

**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.

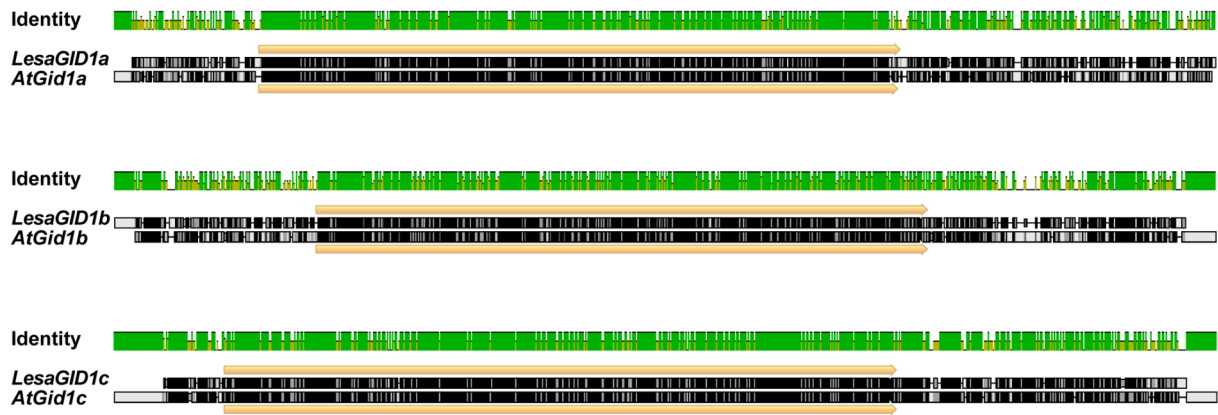
**Supplemental Figure S3.** Comparison of *L. sativum* and Arabidopsis GID1 transcript secondary structures and stability motifs in 5' and 3' UTRs.

**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.

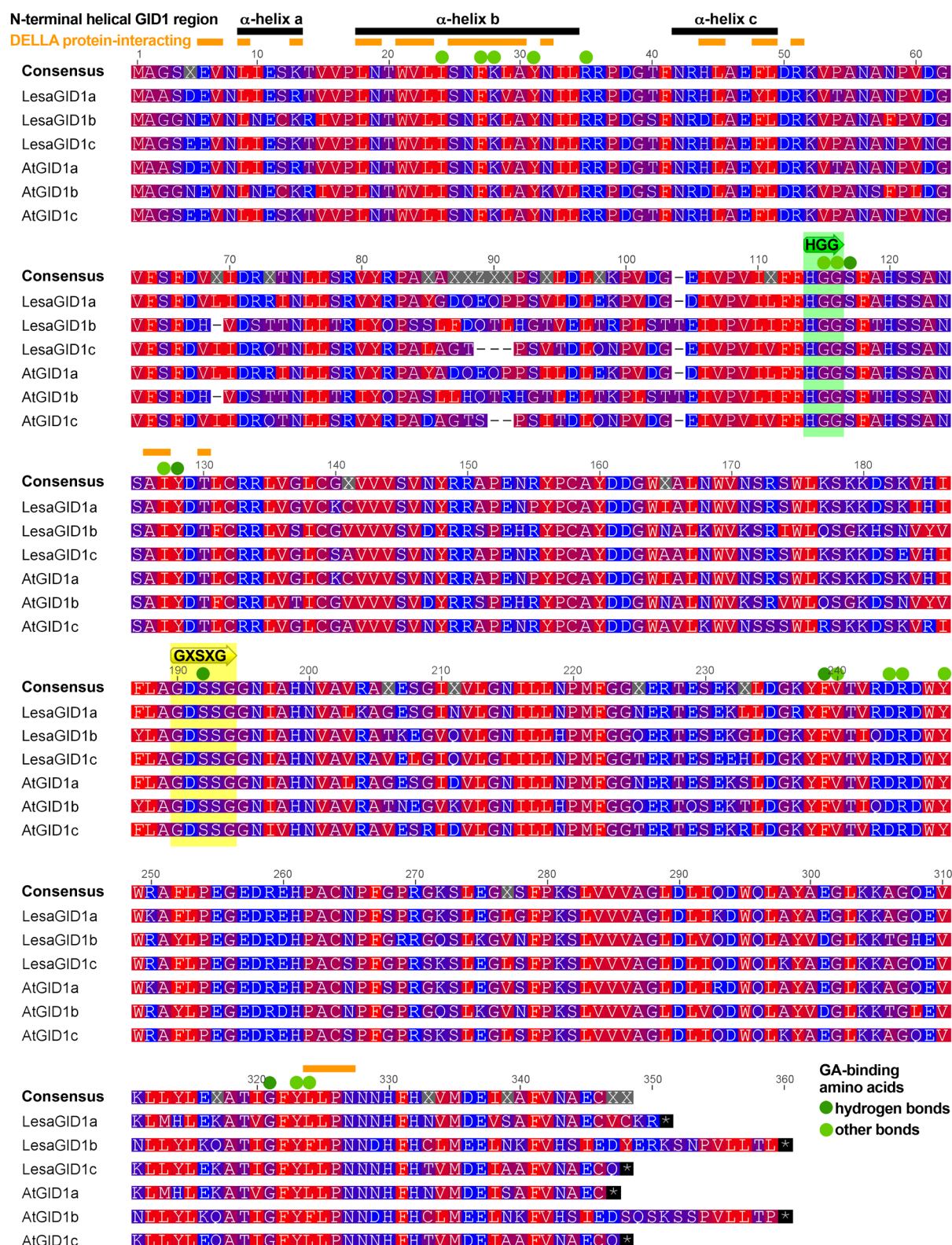
**Supplemental Table S2.** cDNA clones obtained of the early micropylar endosperm SSH library.

