

Supplementary Figures

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Figure S5. Organization of the conserved *cis*-elements in the promoter regions of *ASKβ* and its 32 co-expressed genes.

Figure S6. The expression patterns of *ASKs* in *Arabidopsis*. Information was obtained from public databases.

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ASKα -----MASLPLGPQ--PHALAPPLQLHDGDALKRRPELDSDKEMSAAVIEGNDVAVTGH 52
ASKβ -----MTSIPLGPQPPLAPQPPLHGGDLSLKRPPDIDNDKEMSAAVIEGNDVAVTGH 54
ASKγ -----MADDKEMPAAVVDGHDQVTGH 22
ASKα -----MASVGIAPNPGARDSTG---VDKLPPEEMDMKIRDDKEMEATVVDGNGTETGHI 51
ASKβ -----MASVGIEPSAAVRESTGNVTDADRLPEEMDMKIQDDKEMEATVINGNVTETGHI 55
ASKγ -----MASVGTLPASSMATQSNASICAELKPEGINEMKIQDDKEMEAAVVDGNGTETGHI 56
ASKκ -----MASSGLNGVGTSSAKGLKSSSSVDWLRDLAETRIKRDVETDDEERDSEPDIDGGAEPGHV 65
ASKδ -----MESHLLNGVGTSSAKNTKNTSSVDWLRDMLKIRDKTEADDEERDSEPDIDGGAEPGHV 64
ASKθ MNVVRRLTSIASGRNFVSSDNDVGETETPRSKPNQNR-----ETESTETTSYKEDSVSSSENSDHLPEKIREDDMDCGIIKNGTETSGRI 84
ASKθ MNVMRRLTSIASGRNTSSDPPGGDYALKRAKLDQENDNLCDPDMQVDQNSSCFEMKADVLSSQESVAGTSNVPVSEKPVDDQLPDVMIEMKIRDERNANREDKMETTVVNGSGTETGQQ 120

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▼
nucleotide binding ATP binding

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ASKα ISTTIGKNGPEPKQTSYMAERVWGTGSGFVIFQAKCLETGESVAIKVLQDRRYKNEQLQMRPMDHPNVIKLCFFSTTSRDELFLNLVMEVPELTVRVLRYHTYSSNQRMPFIYVK 172
ASKβ ISTTIGKNGPEPKQTSYMAERVWGTGSGFVIFQAKCLETGESVAIKVLQDRRYKNEQLQMRMDHPNVIKLCFFSTTTRDELFLNLVMEVPELTVRVLKHYTSSNQRMPFIYVK 174
ASKγ ISTTIGKNGPEPKQTSYMAERVWGTGSGFVIFQAKCLETGESVAIKVLQDRRYKNEQLQMRVMDHPNVIKLCFFSTTSKDELFLNLVMEVPELTVRVLKHYSSNQRMPFIYVK 142
ASKα IVTTIGRNGOPKQTSYMAERVWGTGSGFVIFQAKCLETGESVAIKVLQDRRYKNEQLQMRLLDHPNVIKLCFFSTTEKDELFLNLVLEVPETVHRVIKHYKLNQRMLPIYVK 171
ASKβ IVTTIGRNGOPKQTSYMAERVWGTGSGFVIFQAKCLETGESVAIKVLQDRRYKNEQLQMRLLDHPNVIKLCFFSTTEKDELFLNLVLEVPETVHRVIKHYKLNQRMLPIYVK 175
ASKγ IVTTIGKNGOPKQTSYMAERVWGTGSGFVIFQAKCLETGESVAIKVLQDRRYKNEQLQMRLLDHPNVIKLCFFSTTEKDELFLNLVLEVPETVHRVSKHYSSNQRMPFIYVK 176
ASKκ IRTTLRGRNGSQSGRTVSYSEHWGTGSGFVIFQAKCRETEGEVAIKVLQDRRYKNEQLQMRLLDHPNVAIKHSFFSRDNEEYFLNLVLEVPETVNRVRSYRTNQLMPLIYVK 185
ASKδ ITTLLPGRNGSQSGRTVSYIAEHVWGTGSGFVIFQAKCRETEGEVAIKVLQDRRYKNEQLQMRLLDHPNVIKHSFFSRDNEEYFLNLVLEVPETVNRVRSYRTNQLMPLIYVK 184
ASKθ ITTTKKGKLDKDKTISYRAEHWGTGSGFVIFQAKLETEGEVAIKVLQDRRYKNEQLQMRLLDHPNVIKHSFFSTTEKDELFLNLVLEVPETVIRNRSYRTNQLMPLIYVK 204
ASKθ ITTTVGGRDGPKQTSYMAQRVWGTGSGFVIFQAKCLETGESVAIKVLQDRRYKNEQLQMRLLDHPNVIKHSFFSTTEKDELFLNLVLEVPETVIRNRSYRTNQLMPLIYVK 240

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phosphorylation site within activation loop of tyrosine phosphorylation of MPK6

