SV=1
Q94LW4	Nucleus	11	Homeobox protein knotted-1-like 11 OS=Oryza sativa subsp. japonica OX=39947 GN=HOS59 PE=2 SV=2; OsKNOT3
Q6K9C3	Nucleus	10	Serine/arginine-rich splicing factor RSZ23 OS=Oryza sativa subsp. japonica OX=39947 GN=RSZ23 PE=2 SV=1; OsB3-1
P31674	Cytoplasm Nucleus	5	Small ribosomal subunit protein uS19 OS=Oryza sativa subsp. japonica OX=39947 GN=RPS15 PE=2 SV=2
Q06967	Cytoplasm Nucleus	5	14-3-3-like protein GF14-F OS=Oryza sativa subsp. japonica OX=39947 GN=GF14F PE=1 SV=2
Q8W0W4	Nucleus	3	TATA-binding protein 2 OS=Oryza sativa subsp. japonica OX=39947 GN=TBP2 PE=1 SV=2
P46465	Cytoplasm Nucleus	3	26S proteasome regulatory subunit 6A homolog OS=Oryza sativa subsp. japonica OX=39947 GN=TBP1 PE=2 SV=2
Q75LV5	Nucleus	3	U3 snoRNP-associated protein-like YAOH OS=Oryza sativa subsp. japonica OX=39947 GN=Os03g0625900 PE=2 SV=1
P55857	Nucleus	3	Small ubiquitin-related modifier 1 OS=Oryza sativa subsp. japonica OX=39947 GN=SUMO1 PE=1 SV=1
Q75HE5	Nucleus	3	NAC domain-containing protein 2 OS=Oryza sativa subsp. japonica OX=39947 GN=NAC002 PE=1 SV=1; OsNAC19
Q0D6V7	Nucleus	2	Ribosome biogenesis protein BOP1 homolog OS=Oryza sativa subsp. japonica OX=39947 GN=BOP1 PE=2 SV=1
Q2R9D2	Nucleus	2	B3 domain-containing protein Os11g0197600 OS=Oryza sativa subsp. japonica OX=39947 GN=Os11g0197600 PE=2 SV=1;OsB3-2
Q75LL6	Nucleus	2	Transcriptional adapter ADA2 OS=Oryza sativa subsp. japonica OX=39947 GN=ADA2 PE=1 SV=2
Q7Y0Y8	Cytoplasm Nucleus	2	Histone deacetylase 1 OS=Oryza sativa subsp. japonica OX=39947 GN=HDAC1 PE=1 SV=1
Q6I5Y0	Nucleus	2	Cyclin-dependent kinase C-1 OS=Oryza sativa subsp. japonica OX=39947 GN=CDKC-1 PE=2 SV=1
Q9FXM3	Cytoplasm Nucleus	1	Replication factor C subunit 2 OS=Oryza sativa subsp. japonica OX=39947 GN=RFC2 PE=2 SV=1
P0C455	Nucleus	1	Large ribosomal subunit protein bL33c OS=Oryza sativa OX=4530 GN=rpl33 PE=3 SV=1
Q0DY81	Nucleus	1	Nuclear matrix constituent protein 1a OS=Oryza sativa subsp. japonica OX=39947 GN=NMCP1A PE=2 SV=1
Q650T9	Nucleus	1	DEAD-box ATP-dependent RNA helicase 7 OS=Oryza sativa subsp. japonica OX=39947 GN=Os09g0520700 PE=2 SV=1

Note: Transcription factors being highlighted in red.

Supplementary Table 4 | Primers used in this study.