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



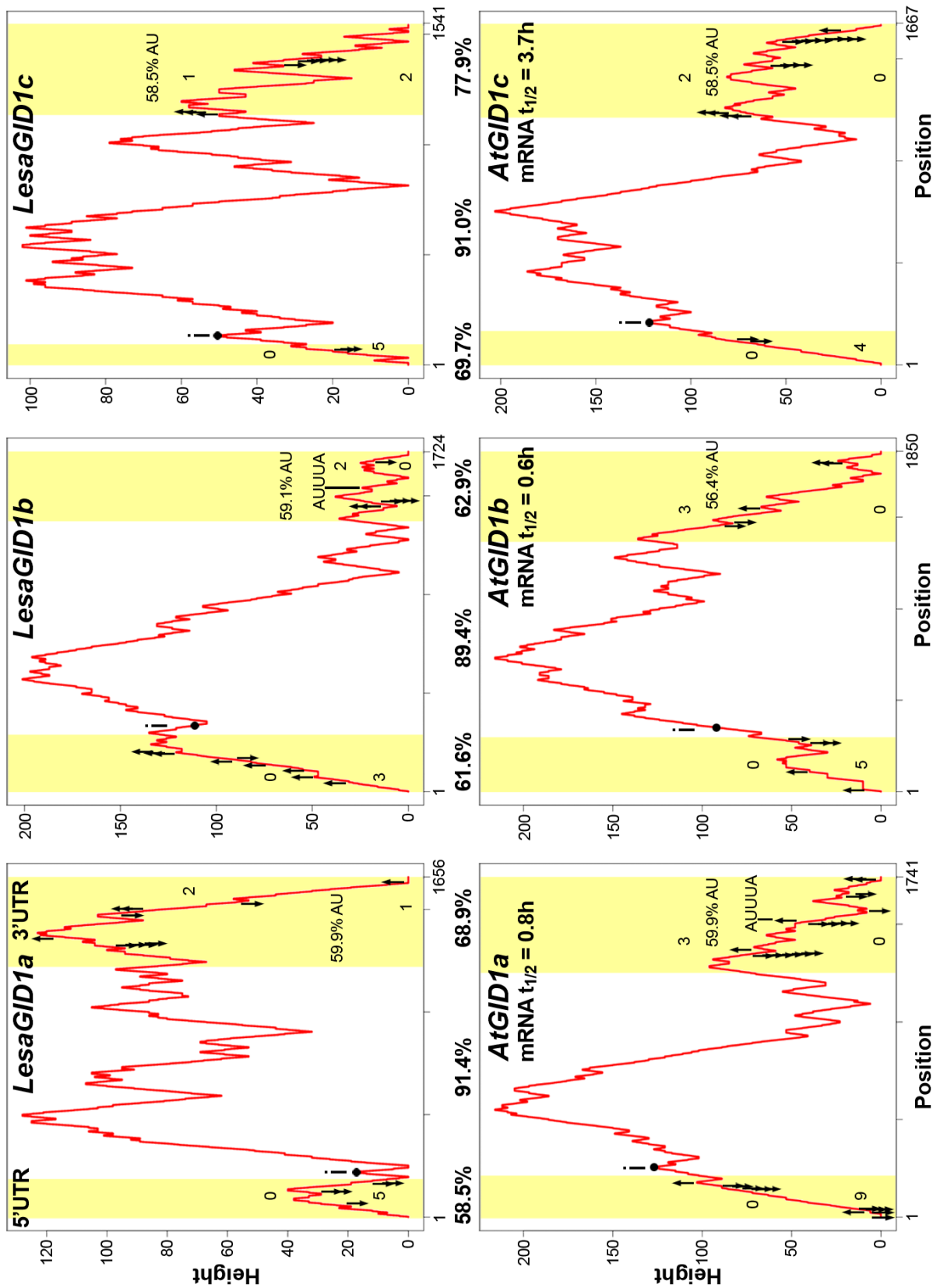
**Supplemental Figure S1.** Transcript sequence alignments of the Brassicaceae GID1 family members of *Lepidium sativum* (*LesagID1a*, *LesagID1b*, *LesagID1c*) and *Arabidopsis thaliana* (*AtGID1a*, *AtGID1b*, *AtGID1c*).