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ASKα LYTQIFRGLAYIHTAPGVCHRDKVQPNLLVDPLTHQVKLIDFGSAKVLVKGEPNISITCSRWRAPDLIFGATEYTSIDVWSAGCVLAELLGQPLPFGENSVDQLVEIKVLGTPTR 292
ASKβ LYTQIFRGLAYIHTAPGVCHRDKVQPNLLVDPLTHQVKLIDFGSAKVLVKGEPNISITCSRWRAPDLIFGATEYTSIDVWSAGCVLAELLGQPLPFGENSVDQLVEIKVLGTPTR 294
ASKγ LYMVQIFRGLAYIHTAPGVCHRDKVQPNLLVDPLTHQVKLIDFGSAKVLVKGEPNISITCSRWRAPDLIFGATEYTSIDVWSAGCVLAELLGQPLPFGENAVDQLVEIKVLGTPTR 262
ASKα LYTQIFRGLAYIHTAPGVCHRDKVQPNLLVDPLTHQVKLIDFGSAKVLVKGEPNISITCSRWRAPDLIFGATEYTTAIDVWSAGCVLAELLGQPLPFGESVDQLVEIKVLGTPTR 291
ASKβ LYTQIFRGLAYIHTAPGVCHRDKVQPNLLVDPLTHQVKLIDFGSAKVLVKGEPNISITCSRWRAPDLIFGATEYTTAIDVWSAGCVLAELLGQPLPFGESVDQLVEIKVLGTPTR 295
ASKγ LYTQICRALAYIHGGVGVCHRDKVQPNLLVDPLTHQVKLIDFGSAKVLVKGEPNISITCSRWRAPDLIFGATEYTTAIDVWSAGCVLAELLGQPLPFGESVDQLVEIKVLGTPTR 296
ASKκ LYTQICRALAYIHTAPGVCHRDKVQPNLLVDPLTHQVKLIDFGSAKVLVKGEPNISITCSRWRAPDLIFGATEYTTAIDVWSAGCVLAELLGQPLPFGESVDQLVEIKVLGTPTR 305
ASKδ LYTQICRALAYIHTAPGVCHRDKVQPNLLVDPLTHQVKLIDFGSAKVLVKGEPNISITCSRWRAPDLIFGATEYTTAIDVWSAGCVLAELLGQPLPFGESVDQLVEIKVLGTPTR 304
ASKθ LYTQICRAMNVLHQVGVCHRDKVQPNLLVDPLTHQVKLIDFGSAKVLVKGEPNISITCSRWRAPDLIFGATEYTTAIDVWSAGCVLAELLGQPLPFGESVDQLVEIKVLGTPTR 324
ASKθ LYTQICRALNVLHRVGVCHRDKVQPNLLVDPLTHQVKLIDFGSAKVLVKGEPNISITCSRWRAPDLIFGATEYTTAIDVWSAGCVLAELLGQPLPFGESVDQLVEIKVLGTPTR 360