Primer name	Vector	Forword Primer	Reverse Primer	Purpose
Turbo-PIF4	dCas9-TD	ATATATGGTCTCGATTGTAGAAATACAAACCG AGACGGTTTTAGAGCTAGAAATAGC	ATTATTGGTCTCGAAACCGTCTCGGTTTGTATT TCTACAATCTCTTAGTCGACTCTAC	Target <i>PIF4</i> promoter in Arabidopsis
mini- <i>PIF4pro</i>	pGreenII 800-miniLUC	CACTATAGGGCGAATTGGGTACCGAGTATCGG GCTTTACTCAGAAGCCCATAG	CCTTATATAGAGGAAGGGTCTTGTCTAGAACC AAGTCCATGAGTCCGTTCTCTTG	LUC/REN assay
62- <i>TCP14</i>	pGreenII 62-SK	gaggacagcccaagctgATGCAAAAGCCAACATCAAGT ATC	ggtcgacggatcgcataCTAATCTTGCTGATCCTCCTCA TCAC	LUC/REN assay
62- <i>GTL2</i>	pGreenII 62-SK	gaggacagcccaagctgATGGAGCAAGGAGGAGGTGG TGG	ggtcgacggatcgcataTTACTGAACCATTGTCAAGAAA GGTGG	LUC/REN assay
62- <i>FHY3</i>	pGreenII 62-SK	gaggacagcccaagctgATGGATATAGATCTTCGACTA CATTTCAGGTG	ggtcgacggatcgcataTTACGAGTGTCTAGACGCGTCC TC	LUC/REN assay
62- <i>LSH3</i>	pGreenII 62-SK	gaggacagcccaagctgATGGATATGATTCCCCAATTG ATGG	ggtcgacggatcgcataTTACTTCTCAAACCTTTAATTGA GTAGTAGAAC	LUC/REN assay
AbAi- <i>PIF4</i>	pAbAi	CTTGAATTCGAGCTCGGTACCCATTTTCAGGAA AACTTAGCATGAAG	ATACAGAGCACATGCCTCGAGAGGTGGTTTCT TATCTGTACCTTATC	Yeast one hybrid
AD- <i>TCP14</i>	pGAD-T7	GTACCAGATTACGCTCATATGATGCAAAAGCC AACATCAAGTATC	GATTCATCTGCAGCTCGAGCTCATCTTGCTGAT CCTCCTCATCAC	Yeast one hybrid
AD- <i>GTL2</i>	pGAD-T7	GTACCAGATTACGCTCATATGATGGAGCAAGG AGGAGGTGGTGG	GATTCATCTGCAGCTCGAGCTCCTGAACCATTG TCAAGAAAGGTGG	Yeast one hybrid
AD- <i>FHY3</i>	pGAD-T7	GTACCAGATTACGCTCATATGATGGATATAGA TCTTCGACTACATTTCAGGTG	GATTCATCTGCAGCTCGAGCTCCGAGTGTCTAG ACGCGTCCTC	Yeast one hybrid
AD- <i>LSH3</i>	pGAD-T7	GTACCAGATTACGCTCATATGATGGATATGATT CCCCAATTGATGG	GATTCATCTGCAGCTCGAGCTCCTTCTCAAACCT TTAATTGAGTAGTAGAAC	Yeast one hybrid
GEX- <i>TCP14</i>	pGEX4T-1	cgcgtggatccccggaattcATGCAAAAGCCAACATCAA GTATC	gtcacgatcgccgctcgagCTAATCTTGCTGATCCTCC TCATCAC	EMSA assay
GEX- <i>GTL2</i>	pGEX4T-1	cgcgtggatccccggaattcATGGAGCAAGGAGGAGGTG GTGG	gtcacgatcgccgctcgagTTACTGAACCATTGTCAAG AAAGGTGG	EMSA assay
GEX- <i>FHY3</i>	pGEX4T-1	cgcgtggatccccggaattcATGGATATAGATCTTCGACT ACATTTCAGGTG	gtcacgatcgccgctcgagTTACGAGTGTCTAGACGCG TCCTC	EMSA assay
GEX- <i>LSH3</i>	pGEX4T-1	cgcgtggatccccggaattcATGGATATGATTCCCCAATT GATGG	gtcacgatcgccgctcgagTTACTTCTCAAACCTTTAAT TGAGTAGTAGAAC	EMSA assay