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  $\alpha$ -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.







## *LesbGID1c* 5'UTR

TNNTNTTCGGCTCAAATCTTCGATCTGGGCTTTCGTGTTTCTGTTCGTTTGATTGGTAAATAAAGGAGATCTTTTTC

TTTTTCNT  
UUUUC

UUUUC  
UUUUUU  
UUUUUU  
UUUUU  
UUUUU  
UUUUU

## *AtGID1c* 5'UTR

ACGUUUAAAAGCAGGUUUCUUUCUAUUUCCAGAUAAAAAACUUUACUCAUCGAGACUCGUUUAGUGAUUCGAAAUUUCCC

UUCUCGGCUCAAAUCUUCGAUCUGGGCUUUCGUGUCUUUUUGCGUUUUGAUUGGUAAUAAAAGAAGCUUUUUAAAAACUU

UUUCC  
UUUCC  
UUUCC  
UUUUU

UUUUU  
UUUUUG  
GUUUUG

UUUUU  
UUUUU  
UUUUU  
UUUUU



## *LesnGID1b* 3'UTR

CAACAACAAGCTCTCTGTTCAATGTTGCTGAATGCTGATACATACATAAAGAGAAGAAGAAAAGAAGATTAGAGGATCAGT

TTGCTTTGGCCATCTGTGATGGGTTTTTGTACAGTTTACATATGTAGTGTATTATGTGAGATCCTTGTTGCGCCTCAAG  
UGCUUU → GUUUUU → UUUUGU → UUGUU →  
UUGCUU → UUUUUG →

TAAAGACCATTAGGTTTAAAGTTTAAAGCAAAACGTGCGTACTAGTATGGGTAGACTTTAAATTGGTTC TAGAGTACAGTT  
AAUUA →

GGTAAATTACAAGACAACCTAACTTGTCTTCAACATGTTGTTGAAAAAACTTATCCTTCGGTTTGTTTATATCATTACCTT  
UUGUU → T → UUUUGU

TTGTGCTCTCGTGCTATTAATAAAAAAAAAAAAAA  
UUUUGU →  
UUUUGU

## *AtGID1b* 3'UTR

CAACGACAAUGUCUGGUCAUGUUGCUGAUAUAUACCACAUGAAGAGUAGAAGAAGACUAGAGGAUCGGUUUGUUUUGC  
UUUUUG → UUGUU →

CUAUCUAUGAUUGGGUUGUGUACAGUUUCCACAAGUGGUGUCUAGUGUCAAUAGCGUUUCUUUUUGUUGUCCUUGGUCUCC  
UUUUGU →

GG AAGCAUAAUAAGUCUGUCUUUCUGUGAGGUCUUGGUGCGCCUGGCGAGAGACCACUUCGGUUAUCGGCAUCUAUCGUU  
AAUAAG →

UUAGGGCUAUACCGGGGAAUGGUACUUUGUUUGCGUACUAGUAUGGGUAGGCUUAGUUGGUUCUAGCUUAGAGUACAGAG  
UUGUU →

GGUAAAUUACAAGACAACUACUUGUCUUCAACAUGUUGUGAAAAAAACUAAUCCUUGGUGAGGAUUUGUAUGUUUAUAUU

AACUUUUUGCUUUUCUAUGCUAUUAAUAGAGUAUGUCUUUGUGGUUGUAGUUUCACUUCUUCUUGUUUUAGUUC AUGCA  
UGCUUU → UUGCUU → UUGUU →

UU

## *Les*GID1c 3'UTR

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

AGCTCTTTGTAGTGATATATCCAAAAGTACGGCGTTTAACTACTACCTCAGCCGCTGCGTTTGCGTCTGCGTTTGTGAAA

CCGTGTGAAGCTGGATTCTGATAGCAAAGCAGGAAGAAGAACAGTGAAGCCGGTAA TGTTGGTTTTAGTGT TAGTTTTTC  
AGUUUU →

AACTCTAAC TAGAGCTGAGTTTTTTTCATCTTGCGGTTAATAGTAACTTCGGTATGTTGCTATCATGATATTTTCCGTA  
AGUUUU →  
GUUUUU →  
UUUUUU →  
UUUUUU →