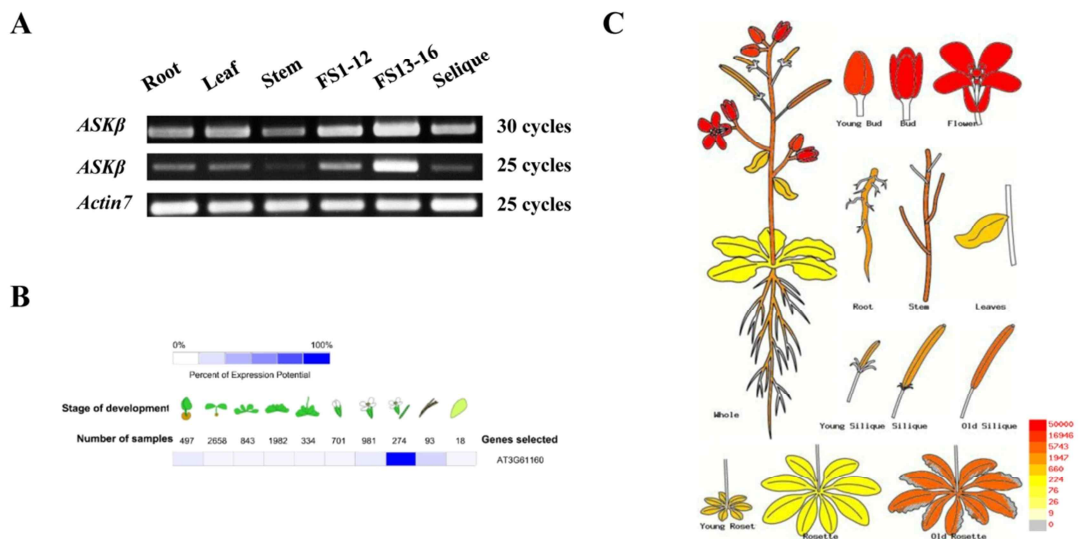
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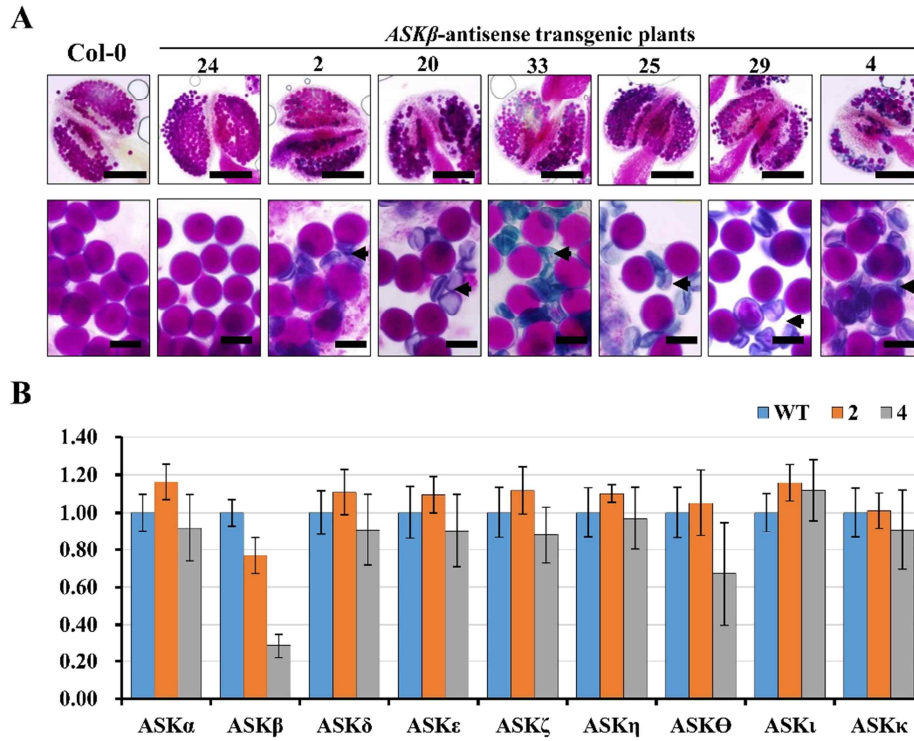
ASKα EEIRCMNPNTDFRFPQIKAHFWHKIFHKRMPPEAIDLASRLQYSPSLRCTALEACAHPPFDELREPNARLPNGRPLPPLFNFK--QELSGASPELINRLIPEHVRQMGSTGLQNS--- 407
ASKβ EEIRCMNPNTDFRFPQIKAHFWHKIFHKRMPPEAIDLASRLQYSPSLRCTALEACAHPPFDELREPNARLPNGRPLPPLFNFK--QELSGASPELINRLIPEHVRQMGSTGLQNS--- 412
ASKγ EEIRCMNPNTDFRFPQIKAHFWHKIFHKRMPPEAIDLASRLQYSPSLRCTALEACAHPPFDELREPNARLPNGRPLPPLFNFK--QEVAGSSPELVNKLIPDHIKRLGLSFLNGSGT 380
ASKα EEIKCMNPNTDFRFPQIKAHFWHKIFHKRMPPEAVDLVSRLLQYSPNLSAALDVLVHPFFDELREPNARLPNGRPLPPLFNFKPHELKGVPEVMVAKLVPEHARKQCPWLSL---- 405
ASKβ EEIKCMNPNTDFRFPQIKAHFWHKIFHKRMPPEAVDLVSRLLQYSPNLSAALDVLVHPFFDELREPNARLPNGRPLPPLFNFKPHELKGVPEVMVAKLVPEHARKQCPWLSL---- 409
ASKγ EEIKCMNPNTDFRFPQIKAHFWHKIFHKRMPPEAVDLVSRLLQYSPNLSAALDVLVHPFFDELREPNARLPNGRPLPPLFNFKPHELKGVPEVMVAKLVPEHARKQCPWLSL---- 410
ASKκ EEIKCMNPNTDFRFPQIKAHFWHKIFHKRMPPEAVDLVSRLLQYSPNLSAALDVLVHPFFDELREPNARLPNGRPLPPLFNFKPHELKGVPEVMVAKLVPEHARKQCPWLSL---- 421
ASKδ EEIKCMNPNTDFRFPQIKAHFWHKIFHKRMPPEAVDLVSRLLQYSPNLSAALDVLVHPFFDELREPNARLPNGRPLPPLFNFKPHELKGVPEVMVAKLVPEHARKQCPWLSL---- 410
ASKθ EEIKCMNPNTDFRFPQIKAHFWHKIFHKRMPPEAVDLVSRLLQYSPNLSAALDVLVHPFFDELREPNARLPNGRPLPPLFNFKPHELKGVPEVMVAKLVPEHARKQCPWLSL---- 420
ASKθ EEIKMNPNTDFRFPQIKAHFWHKIFFRQVSPPEAVDLVSRLLQYSPNLSAALDVLVHPFFDELREPNARLPNGRPLPPLFNFKPHELKGVPEVMVAKLVPEHARKQCPWLSL---- 431
ASKθ EEIRCMNPNTDFRFPQIKAHFWHKIFHKRMPPEAVDLVSRLLQYSPNLSAALDVLVHPFFDELREPNARLPNGRPLPPLFNFKPHELKGVPEVMVAKLVPEHARKQCPWLSL---- 472

