

Supplementary material to:

Members of the gibberellin receptor gene family (*GIBBERELLIN INSENSITIVE DWARF1*) play distinct roles during *Lepidium sativum* and *Arabidopsis thaliana* seed germination

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Supplemental data

Supplemental Figure S1. GID1 transcript sequence alignments of *L. sativum* and *Arabidopsis*.

Supplemental Figure S2. GID1 protein sequence alignments of *L. sativum* and *Arabidopsis*.

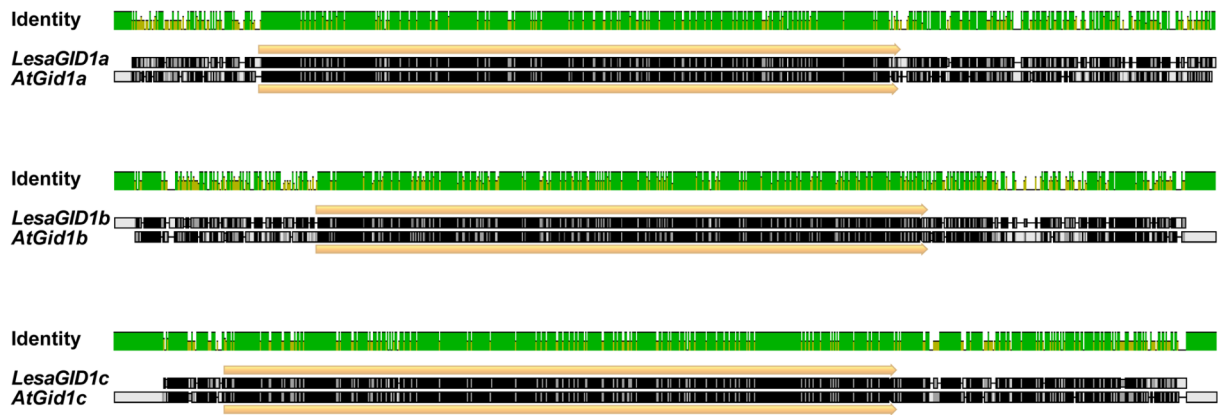
Supplemental Figure S3. Comparison of *L. sativum* and *Arabidopsis* GID1 transcript secondary structures and stability motifs in 5' and 3' UTRs.

Supplemental Figure S4. *L. sativum* and *Arabidopsis* GID1 5' and 3'UTRs motifs associated with mRNA stability.

Supplemental Table S1. Angiosperm phylogeny and GID1 receptor sequence accession numbers of the molecular phylogenetic analysis.

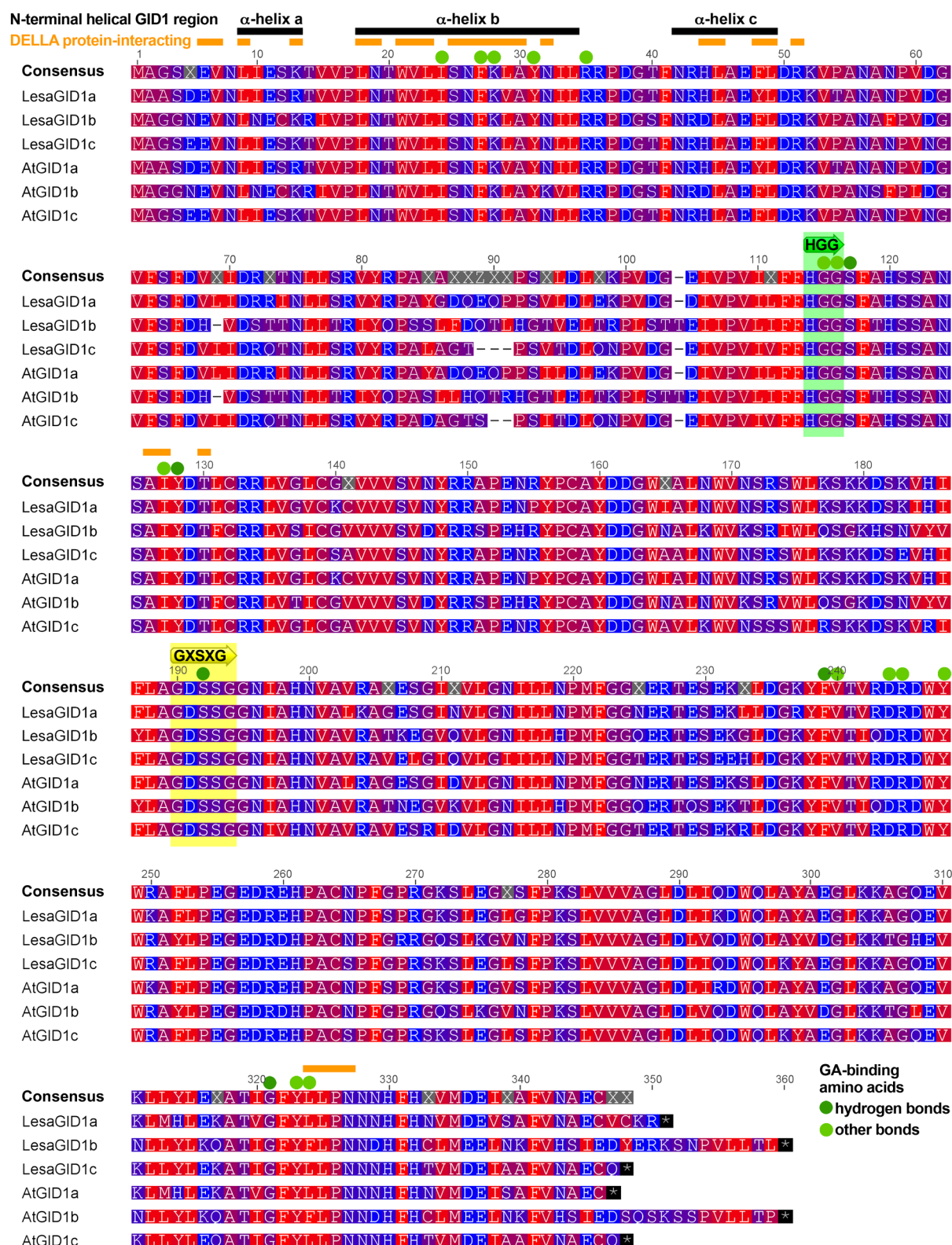
Supplemental Table S2. cDNA clones obtained of the early micropylar endosperm SSH library.

Supplemental Table S3. Primer sequences that were used for the quantitative PCR analyses.