TAATAATCTTATA TACATA TATCAACGATATGTA TAAATAACA TGAGCCATGTAA TGTTGTGTTTAA TGTGCAAG  
UAUCUU → UUGUU →

TAATTGTAAAAAAAAAAAAA

## *At*GID1c 3'UTR

GAAACACUCUUAUCUCUCACUGUAAUCUCUUCACUAAACAAACGGGUGAUAUCCACCAUGGAAGGUGAAAGCCCGAGAUUCUC  
UUAUCU → UCUCUU →  
AUCUCU → AUCUCU → GARE →

GUUUUAGAAGCUCUUUGUAGUGAGUCAAAAGAACGGCGUUUAACUACUACC GCGUGGGUGGUGGUGCGUCGUCGCGUUUGUG

AACCGUCCAAAAGCUGGAUUCUGAAAGCAAAGCAGGAAGAAGAACAGUGUAGUCGGUAAUUAUGUUUGGCUUUCUAGCGUUA

GCUUUUGACUUUAAACUAGAGCUGAGUUUUUUCAGCUUGUGGUUAAUAGUAACUUUGGUUAUGUUACUAUUUAUGAUUUUUUC  
GUUUUU →  
UUUUUU →  
AGUUUU →

GGUAAAUAUCUAUCUAGUACAUAUACAUGCAUACAUCAACAAUAUGUUUAAUUAAGCUUUUUUUGUUUUUGUAUAAUUA  
UUGUU →  
UUUUUU →  
UUUUUU →  
UUUUUU →  
UUUUUU →  
GUUUUU →

UAAGUUUUUGUAGCUAUGUGGUGUUGUUGUUUGCUUACC UAAAAGUGAUCUUUUAUUUUUUU  
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](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
<b>Rosids (core eudicots)</b>			
<b>Cucurbitales</b>			
<i>Cucumis sativus</i>	Cucsa.1637401	Cucsa.084780	
<i>Cucurbita maxima</i>	AM745266	AM745267	
<b>Fabales</b>			
<i>Glycine max</i>	AK285463	AK286926	
<i>Medicago truncatula</i>	BN001191	BN001192	
<b>Malpighiales</b>			
<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	
<b>Malvales</b>			
<i>Gossypium hirsutum</i>	FJ790128 FJ790130	DQ829776 FJ790126 FJ790127	
<b>Brassicales</b>			
<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	
<b>Vitaceae</b>			
<i>Vitis vinifera</i>	XM_00226572	XM_00227166	

**Angiosperm phylogeny**

**Angiosperm GID1 receptor group**

	<b>Eudicot GID1ac</b>	<b>Eudicot GID1b</b>	<b>Monocot GID1</b>
<b>Asterids (core eudicots)</b>			
<b>Lamiales</b>			
<i>Mimulus guttatus</i>		mgf013441m mgf013028m	
<b>Solanales</b>			
<i>Solanum lycopersicum</i>	AK322582	BN001197 AK328124	
<b>Asterales</b>			
<i>Helianthus annuus</i> <sup>a</sup>	Heli_annu.DY905340	Heli_annu.CSA1.2356	
<i>Helianthus ciliaris</i> <sup>a</sup>	Heli_cili.EL415899	Heli_cili.CSA.12537	
<i>Helianthus exilis</i> <sup>a</sup>	Heli_exil.CSA1.102		
<i>Helianthus paradoxus</i> <sup>a</sup>	Heli_para.CSA1.406	Heli_para.EL481749	
<i>Helianthus petiolaris</i> <sup>a</sup>	Heli_peti.CSA1.4196	Heli_peti.DY944716	
<i>Helianthus tuberosus</i> <sup>a</sup>	Heli_tube.EL43821	Heli_tube.CSA1.448	
<i>Lactuca perennis</i> <sup>a</sup>	Lact_pere.CSA1.2657	Lact_pere.DW090471	
<i>Lactuca saligna</i> <sup>a</sup>	Lact_sali.CSA1.630	Lact_Sali.DW050958	
<i>Lactuca sativa</i> <sup>a</sup>		Lact_sati.D4973435	
<i>Lactuca serrida</i> <sup>a</sup>		Lact_serr.DW115969	
<i>Lactuca virosa</i> <sup>a</sup>		Lact_viro.DW164935	
<b>Ericales</b>			
<i>Actinidia deliciosa</i>		DQ279922	
<b>Basal eudicots</b>			
<b>Ranunculales</b>			
<i>Aquilegia formosa</i> x <i>Aquilegia pubescens</i>	BN001198		
<b>Monocots</b>			
<b>Liliales</b>			
<i>Allium cepa</i>			BN001199 BN001200
<b>Poales</b>			
<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

<sup>a</sup> Partial EST sequences from 'The Compositae Genome Project' ([http://compgenomics.ucdavis.edu/compositae\\_index.php](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	lactoylglycyltransferase / 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 <sup>+</sup> -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

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

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

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

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	pectinacetyltransferase	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	TCCCGTAGTCGCAAGGAAGCTCTGT
<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