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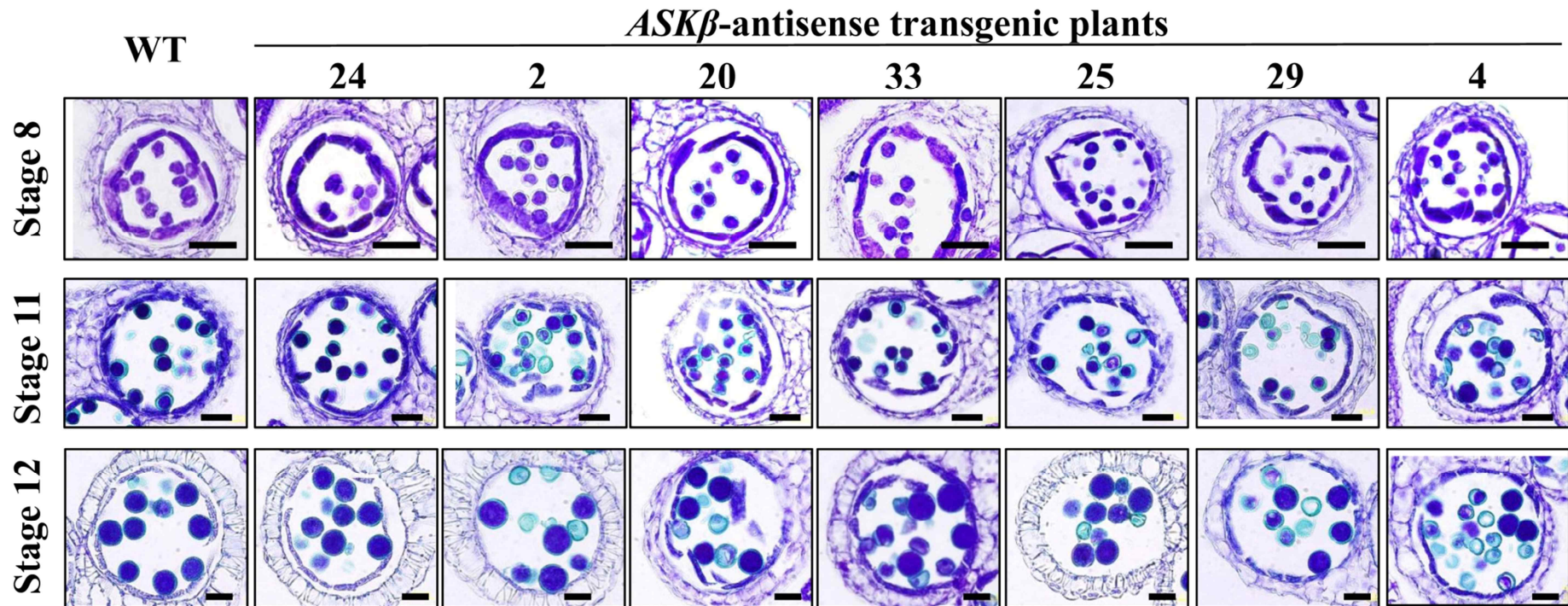
Supplementary Fig. S1. Sequence alignment of ASKs showing functional domains. Shaded region represents protein kinase domain. The conserved phosphate-binding residues that interact with prime-phosphorylated substrate (arginine 142, arginine 226, and lysine 251 in ASK_β) are highlighted in cyan. ATP binding and tyrosine phosphorylation site within the activation loop of MPK6 (de la Fuente van Bentem et al., 2008) are marked. Red line indicates the nucleotide-binding domain.



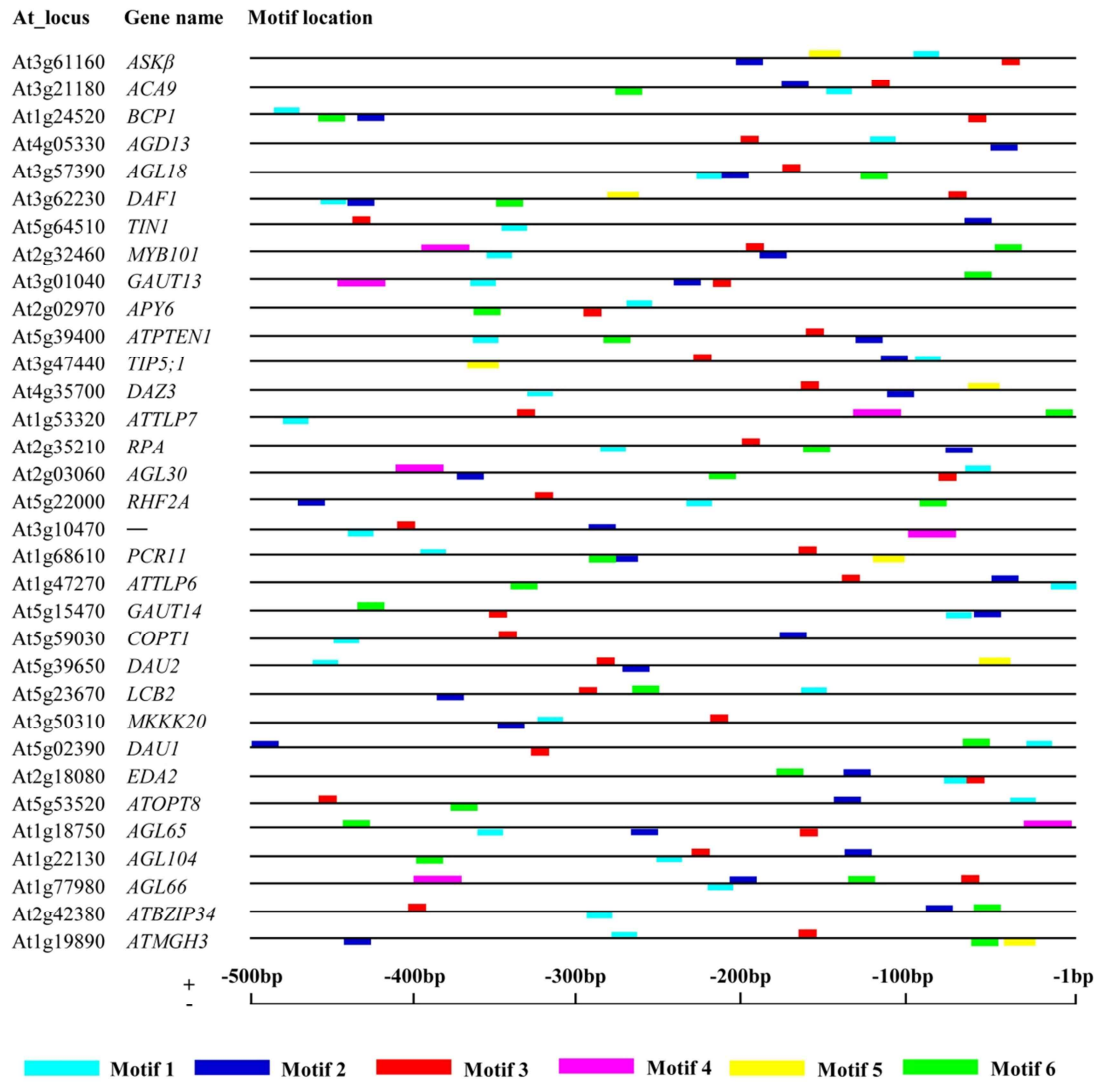
Supplementary Fig. S2. Expression characteristics of *ASKβ* in *Arabidopsis*. **A.** *ASKβ* expression levels in different tissues determined by semi-quantitative RT-PCR. **B.** Expression potential found in Genevestigator (<https://www.genevestigator.com/gv/>). Developmental stages (from left to right): germinating seeds, seedling, young rosette, developed rosette, bolting, young flower, developed flower, flower and silique, mature silique, and senescence. **C.** Expression patterns presented in the HanaDB-AT microarray database (<http://evolver.psc.riken.jp/seiken/graphic.cgi>).