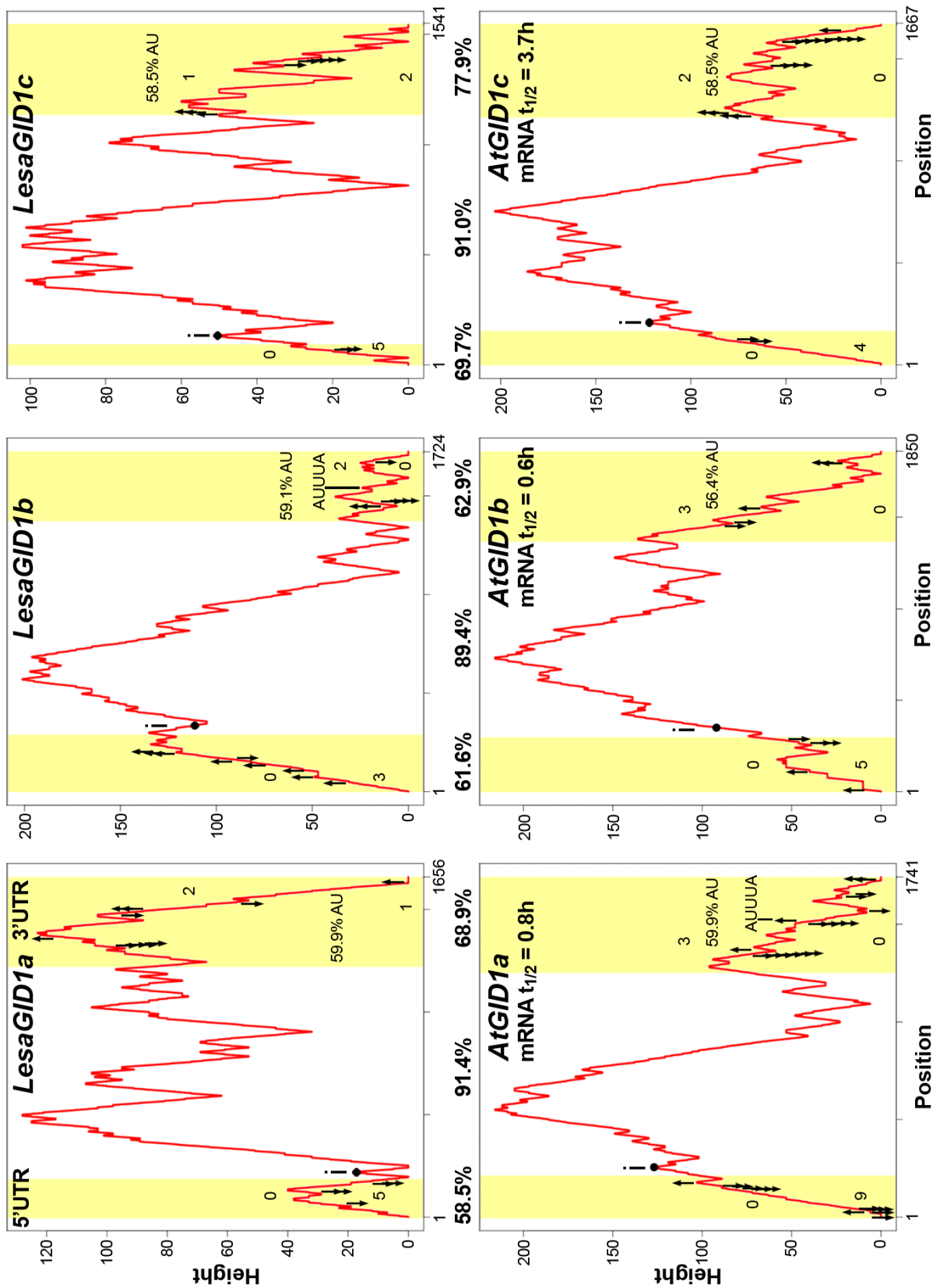
Supplemental Figure S1. Transcript sequence alignments of the Brassicaceae GID1 family members of *Lepidium sativum* (*LesaGID1a*, *LesaGID1b*, *LesaGID1c*) and *Arabidopsis thaliana* (*AtGID1a*, *AtGID1b*, *AtGID1c*).

Full-length coding sequences including 5' and 3' UTR-sequences of *GID1a*, *GID1b*, and *GID1c* from *L. sativum* and *Arabidopsis* were aligned using the Geneious Alignment Algorithm (gap open penalty: 12, gap extension penalty: 3). The identity plots and the pairwise alignment of the corresponding putative cDNA orthologous sequences of the two species are presented. Different vertical colouring represents the identity at each base position between the two sequences: black = the bases at these positions are identical, grey = base positions that are only present in one of the sequences, white = the bases at these positions are not identical. The coding sequences are indicated as orange arrows. Nucleotide coding sequence similarity between the corresponding orthologous sequences from *L. sativum* and *Arabidopsis* are 91.4% for the *GID1a*, 89.4% for the *GID1b*, and 91.0% for the *GID1c* sequences.



Supplemental Figure S2. Sequence alignment of the predicted GID1 proteins of *Lepidium sativum* (*LesGID1a*, *LesGID1b*, *LesGID1c*) and *Arabidopsis thaliana* (*AtGID1a*, *AtGID1b*, *AtGID1c*).

Alignment of LesaGID1a, LesaGID1b, LesaGID1c, AtGID1a, AtGID1b and AtGID1c protein sequences using the BLOSUM62 algorithm (gap open penalty: 12, gap extension penalty: 3). Similarity between the corresponding sequences from *L. sativum* and Arabidopsis was 96.2% for GID1a, 92.8% for GID1b, and 94.8% for GID1c. Amino acids are color-coded according to their hydrophobic characteristics, with red being most hydrophobic and blue being most hydrophilic. The α -helices a, b and c of the N-terminal helical GID1 region known to be important for DELLA repressor binding (Murase *et al.*, 2008) are shown as black bars at the top. Residues known crystal structures for DELLA repressor binding (Murase *et al.*, 2008) are indicated as orange bars. Green circles indicate important residues for GA3 and GA4 binding based on the crystal structures (Murase *et al.*, 2008); *dark green*: hydrogen bonds with GA, *light green*: other bonds with GA. The HGG and GX SXG motives, known as conserved motifs in hormone sensitive lipases, are highlighted as green (HGG) and yellow (GX SXG) boxes and are indicated by arrows. Accession numbers: LesaGID1a, HQ003455; LesaGID1b, HQ003456; LesaGID1c, HQ003457; AtGID1a, At3g05120; AtGID1b, At3g63010; AtGID1c, At5g27320. Based on the similarities and the presence of all the required sequence motifs we conclude that the *L. sativum* proteins are functional GID1 proteins and are encoded by *L. sativum* gene orthologs of the corresponding Arabidopsis GID1a, GID1b, and GID1c genes.