qPCR- <i>eIF4a</i>	-	CGTGACCACACAGTCTCTGCAAC	GATAACCAGGGAGACTTGTGAC	qRT-PCR
qPCR- <i>PIF4</i>	-	GTTATTATGGCGAGATGGACAAGTGG	GTCGGGTTCGAATGGGTCTTC	qRT-PCR
qPCR- <i>TCP14</i>	-	GAAATACAAACCGAGACGCGGTATG	GTGGACCATTGTGCCTACTTGTAATGG	ChIP-qPCR
qPCR- <i>GTL2</i>	-	CCATTACAAGTAGGCACAATGGTCCAC	CACGTTGCATTGAAAGGGCACC	ChIP-qPCR
qPCR- <i>FHY3</i>	-	GAAATACAAACCGAGACGCGGTATG	GTGGACCATTGTGCCTACTTGTAATGG	ChIP-qPCR
qPCR- <i>LSH3</i>	-	CTCGTTGAGAGCATTGAACTCGG	GTCAAATCACAATCATCTATAGCGTTATGG	ChIP-qPCR
Turbo-BolPIF4	dCas9-TD	ATATATGGTCTCGATTGTACAGATCAGAAACC ACCTCGTTTTAGAGCTAGAAATAGC	ATTATTGGTCTCGAAACGAGGTGGTTTCTGATC TGTACAATCTCTTAGTCGACTCTAC	Target <i>BolPIF4</i> promoter in cabbage
mini- <i>BolPIF4pro</i>	pGreenII 800-miniLUC	GGTCGACGGTATCGATAAGCTTGCTGATGTGT CATGTTCTCGAG	GGAAGGGTCTTGCTAGAACTAGTGTGTCAGATC TCTGGAGACATGG	LUC/REN assay
62- <i>BolGTL2</i>	pGreenII 62-SK	gaggacagcccaagctgATGGAGCAAGGAGGTGGTGG TG	ggtcgacggtatcgataTACTGAACCATTGTCAAGAAA GGTGGC	LUC/REN assay
62- <i>BolTGA6</i>	pGreenII 62-SK	gaggacagcccaagctgATGGCTGATACCAGTTCAAGG ACTG	ggtcgacggtatcgataTCACTCTCTTGGCCTGGCAAGC	LUC/REN assay
62- <i>BolC3H</i>	pGreenII 62-SK	gaggacagcccaagctgATGGATTTTAACGCCGGAGTT CC	ggtcgacggtatcgataTCAGTTGGTAGTGTCTTCCCCA GAG	LUC/REN assay
AbAi- <i>BolPIF4</i>	pAbAi	CTTGAATTCGAGCTCGGTACCGAGACTTGTGTG CCTCATATTCAATG	ATACAGAGCACATGCCTCGAGCCTCTCACTTG CTCTCTAGTCTC	Yeast one hybrid
AD- <i>BolGTL2</i>	pGAD-T7	GTACCAGATTACGCTCATATGATGGAGCAAGG AGGTGGTGGTG	GATTCATCTGCAGCTCGAGCTCCTGAACCATTG TCAAGAAAGGTGGC	Yeast one hybrid
AD- <i>BolTGA6</i>	pGAD-T7	GTACCAGATTACGCTCATATGATGGCTGATAC CAGTTCAAGGACTG	GATTCATCTGCAGCTCGAGCTCCTCTCTTGGCC TGGCAAGC	Yeast one hybrid
AD- <i>BolC3H</i>	pGAD-T7	GTACCAGATTACGCTCATATGATGGATTTTAAC GCCGGAGTTCC	GATTCATCTGCAGCTCGAGCTCAGTTGGTAGTG TCTTCCCCAGAG	Yeast one hybrid
GEX- <i>BolGTL2</i>	pGEX4T-1	cgcgtggatccccggaattcATGGAGCAAGGAGGTGGTG GTG	gtcacgatgcggccgctcgagTACTGAACCATTGTCAAG AAAGGTGGC	EMSA assay
GEX- <i>BolTGA6</i>	pGEX4T-1	cgcgtggatccccggaattcATGGCTGATACCAGTTCAAG GACTG	gtcacgatgcggccgctcgagTCACTCTCTTGGCCTGGCA AGC	EMSA assay
GEX- <i>BolC3H</i>	pGEX4T-1	cgcgtggatccccggaattcATGGATTTTAACGCCGGAGT TCC	gtcacgatgcggccgctcgagTCAGTTGGTAGTGTCTTCC CCAGAG	EMSA assay
Turbo-OsPIF4	dCas9-TDmo	CCTCGGATACTTTCGGTCTTCAACACAAGCGGCA GCGCGCGG	GTGTTGAAGACCGAAAGTATCCGAGGTTTCAGAG CTATGCTGGAACAGC	Target <i>OsPIF4</i> promoter in rice
AbAi- <i>OsPIF4</i>	pAbAi	CTTGAATTCGAGCTCGGTACCGTGTGAGTGCTC	ATACAGAGCACATGCCTCGAGCTTCACACACC	Yeast one hybrid

AD- <i>OsNAC19</i>	pGAD-T7	AGCTCCTATCGC GTACCAGATTACGCTCATATGatggggatggggatgagg agg	ATATTCGACCTGAC GATTCATCTGCAGCTCGAGCTCtcagaacgggaccatgc ccatgc	Yeast one hybrid
AD- <i>OsB3-1</i>	pGAD-T7	GTACCAGATTACGCTCATATGCTCATGGCTCGC GTGTACGTGG	GATTCATCTGCAGCTCGAGCTCTTACGCGTTAT TTGCGTAGGGGGAC	Yeast one hybrid
AD- <i>OsB3-2</i>	pGAD-T7	GTACCAGATTACGCTCATATGATGGTGGTTAG GGAAAAGCAAGGTG	GATTCATCTGCAGCTCGAGCTCTTACTTCGGGT CAGAACGGAGTTTGTG	Yeast one hybrid
AD- <i>OsKNOT3</i>	pGAD-T7	GTACCAGATTACGCTCATATGATGGCGTTCCAC TACCAGGAC	GATTCATCTGCAGCTCGAGCTCCTACCAAGATT GCTCGGCCTTGCC	Yeast one hybrid