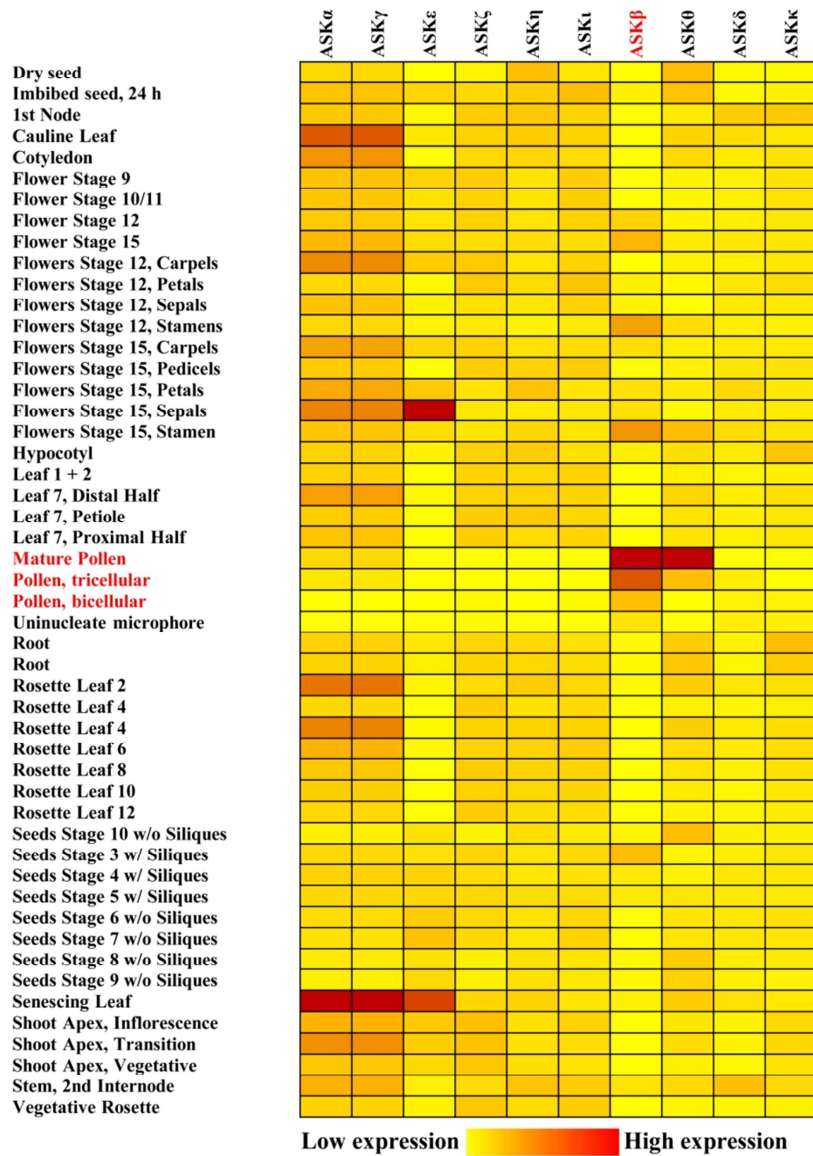
Supplementary Fig. S3. Phenotype of anther and mature pollen grain, along with gene expression levels of ASKs in WT and *ASKβ* antisense transgenic. **A**, whole anthers and mature pollen grain of wild type and *ASKβ* antisense transgenic lines. Upper, anthers of wild type and independent *ASKβ* antisense transgenic lines have been stained to determine pollen viability. Bar=200 μm. Lower, analysis of mature pollen grains from wild type and *ASKβ* antisense transgenic lines. Bar=20μm. Numbers indicate the independent *ASKβ* antisense transgenic lines. Black arrows indicate the defected mature pollen grains. **B**, Expression patterns of 9 ASK genes in WT, antisense transgenic line 2 and line 4. No expression signal was for *ASKγ*. Expression levels were normalized to that of *ACTIN7*. Data were obtained from three biological replicates and the error bar represents standard deviation.