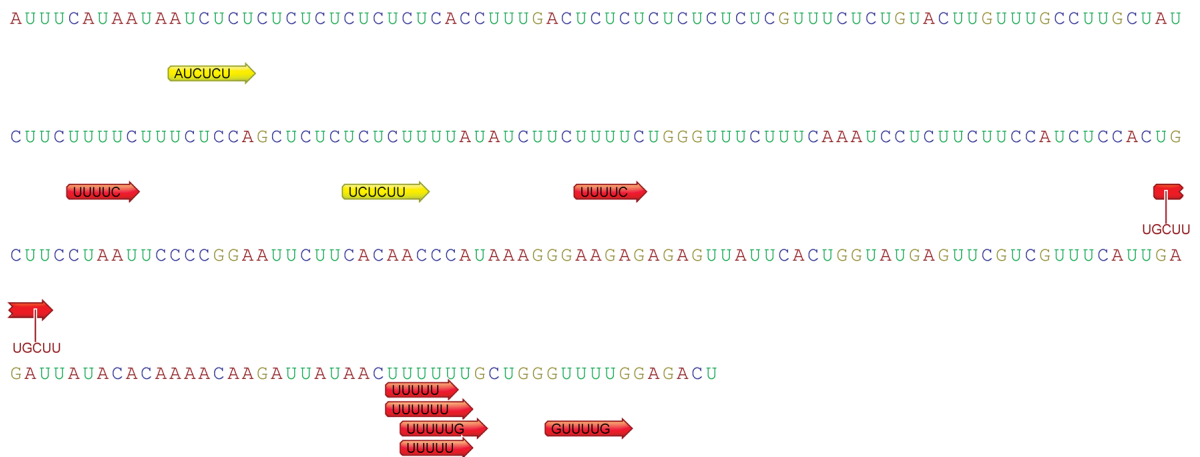
Supplemental Figure S3: Comparison of *L. sativum* and Arabidopsis GID1 transcript secondary structures and stability motifs in 5' and 3' UTRs (untranslated regions).

Secondary structures of *L. sativum* and Arabidopsis GID1 transcripts were predicted using the Vienna RNA Websuite tool RNAfold (Hofacker and Stadler, 2006) and were graphically represented using the mountain plot output, which plots secondary structures as height versus position. The height represents the number of bases which enclose a base at a peak or plateau position, which leads to loops being shown as plateaus and hairpins being represented as peaks. The positions of intron splice sites and different regulatory motifs are marked in each mountain plot diagram, as well as mRNA half lives (as determined in Arabidopsis cell cultures by Narsai *et al.*, 2007) and AU contents in 3' UTRs. Global UTR motifs associated with stabilizing and destabilizing of mRNAs as determined by Narsai *et al.* (2007) were marked using arrows pointing upwards (stabilizing motifs) or downwards (destabilizing motifs). The numbers of motifs related to the mRNA 5'-3' decapping pathway as defined by Jiao *et al.* (2008) were indicated above (repressing mRNA uncapping) and underneath (enhancing mRNA uncapping) the mountain plot. Comparison of GID1 secondary structures and stability motifs in 5' and 3' UTRs suggests rapid regulation of transcript abundances.

LesbGID1b 5'UTR



AtGID1b 5'UTR



***Les*GID1c 5'UTR**

TNNTNTTCGGCTCAAATCTTCGATCTGGGCTTTCGTGTTTCTGTTCGTTTGATTGGTAATAAAAGGAGATCTTTTTC
UUUUC
UUUUUU
UUUUUU
UUUUU
UUUUU
UUUUU

ATTTTCNT
UUUUC

***At*GID1c 5'UTR**

ACGUUUAAAAGCAGGUUUCUUUCUAUUUCCAGAUAAAAAACUUUACUCAUCGAGACUCGUUUAGUGAUUCGAAAUUCC

UUCUCGGCUCAAAUCUUCGAUCUGGGCUUUCGUGUCUUUUUGCGUUUUGAUUGGUAAUAAAAGAAGCUUUUUAAAAACUU
UUUUU
UUUUUG
GUUUUG
UUUUU
UUUUU
UUUUU
UUUUU

UUUCC
UUUCC
UUUU
UUUU

LesbGID1a 3'UTR

AUGUUAAACCCAAUGUUCGAGAAAGGAGGCUGUUUUAAUAGAGCCAACAAGUCUUUCAAAACUAAACAAAACAGGUGACGGCC

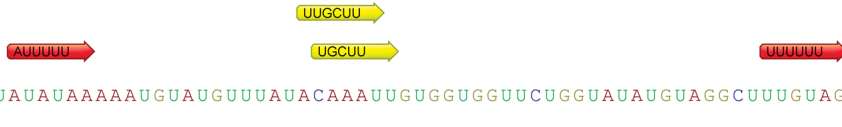
GARE →

UGUGGAUUCUCUCGAGUAGUUUUUUUUUGGUGUUUAGUACUUAAGUGUGUGGCGGUUCCGACAGCGUUUGAGUCUU



UUCUAAUCGUUGGAUUCGAGUGAAAGAACAGCCAAGCGGUCAGAGACUCGGAAAGGAACAGAGCAGAAGUAAUAAUUU

UCUCCUCUUUUUUUUUGGUCUGUAAUGUUUGUUUUAGCCUAAUUCUUAAACUAAAGCUGUUUUUUUUCAGCUUGGGAAUG



UUAUCUUGUAUUUGUAAAAAAAAAAAAAAAA



AtGID1a 3'UTR

CACUGGGUUAGAGAAAGAAGGUUGUUUUAAACAAAGCCAAGACAUCUUUCAAAACUAAACACACAGGUGAAUGUAUUUGCCUGUG

UUGUU →

GARE →

GAUUCUCUCGUUUAGUUUUUUUUUUUGUUUAGUAUCUAAGUGUGGCGGUUCGCGGCAGCCUUUGGAUGACUGUUUAA



ACGCUUGGAUUCUGAAACGCUAAAGCUUGUGGAAGAACAGUGAGGCGUUUAGAGACUUGGAAAGGAACCAAGCACUAGUAAA

AAUUUCUCCUUUUUUUUGUCUGUAAUAAUUGGCAUUUAGCUUUUACCUUGAGCCUUUUUACUAAACUAAAAGCUGAUUUUUU

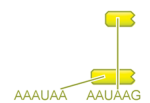


CAGCAUGAGAGUGGUAUUAGAUUUCUUAUUAAUUAUAUAAUUUCAAGAAUGUAAUGUUUAUACACAAAUUUUAGUGAUUUU

AAUUUU → AUUUUG →

GGUAAAUGUAUGUAGGGUCUGCACUCUGCAGUUGUAUUUUUGCUCUUUUUUAUUUGUACUCUAAUGGAUUUUUACAAAAA

UUGUU →



*Les*GID1b 3'UTR

CAACAACAAGCTCTCTGTTCA TGTTGCTGAATGCTGATACATACATAAAGAGAAGAAGAAAAGAAGATTAGAGGATCAGT

TTGCTTTGGCCATCTCTGATGGGTTTTTTGTACAGTTTACATATGTAGTGTATTATGTGAGATCCTTGTTGCGCCTCAAG
UGCUUU → GUUUUU → UUUUGU → UUGUU →
UUGCUU → UUUUUG →

TAAAGACCATTAGGTTTAAGTTTAGAGCAAAACGTGCGTACTAGTATGGGTAGACTTTAAATTGGTTC TAGAGTACAGTT
AAUUA →

GGTAAATTACAAGACAAC TAAC TTGCTCTCAACA TG TGTGAAAAAACTTATCCTTCGGTTTGTATA TCATTACCTT
UUGUU → T → UUUUGU

TTGTCCTCTCGTGTATTA AAAAAAAAAAAAAAAAAA
UUUUGU → UUUUGU

*At*GID1b 3'UTR

CAACGACAAUGUCUGGUCAUGUUGCUGAUAUAUACCACAUGAAGAGUAGAAGAAGACUAGAGGAUCGGUUUGUUUGC
UUUUUG → UUGUU →

CUAUCUAUGAUUGGGUUGUGUACAGUUUCCACAAGUGGUGUCUAGUGUCAAUAGCGUUUCUUUUUGUUGUCCUUGGUCUCC
UUUUGU →

GG AAGCAUAAUAAGUCUGUCUUUCUGUGAGGUCUUGGUGCGCCUGGCGAGAGACCACUUCGGUUAUCGGCAUCUAUCGUU
AAUAAG →

UUAGGGCUAUACCGGGGAAUGGUACUUUGUUUGCGUACUAGUAUGGGUAGGCUUAGUUGGUUCUAGCUUAGAGUACAGAG
UUGUU →

GGUAAAUUACAAGACAACUAACUUGUCUUCAACAUGUUGUGAAAAAAACUAAUCCUUGGUGAGGAUUUGUAUGUUUAUAUU

AACUUUUUCUUUCUAUGCUAUUAAUAGAGUAUGUCUUUGGUGUAGUUUCACUUCUUCUUGUUUUAGUUC AUGCA
UGCUUU → UUGCUU → UUGUU →

UU

*Les*GID1c 3'UTR

AAACAGTC TCATCTCTCAC TGTAATCTCTTCAC TAACAAACGGGTTTATCCACGGCTAACCCGAGATTCCTCGTTTTAGA
AUCUCU → AUCUCU → GARE →
UCUCUU →

AGCTCTTTGTAGTGATATATCCAAAAGTACGGCGTTTAACTACTACCTCAGCCGCTGCGTTTGCGTCTGCGTTTGTGAAA

CCGTGTGAAGCTGGATTCTGATAGCAAAGCAGGAAGAAGAACAGTGAAGCCGGTAA TGTTGGTTTTAGTGT TAGTTTTTC
AGUUUU →

AACTCTAAC TAGAGCTGAGTTTTTTTCATCTTGCGGTTAATAGTAACTTCGGTTATGTTGCTATCATGATATTTTCCGTA
AGUUUU →
GUUUUU →
UUUUUU →
UUUUUU →

TAATAATCTTATA TACATA TATCAACGATATGTA TAAATAACA TGAGCCATGTAA TGTTGTGTTTAA TGTGCAAG
UAUCUU → UUGUU →

TAA TTGTAAAAAAAAAAAAA

*At*GID1c 3'UTR

GAAACACUCUUAUCUCUCACUGUAAUCUCUUCACUAAACAAACGGGUGAUAUCCACCAUGGAAGGUGAAAGCCCGAGAUUCUC
UUUAUCU → UCUCUU →
AUCUCU → AUCUCU → GARE →

GUUUUAGAAGCUCUUUGUAGUGAGUCAAAAGAACGGCGUUUAACUACUACC GCGUGGGUGGUGGUGCGGUCUGCCGCUUUGUG

AACCGUCCAAAAGCUGGAUUCUGAAAGCAAAGCAGGAAGAAGAACAGUGUAGUCGGUAAUUAUGUUUGGCUUUCUAGCGUUA

GCUUUUGACUUUAAACUAGAGCUGAGUUUUUUCAGCUUGUGGUUAAUAGUAACUUUGGUUAUGUUACUAUUUAUGAUUUUUUC
GUUUUU →
UUUUUU →
AGUUUU →

GGUAAAUAUCUAUCUAGUACAUAUACAUGCAUACAUCAACAAUAUGUUUAAUUAUAGCUUUUUUUGUUUUUGUAUAAUUA
UUGUU →
UUUUUG → UUUUGU →
UUUUUG → UUUUUU →
UUUUUU → GUUUUU →

UAAGUUUUUGUAGCUAUGUGGGUUGUGUUUGCUUACC UAAAAGUGAUCUUUUAUUUUUU
UUGUU →

UUGCUU →

Supplemental Figure S4: *L. sativum* and Arabidopsis GID1 5' and 3'UTRs (untranslated regions) with motifs associated with mRNA stability

Various motifs associated with mRNA 5'-3' decapping as determined by Jiao *et al.* (2008) and with global mRNA decay (Narsai *et al.*, 2007) are marked in the 5' and 3'UTRs of *L. sativum* and Arabidopsis GID1 sequences. Motifs associated with stabilization are indicated in yellow, motifs associated with destabilization are indicated in red. The GA responsive *cis*-acting element GARE is marked in blue, and the classical AUUUA pentamer, associated with the main deadenylation pathway is indicated in turquoise.

Supplemental Table S1. Angiosperm phylogeny and GID1 receptor sequence accession numbers of the three individual GID1 receptor groups revealed by molecular phylogenetic analysis presented in Figure 1: eudicot GID1ac, eudicot GID1b, monocot GID1. For generating the unrooted phylogenetic tree translated protein sequences of 37 available GID1 full-length or near full-length cDNA sequences (in red) from different species were aligned. Additional sequences contained in the table were assigned to the different GID1 receptor groups based on the sequence similarities of their translated (partial) cds (best BLAST hit). Sequences are available from the following databases:

<http://www.phytozome.net/> (*Cucumis*, *Manihot*, *Carica*, *Mimulus*, and *Brachypodium*)

http://compgenomics.ucdavis.edu/compositae_index.php (*Lactuca* and *Helianthus*)

<http://www.ncbi.nlm.nih.gov/> (all others)

| Angiosperm phylogeny | Angiosperm GID1 receptor group | | |
|-------------------------------|---------------------------------|----------------------------------|--------------|
| | Eudicot GID1ac | Eudicot GID1b | Monocot GID1 |
| Rosids (core eudicots) | | | |
| Cucurbitales | | | |
| <i>Cucumis sativus</i> | Cucsa.1637401 | Cucsa.084780 | |
| <i>Cucurbita maxima</i> | AM745266 | AM745267 | |
| Fabales | | | |
| <i>Glycine max</i> | AK285463 | AK286926 | |
| <i>Medicago truncatula</i> | BN001191 | BN001192 | |
| Malpighiales | | | |
| <i>Ricinus communis</i> | XM_002512264 | XM_002524721 | |
| <i>Populus trichocarpa</i> | XM_002328371 | XM_002302777 | |
| <i>Manihot esculenta</i> | cassava22764 cassava36647 | cassava29555 cassava 24655 | |
| Malvales | | | |
| <i>Gossypium hirsutum</i> | FJ790128 FJ790130 | DQ829776 FJ790126 FJ790127 | |
| Brassicales | | | |
| <i>Arabidopsis thaliana</i> | At3g05120 At5g27320 | At3g63010 | |
| <i>Arabidopsis lyrata</i> | XP_002882394 XP_002874383 | XP_002876701 | |
| <i>Lepidium sativum</i> | HQ003455 HQ003457 | HQ003456 | |
| <i>Carica papaya</i> | evm.model supercontig_84.118 | evm.model supercontig_731.1 | |
| Vitaceae | | | |
| <i>Vitis vinifera</i> | XM_00226572 | XM_00227166 | |