Supplementary Fig. S4. Comparison of anther development between wild-type and *ASKβ*-antisense plants. Semi-thin sections of representative locules were stained with toluidine blue and photographed. The developmental stages of anthers are marked on the left: stage 8 for uninucleate microspores, stage 12 for bicellular, and stage 13 for mature pollen grains. Tapetum degradation usually occurs during stage 10 and 11. Bar = 20 μ m.



Supplementary Fig. S5. Organization of the conserved *cis*-elements in the promoter regions of *ASKβ* and its 32 co-expressed genes. The conserved sequences were identified with MEME version 4.9.1 (Bailey et al., 2009).



Supplementary Fig. S6. The expression patterns of *ASKs* in Arabidopsis. Information was obtained from public databases.

Supplementary Table S1. List of primers used in this study.

Primer Name	Primer Sequence		Product Size(bp)	Purpose
	Forward (5'-3')	Reverse (5'-3')		
<i>ASKβ -P1</i>	ATGCGATTTTGGGAGCGCCA	TGTGCCACGGCTGAGCTTTGA	314	<i>ASKβ</i> gene expression analysis
<i>ASKKSβ -P2</i>	CGATGAATGTGGTGC GGAGATTAACG	CATCTGCGTAGAGAAGCAGCCATTAACC	1354	<i>ASKβ</i> full CDS region, for antisense construct, gDNA PCR
<i>ASKβ -P3</i>	GCGGAGATTAACGAGTATTGCC	CAGAATCTTTCTCGTACGACG	145	<i>ASKβ</i> gene expression, qRT-PCR
<i>ASKθ</i>	GCTTCGGGTCGGACCTCC	CTCGCGGTTGGCATTTCG	275	<i>ASKθ</i> gene expression
<i>TDF1</i>	GAGCGATTTCTTCTCTCGGACC	GATGTATTCGGCTTCGATGTTGAAATG	112	Gene expression analysis
<i>MYB80</i>	GTCTCCTGCCGTTGCAGCTTGGA	AATCTCCTCTTGATCAACCACTTCTCCC	124	Gene expression analysis
<i>DAF1</i>	CTCAGGAAGTGCAGTGGACATCATT	CTAATGCAGCCCTTTGGTAATAGC	218	Gene expression analysis
<i>BCP1</i>	TACTCCTGGTGACGGTGACGTTGCA	AACGACGACCGCAGAGACGC	133	Gene expression analysis
<i>PCR11</i>	CGGGTATGGAGGAAGCAGTCTCTAC	CCGATGACCAAGTCCAAATCGC	177	Gene expression analysis
<i>ACA9</i>	TCTCTGTGATTGACAGAGAGGTAAGAGA	TCGTCTACCCAGCTTTCTTC	225	Gene expression analysis
<i>TIP5;1</i>	CGAAAGAAATTGATGAGAAGAATGATT	AGCCATCAATTTCTTGAAGACATG	165	Gene expression analysis
<i>ATTLP6</i>	CTCCTCTTCGGAATCGAAGCTCA	TTGAAATTA AAAAGCCTTCTCTTCTCG	113	Gene expression analysis
<i>35S</i>	CAATCCACTTGCTTTGAAGAC	CCATCATTGCGATAAAGGAAAG	135	gDNA PCR for transgenic plant confirmation
<i>ASKα</i>	CACAAATCCTTACTCGTACGGATCTCTC	AACACCAGTAGAGTCTCTTGCTCCAGG	173	<i>ASKα</i> gene expression
<i>ASKη</i>	CTCTATCGCCACAATGATCATTACCAA	ATCATCAGCCATGGCGATAGAGAC	127	<i>ASKη</i> gene expression
<i>ASKγ</i>	CGAAA ACTAGAGCAAAGCAGTCGAGA	GTGAATCATTGTGGGGGTTATGATATT	163	<i>ASKγ</i> gene expression
<i>ASKε</i>	ATTGGGGTCCGCTCTCTCTCTCT	ACTAGAGAAGCCCTAGAATAAAACACTTCC	131	<i>ASKε</i> gene expression
<i>ASKκ</i>	CAAAGAAGGTGTGAAGAAGTTGGGAAA	CCAAAGTCAAGCATTGACGATTGTC	174	<i>ASKκ</i> gene expression
<i>ASKι</i>	AGCGATCTCGAGATGCTTTTCCAG	TGGCCACGTCTAAGGAGGAGACATC	131	<i>ASKι</i> gene expression
<i>ASKζ</i>	GTTAGAGCTGTA AAAAGCACATGACTTCG	CGGGACGACGTTTCAAAGAATCT	113	<i>ASKζ</i> gene expression
<i>ASKδ</i>	CTCTACTGATCAGTTTCTCTCCATTGGTG	TCTTATAGCTTGAACATCCACAAGCACT	209	<i>ASKδ</i> gene expression
<i>At Actin7</i>	AGTGGTTCGTACAACCGGTATTGT	GAGGATAGCATGTGGA ACTGAGAA	96	Internal control

Supplementary Table 2. The orthologue relationship between ASKs and BrASKs. The calculation was carried out using InParanoid Version 4.1 (Sonnhammer and Östlund, 2015). The relationship between *ASKβ* and *BrASKβ* has been shown in red color.