Angiosperm phylogeny

Angiosperm GID1 receptor group

| | Eudicot GID1ac | Eudicot GID1b | Monocot GID1 |
|--|-----------------------|--------------------------|----------------------|
| Asterids (core eudicots) | | | |
| Lamiales | | | |
| <i>Mimulus guttatus</i> | | mgf013441m mgf013028m | |
| Solanales | | | |
| <i>Solanum lycopersicum</i> | AK322582 | BN001197 AK328124 | |
| Asterales | | | |
| <i>Helianthus annuus</i> ^a | Heli_annu.DY905340 | Heli_annu.CSA1.2356 | |
| <i>Helianthus ciliaris</i> ^a | Heli_cili.EL415899 | Heli_cili.CSA.12537 | |
| <i>Helianthus exilis</i> ^a | Heli_exil.CSA1.102 | | |
| <i>Helianthus paradoxus</i> ^a | Heli_para.CSA1.406 | Heli_para.EL481749 | |
| <i>Helianthus petiolaris</i> ^a | Heli_peti.CSA1.4196 | Heli_peti.DY944716 | |
| <i>Helianthus tuberosus</i> ^a | Heli_tube.EL43821 | Heli_tube.CSA1.448 | |
| <i>Lactuca perennis</i> ^a | Lact_pere.CSA1.2657 | Lact_pere.DW090471 | |
| <i>Lactuca saligna</i> ^a | Lact_sali.CSA1.630 | Lact_Sali.DW050958 | |
| <i>Lactuca sativa</i> ^a | | Lact_sati.D4973435 | |
| <i>Lactuca serrida</i> ^a | | Lact_serr.DW115969 | |
| <i>Lactuca virosa</i> ^a | | Lact_viro.DW164935 | |
| Ericales | | | |
| <i>Actinidia deliciosa</i> | | DQ279922 | |
| Basal eudicots | | | |
| Ranunculales | | | |
| <i>Aquilegia formosa</i> x <i>Aquilegia pubescens</i> | BN001198 | | |
| Monocots | | | |
| Liliales | | | |
| <i>Allium cepa</i> | | | BN001199 BN001200 |
| Poales | | | |
| <i>Zea mays</i> | | | BN001194 BN001195 |
| <i>Sorghum bicolor</i> | | | BN001196 |
| <i>Saccharum officinarum</i> | | | BN001193 |
| <i>Brachypodium distachyon</i> | | | Bradi2g25600.1 |
| <i>Oryza sativa</i> | | | AB211399 |
| <i>Triticum aestivum</i> | | | BN001201 |
| <i>Hordeum vulgare</i> | | | AM849822 |

^a Partial EST sequences from 'The Compositae Genome Project' (http://compgenomics.ucdavis.edu/compositae_index.php)

Supplemental Table S2. cDNA clones obtained of the early micropylar endosperm SSH library. Putative gene function was based on the highest BLAST hit, usually Arabidopsis if not indicated otherwise. Based on the data of Ogawa *et al.* (2003) and Preston *et al.* (2009) GA-induction during seed germination of *A. thaliana* Ler was determined by eNorthern (Toufighi *et al.*, 2005) using the BAR website (<http://bar.utoronto.ca/>). Transcripts with a ratio of at least 1.5 between GA and control treatments at least one of the three time points (3h, 6h, 9h) were considered as GA-induced ("Yes").

| Clone number | GenBank accession number | Locus of closest Arabidopsis homologue | Putative gene product / function | Sequence similarity to Arabidopsis (%) , if not indicated otherwise | GA-inducible |
|--------------|--------------------------|--|--|---|--------------|
| pUC19-8h23 | HO208984 | At1g08110 | lactoylglycylglutathione lyase / glyoxylase 1 | 91.8 | No |
| 8h-151 | HO208845 | At1g08770 | PRA1 (prenylated rab acceptor) | 80.2 | No |
| 8h-106 | HO208806 | At1g11350 | universal stress protein (USP) | 87.4 | Yes |
| 8h-38 | HO208897 | At1g15690 | AVP1 (vacuolar-type H ⁺ -pumping pyrophosphatase 1) | 96.2 | Yes |
| 8h-93 | HO208946 | At1g17620 | unknown protein | 83.8 | Yes |
| pTopo-8h19 | HO208958 | At1g17720 | serine/threonine protein phosphatase | 72.5 | Yes |
| 8h-17 | HO208861 | At1g18210 | calcium-binding | 87.9 | No |
| 8h-54 | HO208913 | At1g18540 | 60S ribosomal protein L6 (RPL6A) | 84.8 | No |
| 8h-69 | HO208923 | At1g18540 | 60S ribosomal protein L6 (RPL6A) | 90.6 | No |
| 8h-104 | HO208804 | At1g19770 | PUP14 (purin permease) | 86.8 | No |
| 8h-176 | HO208864 | At1g23010 | multi-copper oxidase type I family | 82.0 | No |
| pTopo-8h13 | HO208953 | At1g30270 | CIPK23 (CBL-interacting protein kinase) | 94.4 | Yes |
| 8h-162 | HO208854 | At1g30690 | SEC14 (cytosolic factor) | 87.1 | Yes |
| 8h-31 | HO208891 | At1g31850 | dehydration-responsive | 91.7 | No |
| 8h-189 | HO208876 | At1g47128 | cysteine proteinase RD21A | 89.5 | Yes |
| 8h-56 | HO208915 | At1g36280 | adenylosuccinate lyase | 93.1 | Yes |
| 8h-158 | HO208851 | At1g53510 | MPK18 (map kinase) | 88.2 | No |
| 8h-187 | HO208874 | At1g56090 | tetratricopeptide repeat (TPR)-containing protein | 85.3 | No |

| | | | | | |
|------------|----------|-----------|--|------|-----|
| 8h-52 | HO208911 | At1g56300 | DNAJ heat shock N-terminal domain-containing | 86.2 | No |
| 8h-141 | HO208835 | At1g60160 | potassium transporter family protein | 93.2 | Yes |
| 8h-111 | HO208811 | At1g63000 | RHM1/ROL1 (rhamnose biosynthesis) | 87.7 | Yes |
| 8h-149 | HO208842 | At1g63000 | RHM1/ROL1 (rhamnose biosynthesis) | 86.6 | No |
| 8h-44 | HO208902 | At1g65930 | isocitrate dehydrogenase | 93.4 | No |
| 8h-129 | HO208824 | At1g64650 | unknown protein | 87.6 | No |
| 8h-185 | HO208872 | At1g64650 | unknown protein | 87.5 | No |
| pTopo-8h2 | HO208959 | At1g69910 | protein kinase family protein | 85.3 | No |
| 8h-2 | HO208881 | At1g70090 | GATL9 (galacturonosyltransferase-like) | 89.7 | No |
| 8h-130 | HO208825 | At1g71920 | histidinol-phosphate aminotransferase | 92.1 | No |
| 8h-91 | HO208944 | At1g72510 | unknown protein | 83.1 | Yes |
| 8h-182 | HO208870 | At1g79850 | Ribosomal protein S17 | 77.2 | No |
| 8h-171 | HO208862 | At1g80120 | unknown protein | 86.2 | No |
| pUC19-8h11 | HO208975 | At2g05220 | 40S ribosomal protein S17 (RPS17B) | 85.3 | No |
| pTopo-8h9 | HO208970 | At2g05755 | integral membrane family protein | 80.4 | Yes |
| 8h-16 | HO208852 | At2g05929 | subtilisin serine protease | 87.7 | No |
| 8h-96 | HO208948 | At2g16365 | F-box family | 85.9 | No |
| 8h-8 | HO208932 | At2g17420 | NADH-dependent thioredoxin reductase 2 | 79.5 | No |
| Puc19-19 | HO208981 | At2g17930 | inositol or phosphatidylinositol kinase/ phosphotransferase | 94.1 | No |
| 8h-48 | HO208906 | At2g22090 | UBA1 (ubiquitin activating enzyme) | 90.0 | No |
| 8h-160 | HO208853 | At2g22500 | mitochondrial dicarboxylate carrier protein | 73.7 | Yes |
| 8h-18 | HO208867 | At2g23310 | RERC1C1 (endoplasmatic reticulum retrieval 1C) | 79.1 | No |
| 8h-163 | HO208855 | At2g24280 | serine carboxypeptidase S28 family | 89.0 | No |
| 8h-153 | HO208847 | At2g28190 | CSD2 (copper/zinc SOD) | 93.1 | No |
| 8h-29 | HO208889 | At2g32070 | CCR4-NOT transcription complex protein | 91.4 | No |
| 8h-135 | HO208829 | At2g32070 | CCR4-NOT transcription complex protein | 91.7 | No |
| 8h-9 | HO208943 | At2g34250 | sec61 (protein transport) | 95.4 | No |
| 8h-128 | HO208823 | At2g34480 | 60S ribosomal protein L18A | 90.5 | No |
| 8h-51 | HO208910 | At2g36460 | putative fructose biphosphate aldolase | 88.2 | No |
| 8h-79 | HO208931 | At2g36460 | putative fructose biphosphate aldolase | 88.1 | No |
| pTopo- | HO208962 | At2g36460 | putative fructose biphosphate aldolase | 88.0 | No |

| | | | | | |
|------------|----------|-----------|---|------|-----|
| 8h23 | | | | | |
| pTopo-8h3 | HO208964 | At2g37640 | EXPA3 (expansin) | 76.5 | Yes |
| pTopo-8h5 | HO208966 | At2g37640 | EXPA3 (expansin) | 76.5 | No |
| pTopo-8h12 | HO208952 | At2g37640 | EXPA3 (expansin) | 81.8 | No |
| 8h-166 | HO208857 | At2g38710 | AMMECR1 family | 91.6 | No |
| 8h-191 | HO208879 | At2g39290 | PGPS 1 (phosphatidylglycerolphosphate synthase 2C) | 91.4 | No |
| 8h-53 | HO208912 | At2g40000 | putative nematode resistant | 90.7 | Yes |
| 8h-119 | HO208814 | At2g40330 | Bet vI allergen family; abscisic acid receptor PYL6 | 80.7 | Yes |
| pUC19-8h22 | HO208983 | At2g41900 | zinc-finger (CCCH-type) family | 89.3 | No |
| pTopo-8h21 | HO208961 | At2g42700 | unknown protein | 89.3 | No |
| pTopo-8h24 | HO208963 | At2g42700 | unknown protein | 85.3 | No |
| 8h-71 | HO208924 | At2g43160 | epsin N-terminal homology domain-containing | 93.2 | No |
| 8h-45 | HO208903 | At2g46330 | AGP16 (arabinogalactan protein 16) | 80.1 | Yes |
| 8h-28 | HO208888 | At2g47640 | small nuclear ribonucleoprotein D2 | 87.7 | No |
| 8h-72 | HO208925 | At2g47640 | small nuclear ribonucleoprotein D2 | 86.9 | No |
| 8h-39 | HO208898 | At3g01360 | unknown protein | 85.6 | No |
| 8h-188 | HO208875 | At3g02880 | leucine-rich repeat transmembrane protein kinase | 78.9 | Yes |
| pUC19-8h14 | HO208978 | At3g03570 | expressed protein | 91.1 | Yes |
| 8h-169 | HO208860 | At3g03640 | Beta glucosidase 25 | 89.4 | No |
| 8h-137 | HO208831 | At3g03710 | RIF10 (resistant to inhibition with FSM 10) | 81.6 | No |
| 8h-165 | HO208856 | At3g05880 | RCI2A (rare cold inducible) | 77.2 | No |
| pUC19-8h12 | HO208976 | At3g07390 | plant IF-like protein | 77.1 | Yes |
| 8h-19 | HO208877 | At3g08030 | unknown protein | 89.1 | No |
| 8h-150 | HO208844 | At3g09630 | 60S ribosomal protein L1 | 80.5 | No |
| 8h-192 | HO208880 | At3g10930 | unknown protein | 74.2 | Yes |
| pTopo-8h7 | HO208968 | At3g10980 | Senescence associated gene 20 SAG20 | 87.6 | No |
| 8h-122 | HO208817 | At3g11400 | EIF3G (translation initiation factor) | 88.8 | No |
| 8h-89 | HO208942 | At3g11510 | 40S ribosomal protein S14 (RPS14B) | 87.7 | No |