OrtoID	Score	<i>Arabidopsis</i>	<i>Brassica rapa</i>
1	872	AT4G00720	Bra037354
2	818	AT1G09840	Bra030803
3	816	AT3G05840	Bra001169; Bra039407
4	812	AT3G61160	Bra003440
5	808	AT5G14640	Bra006263
6	801	AT5G26751	Bra036593
7	782	AT2G30980	Bra021685
8	771	AT4G18710	Bra020994

10 sequences in file At
 18 sequences in file Br
 10 sequences At have homologs in dataset Br
 18 sequences Br have homologs in dataset At
 80 At-At matches
 144 Br-Br matches

#####

8 groups of orthologs

8 in-paralogs from At

9 in-paralogs from Br

Grey zone 0 bits

Score cutoff 40 bits

In-paralogs with confidence less than 0.05 not shown

Sequence overlap cutoff 0.5

Group merging cutoff 0.5

Scoring matrix BLOSUM62

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Group of orthologs #1. Best score 872 bits

Score difference with first non-orthologous sequence - At:266 Br:29

AT4G00720	100.00%	Bra037354	100.00%
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Bootstrap support for AT4G00720 as seed ortholog is 100%.

Bootstrap support for Bra037354 as seed ortholog is 82%.

Group of orthologs #2. Best score 818 bits

Score difference with first non-orthologous sequence - At:29 Br:3

AT1G09840	100.00%	Bra030803	100.00%
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Bootstrap support for AT1G09840 as seed ortholog is 90%.

Bootstrap support for Bra030803 as seed ortholog is 56%. Alternative seed ortholog is Bra019983 (3 bits away from this cluster)

Group of orthologs #3. Best score 816 bits

Score difference with first non-orthologous sequence - At:182 Br:35

AT3G05840	100.00%	Bra001169	100.00%
		Bra039407	10.34%

Bootstrap support for AT3G05840 as seed ortholog is 100%.

Bootstrap support for Bra001169 as seed ortholog is 94%.

Group of orthologs #4. Best score 812 bits

Score difference with first non-orthologous sequence - At:248 Br:18

AT3G61160	100.00%	Bra003440	100.00%
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Bootstrap support for AT3G61160 as seed ortholog is 100%.

Bootstrap support for Bra003440 as seed ortholog is 41%. Alternative seed ortholog is Bra007577 (18 bits away from this cluster)

Group of orthologs #5. Best score 808 bits

Score difference with first non-orthologous sequence - At:163 Br:84

AT5G14640	100.00%	Bra006263	100.00%
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Bootstrap support for AT5G14640 as seed ortholog is 100%.

Bootstrap support for Bra006263 as seed ortholog is 99%.

Group of orthologs #6. Best score 801 bits

Score difference with first non-orthologous sequence - At:172 Br:4

AT5G26751	100.00%	Bra036593	100.00%
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Bootstrap support for AT5G26751 as seed ortholog is 100%.

Bootstrap support for Bra036593 as seed ortholog is 56%. Alternative seed ortholog is Bra009916 (4 bits away from this cluster)

Group of orthologs #7. Best score 782 bits

Score difference with first non-orthologous sequence - At:18 Br:92

AT2G30980	100.00%	Bra021685	100.00%
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Bootstrap support for AT2G30980 as seed ortholog is 78%.

Bootstrap support for Bra021685 as seed ortholog is 99%.

Group of orthologs #8. Best score 771 bits

Score difference with first non-orthologous sequence - At:86 Br:5

AT4G18710	100.00%	Bra020994	100.00%
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Bootstrap support for AT4G18710 as seed ortholog is 100%.

Bootstrap support for Bra020994 as seed ortholog is 61%. Alternative seed ortholog is Bra013341 (5 bits away from this cluster)

Supplementary Table S3. ASKβ co-expressed genes selected using Expression Angler.