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|------------|----------|-----------|--|--------------------------|-----|
| 8h-177 | HO208865 | At3g14090 | unknown protein | 87.4 | No |
| Puc19-8h16 | HO208979 | At3g16270 | unknown protein | 71.6 | No |
| 8h-12 | HO208815 | At3g16640 | TCTP (translationally controlled tumor) | 80.3 | No |
| 8h-26 | HO208886 | At3g16640 | TCTP (translationally controlled tumor) | 88.1 | No |
| 8h-84 | HO208937 | At3g18190 | chaperonin | 83.1 | No |
| 8h-190 | HO208878 | At3g19920 | unknown protein | 85.3 | No |
| 8h-145 | HO208838 | At3g20898 | unknown protein | 83.1 | No |
| Puc19-8h10 | HO208974 | At3g21720 | isocitrate lyase | 94.0 (<i>B. napus</i>) | No |
| 8h-110 | HO208810 | At3g21890 | zinc-finger (B-box type) family | 74.0 | Yes |
| 8h-181 | HO208869 | At3g24830 | 60S ribosomal protein L13A (RPL13aB) | 91.9 | No |
| 8h-143 | HO208837 | At3g25040 | HDEL ER lumen protein | 82.0 | Yes |
| 8h-105 | HO208805 | At3g45970 | EXLA1 (expansin-like) | 85.2 | No |
| pTopo-8h14 | HO208954 | At3g48140 | senescence-associated | 88.9 | Yes |
| 8h-62 | HO208917 | At3g49720 | unknown protein | 89.6 | Yes |
| 8h-174 | HO208863 | At3g52580 | 40S ribosomal protein S14 (RPS14C) | 87.8 | No |
| 8h-179 | HO208866 | At3g55440 | triose-phosphate isomerase (TPI) | 91.3 | No |
| 8h-146 | HO208839 | At3g57090 | binding (BIGYIN) | 84.3 | No |
| Puc19-8h7 | HO208988 | At3g57520 | putative imbibition protein homolog | 91.3 | Yes |
| 8h-64 | HO208972 | At3g57550 | AGK2 (guanylate-kinase) | 91.1 | Yes |
| 8h-99 | HO208949 | At3g59770 | SAC 9 (suppressor of actin) | 90.4 | No |
| Puc19-8h20 | HO208982 | At3g63030 | MBD4 (methyl-CpG-binding domain 4, DNA-binding) | 83.2 | No |
| 8h-107 | HO208807 | At4g00730 | transcription factor/ transcription regulator (Anthocyanless 2) | 74.1 | No |
| 8h-76 | HO208929 | At4g05050 | UBQ11 (ubiquitin) | 88.2 | Yes |
| pTopo-8h15 | HO208955 | At4g11740 | SAY1 (Isolated as a suppressor of a dominant mutant in the Ara4 gene) | 80.8 | No |
| 8h-136 | HO208830 | At4g13010 | oxidoreductase, zinc-binding dehydrogenase family | 85.2 | No |
| 8h-133 | HO208827 | At4g13940 | HOG1 (homology-dependent gene silencing, adenosylhomocysteinase) | 93.6 | No |

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|------------|----------|-----------|--|------|-----|
| 8h-67 | HO208921 | At4g15470 | unknown protein | 80.7 | No |
| pUC19-8h18 | HO208980 | At4g15470 | unknown protein | 90.8 | No |
| 8h-35 | HO208894 | At4g15530 | PPDK (pyruvate orthophosphate dikinase) | 92.9 | Yes |
| 8h-78 | HO208930 | At4g16563 | aspartyl protease family | 87.4 | No |
| 8h-127 | HO208822 | At4g17420 | unknown protein | 92.5 | No |
| 8h-27 | HO208887 | At4g18650 | transcription-factor related | 86.0 | Yes |
| 8h-87 | HO208940 | At4g20860 | FAD-binding domain | 90.0 | No |
| 8h-88 | HO208941 | At4g20860 | FAD-binding domain | 90.0 | No |
| 8h-102 | HO208802 | At4g22820 | AN1-like zinc finger family | 79.5 | No |
| 8h-156 | HO208849 | At4g24220 | VEP1 (vein patterning) | 94.1 | No |
| 8h-5 | HO208908 | At4g24770 | RBP31 (RNA binding) | 76.8 | No |
| 8h-74 | HO208927 | At4g26000 | PEP (nucleic acid binding) | 91.0 | No |
| 8h-101 | HO208801 | At4g27070 | TSB2 (tryptophane synthase beta subunit) | 82.5 | No |
| pTopo-8h1 | HO208950 | At4g27320 | universal stress protein (USP) | 81.8 | Yes |
| 8h-6 | HO208916 | At4g27652 | unknown protein | 73.7 | No |
| 8h-138 | HO208832 | At4g28440 | DNA-binding protein-related | 90.1 | No |
| 8h-22 | HO208884 | At4g29130 | HXK1 (hexokinase, glucose insensitive 1) | 93.9 | Yes |
| 8h-75 | HO208928 | At4g29390 | 40S ribosomal protein S30 (RPS30B) | 91.5 | No |
| 8h-36 | HO208895 | At4g30270 | MERI5B (xyloglucan endo-1,4-Betaglucanase) | 89.3 | No |
| 8h-21 | HO208883 | At4g30280 | XTH18 | 86.9 | Yes |
| 8h-46 | HO208904 | At4g30280 | XTH18 | 87.4 | Yes |
| 8h-47 | HO208905 | At4g30280 | XTH18 | 87.4 | Yes |
| 8h-131 | HO208826 | At4g30280 | XTH18 | 87.4 | Yes |
| pTopo-8h6 | HO208967 | At4g30280 | XTH18 | 85.7 | Yes |
| 8h-55 | HO208914 | At4g30290 | XTH19 | 80.6 | Yes |
| 8h-25 | HO208885 | At4g31130 | unknown protein | 85.7 | No |
| Puc19-8h1 | HO208973 | At4g32020 | unknown protein | 69.6 | No |
| 8h-73 | HO208926 | At4g32130 | unknown protein | 72.5 | No |
| 8h-86 | HO208939 | At4g32390 | phosphate-translocator-related | 90.4 | No |
| 8h-95 | HO208947 | At4g34555 | 40S ribosomal protein S25 | 81.8 | Yes |

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|----------------|----------|-----------|---|------|-----|
| 8h-152 | HO208846 | At4g37580 | HLS1 (hookless, N-acetyltransferase) | 85.6 | Yes |
| 8h-34 | HO208893 | At4g38740 | ROC1 (peptidylprolyl isomerase) | 89.5 | No |
| 8h-20 | HO208882 | At4g38800 | MTN1 (methylthioadenosin nucleosidase) | 89.4 | No |
| 8h-83 | HO208936 | At5g01320 | pyruvate decarboxylase | 83.4 | Yes |
| 8h-167 | HO208858 | At5g01710 | unknown protein | 89.0 | No |
| 8h-139 | HO208833 | At5g02260 | EXPA9 (expansin A9) | 78.2 | Yes |
| 8h-184 | HO208871 | At5g02280 | ATEXPA9 (ARABIDOPSIS THALIANA EXPANSIN A9) (ATEXPA9) | 78.4 | No |
| 8h-49 | HO208907 | At5g02610 | 60S ribosomal protein L35 (RPL35D) | 84.3 | No |
| 8h-50 | HO208909 | At5g02610 | 60S ribosomal protein L35 (RPL35D) | 84.3 | No |
| pTopo- 8h17 | HO208957 | At5g03040 | calmodulin binding (iqd2); (IQ-domain 2) | 89.5 | Yes |
| 8h-164 | HO208971 | At5g03880 | electron carrier | 78.3 | No |
| 8h-40 | HO208899 | At5g07340 | Calnexin | 83.0 | No |
| pTopo- 8h20 | HO208960 | At5g07830 | Beta-glucuronidase AtGUS2 | 91.2 | No |
| 8h-103 | HO208803 | At5g08160 | PK3 serine/threonine protein kinase | 93.2 | No |
| Puc19- 8h4 | HO208987 | At5g10750 | unknown protein | 87.6 | No |
| 8h-30 | HO208890 | At5g10770 | chloroplast nucleoid DNA-binding protein | 82.6 | Yes |
| 8h-157 | HO208850 | At5g10860 | CBS domaine containing | 84.1 | No |
| 8h-41 | HO208900 | At5g11090 | serine-rich protein-related | 81.2 | No |
| 8h-123 | HO208818 | At5g12140 | CYS1 (cystatin) | 83.4 | No |
| 8h-63 | HO208918 | At5g12850 | zinc-finger (CCCH-type) family | 89.6 | Yes |
| 8h-112 | HO208812 | At5g14450 | GDSL-motif lipase/hydrolase family | 90.1 | Yes |
| 8h-148 | HO208841 | At5g15650 | RGP2 (reversibly glycosylated polypeptide-3) | 90.8 | Yes |
| pTopo- 8h16 | HO208956 | At5g15850 | COL1 (constance-like) | 86.0 | Yes |
| 8h-147 | HO208840 | At5g17860 | CAX7 (calcium exchanger) | 89.3 | Yes |
| 8h-134 | HO208828 | At5g17920 | CIMS (cobalamin-independent methionine synthase) | 93.2 | Yes |
| Puc19- 8h9 | HO208989 | At5g20290 | 40S ribosomal protein S8 (RPS8A) | 81.0 | No |
| 8h-168 | HO208859 | At5g25460 | Unknown protein | 93.9 | No |
| 8h-33 | HO208892 | At5g28060 | 40S ribosomal protein S24 (RPS24B) | 78.9 | No |
| 8h-42 | HO208901 | At5g29560 | Calcium-ion-binding | 89.0 | No |

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|------------|----------|-----------|---|------|-----|
| pTopo-8h4 | HO208965 | At5g35160 | Unknown protein | 85.2 | No |
| 8h-82 | HO208935 | At5g35460 | unknown protein | 89.9 | No |
| 8h-120 | HO208816 | At5g35560 | MOK9_2 | 86.6 | No |
| 8h-85 | HO208938 | At5g38890 | exoribonuclease-related | 91.1 | Yes |
| 8h-116 | HO208813 | At5g43940 | ADH2 alcohol dehydrogenase | 92.2 | No |
| Puc19-8h3 | HO208986 | At5g44420 | PDF1.2c (plant defensin 1.2c) (PDF1.2c) | 81.3 | No |
| 8h-68 | HO208922 | At5g45280 | pectinacetylsterase | 90.4 | Yes |
| Puc19-8h24 | HO208985 | At5g45775 | 60S ribosomal protein L11 (RPL11D) | 92.8 | No |
| 8h-65 | HO208919 | At5g48545 | unknown protein | 88.6 | No |
| 8h-125 | HO208820 | At5g51570 | band 7 family protein | 83.1 | No |
| 8h-180 | HO208868 | At5g53570 | RabGAP/TBC domain-containing protein | 84.1 | No |
| 8h-142 | HO208836 | At5g54855 | pollen allergene Ole e1 and extensin family | 90.2 | No |
| 8h-186 | HO208873 | At5g55190 | RAN3 (RAN GTPase gene family) | 93.0 | No |
| pTopo-8h8 | HO208969 | At5g56030 | HSP81-2 (early-responsive to dehydration) | 91.2 | Yes |
| 8h-109 | HO208809 | At5g60390 | elongation factor 1-alpha | 85.6 | No |
| 8h-66 | HO208920 | At5g61230 | Ankyrin repeat family | 76.9 | No |
| 8h-124 | HO208819 | At5g61820 | unknown protein | 73.3 | No |
| 8h-108 | HO208808 | At5g64270 | splicing factor | 92.0 | No |
| 8h-155 | HO208848 | At5g64310 | Arabinogalactan protein 1 | 69.9 | Yes |
| 8h-92 | HO208945 | At5g64400 | unknown protein | 82.7 | No |
| 8h-14 | HO208834 | At5g65140 | trehalose-6-phosphate phosphatase | 92.0 | Yes |
| 8h-15 | HO208843 | At5g66590 | allergen V5/Tpx-1-related | 84.4 | No |
| 8h-80 | HO208933 | At5g66590 | allergen V5/Tpx-1-related | 82.9 | No |

Supplemental Table S3. Primer sequences that were used for the quantitative PCR analyses.

| amplified DNA | Primer Specificity | Accession number | forward Primer (5'-3') | reverse Primer (5'-3') |
|------------------|-----------------------------|-------------------------|-------------------------|----------------------------|
| <i>LesaGID1a</i> | <i>Lepidium sativum</i> | HQ003455 (At3g05120) | AGCGGGTGAGTCTGGAATCAAT | AAGTTTCTCAGACTCTGTTCTC |
| <i>LesaGID1b</i> | <i>Lepidium sativum</i> | HQ003456 (At3g63010) | AGCTCACAATGTTGCTGTGAG | TCAGTCCTCTCTTGTCCAC |
| <i>LesaGID1c</i> | <i>Lepidium sativum</i> | HQ003457 (At5g27320) | GCATAATGTCGCGGTTAGAG | GTCCCTCCAAACATAGGGTT |
| <i>AtGID1a</i> | <i>Arabidopsis thaliana</i> | At3g05120 | AGAGACCGCGATTGGTACTG | TCGGGCTAAACGGATTACAC |
| <i>AtGID1b</i> | <i>Arabidopsis thaliana</i> | At3g63010 | GGATCGGTTTGTTCCTGCCTA | TTATGCTTCCGGAGACCAAG |
| <i>AtGID1c</i> | <i>Arabidopsis thaliana</i> | At5g27320 | AAGAGCGGTTGAGTCAAGGA | TTCCCATCCAAACGTTTCTC |
| <i>EXLA1</i> | <i>Lepidium sativum</i> | HO208805 | ATGGCTAAGCCTGTTCTGGTGCT | TCCCGTAGTCGCAAGGAACTCTGT |
| <i>EXPA9</i> | <i>Lepidium sativum</i> | HO208871 | ATGTCAACGACGGTGAAGGCCA | ATAGTGCCTTGAGCATCAGCCCCA |
| <i>XTH18</i> | <i>Lepidium sativum</i> | HO208883 | TGGGGGTTCCATGTGATGCAGT | GGCTCAGGAGACAAAGAACAACAGT |
| <i>XTH19</i> | <i>Lepidium sativum</i> | HO208914 | GGGGGCACAGAGAACTACATGGT | TTAGCTGCACTCTGGAGGAACACCAC |