UNIQUID	R-value to Bait	Annotation	GeneChip-ID
A13g01160	1.0000	Protein kinase superfamily protein	251358_at
A12g45800	0.9910	PLIM2b_GATA type zinc finger transcription factor family protein	266915_at
A12g45400	0.9910	Pleckstrin homology (PH) and lipid-binding START domains-containing protein	251854_at
A11g13970	0.9910	Protein of unknown function (DUF1336)	262664_at
A12g62180	0.9900	Plant invertase/pectin methylesterase inhibitor superfamily protein	251250_at
A13g04700	0.9890	Protein of unknown function (DUF1685)	257532_at
A12g25165	0.9870	RALFL25_ralf-like 25	257819_at
A12g50030	0.9870	Plant invertase/pectin methylesterase inhibitor superfamily protein	248534_at
A13g01240	0.9870	unknown protein	259266_at
A12g16500	0.9860	Protein kinase superfamily protein	250121_at
A12g13350	0.9860	Calcium-dependent lipid-binding (CaLB domain) family protein	265368_at
A12g48140	0.9840	Pectin lyase-like superfamily protein	248714_at
A12g43120	0.9840	SAUR-like auxin-responsive protein family	252733_at
A12g15110	0.9830	Pectate lyase family protein	246545_at
A12g20210	0.9830	DELTA-VPE_DELTA_VAPE_delta vacuolar processing enzyme	257121_at
A12g21180	0.9830	ACA9_ATACA9_autoinhibited Ca(2+)-ATPase 9	258035_at
A11g01780	0.9830	PLIM2b_GATA type zinc finger transcription factor family protein	261559_at
A12g15600	0.9820	SP1L4_SPIRAL1-like4	246540_at
A12g20410	0.9810	ATMGD2_MGD2_monogalactosyldiacylglycerol synthase 2	246075_at
A12g31500	0.9810	CPK24_calcium-dependent protein kinase 24	263450_at
A11g68110	0.9810	ENTH/ANTH/VHS superfamily protein	260011_at
A11g10770	0.9810	Plant invertase/pectin methylesterase inhibitor superfamily protein	262760_at
A12g26110	0.9810	Anther-specific protein agp1-like	258077_at
A12g26700	0.9800	RmC-like cupins superfamily protein	246841_at
A12g18220	0.9800	Phosphatidic acid phosphatase (PAP2) family protein	257065_at
263659_at	0.9800		263659_at
A12g12000	0.9790	Protein kinase protein with adenine nucleotide alpha hydrolases-like domain	250349_at
A12g20320	0.9790	DENN (AEX-3) domain-containing protein	265306_at
A12g01700	0.9780	AGP11_ATAGP11_arabinogalactan protein 11	259189_at
A12g46770	0.9780	unknown protein	248840_at
A12g02140	0.9780	LCR72_PDF2_6_low-molecular-weight cysteine-rich 72	266115_at
A11g24520	0.9770	BCP1_homolog of Brassica campestris pollen protein 1	265022_at
A12g28150	0.9770	AXY4L_TBL22_TRICHOME BIREFRINGENCE-LIKE 22	257309_at
A12g36490	0.9770	ATSFH12_SFH12_SEC14-like 12	246208_at
A12g25170	0.9770	RALFL26_ralf-like 26	257821_at
A12g26060	0.9760	Plant self-incompatibility protein S1 family	246878_at
A12g20865	0.9760	AGP40_arabinogalactan protein 40	257986_at
A11g18990	0.9760	Protein of unknown function, DUF593	259464_at
A12g14380	0.9760	AGP6_arabinogalactan protein 6	250174_at
A12g27180	0.9760	unknown protein	263084_at
A12g47000	0.9750	Peroxidase superfamily protein	248822_at
A12g17980	0.9750	AtC2_C2_Calcium-dependent lipid-binding (CaLB domain) family protein	258216_at
A12g50830	0.9750	unknown protein	248470_at
A12g02250	0.9750	Plant invertase/pectin methylesterase inhibitor superfamily protein	255515_at
A12g26860	0.9750	Plant self-incompatibility protein S1 family	258278_at
A12g04180	0.9750	ACA3_ATACA3_alpha carbonic anhydrase 3	245700_at
A12g15140	0.9740	Galactose mutarotase-like superfamily protein	250154_at
A12g34220	0.9740	Protein of unknown function (DUF810)	255835_at
A12g45280	0.9740	ATSYYP2_SYPP2_syntaxin of plants 72	252571_at
A12g44560	0.9740	FLA3_FASCLIN-like arabinogalactan protein 3 precursor	257392_at
A12g64790	0.9740	O-Glycosyl hydrolases family 17 protein	247253_at
A12g47050	0.9740	Plant invertase/pectin methylesterase inhibitor superfamily protein	266764_at
A12g62710	0.9740	Glycosyl hydrolase family protein	251228_at
A12g62640	0.9730	Protein of unknown function (DUF3511)	251180_at
A12g05610	0.9730	Plant invertase/pectin methylesterase inhibitor superfamily	258889_at
A11g54070	0.9730	Dormancy/auxin associated family protein	263144_at
A12g02720	0.9730	Pectate lyase family protein	267476_at
A12g28750	0.9730	unknown protein	256584_at
A12g27790	0.9720	Calcium-binding EF hand family protein	253833_at
A12g34440	0.9720	AtPERK5_PERK5_Protein kinase superfamily protein	253262_at
A11g70790	0.9720	Calcium-dependent lipid-binding (CaLB domain) family protein	262291_at
A12g55930	0.9720	ATOPT1_OPT1_oligopeptide transporter 1	248037_at
A12g26260	0.9720	MIOX4_myo-inositol oxygenase 4	254001_at
A12g04930	0.9710	DES-1-LIKE_fatty acid desaturase family protein	255276_at
A12g24370	0.9710	Protein kinase protein with adenine nucleotide alpha hydrolases-like domain	265681_at
A11g73860	0.9710	P-loop containing nucleoside triphosphate hydrolases superfamily protein	260381_at
A11g14420	0.9710	ATS9_Pectate lyase family protein	261528_at
A12g02810	0.9710	Protein kinase superfamily protein	258600_at
A11g52580	0.9700	ATRBL5_RBL5_RHOMBOLD-like protein 5	262146_at
A12g06260	0.9700	GATL4_GoIS9_galacturonosyltransferase-like 4	256392_at
A12g47540	0.9700	Mo25 family protein	248751_at
A12g51290	0.9700	Protein of unknown function (DUF630);Protein of unknown function (DUF632)	252101_at
A11g78460	0.9700	SOUL_heme-binding family protein	263126_at
A12g36020	0.9690	HVA22J_HVA22-like protein J	263950_at
A12g07820	0.9690	Pectin lyase-like superfamily protein	258639_at
A11g52240	0.9680	ATROPGEF11_PIRF1_ROPGEF11_RHO guanyl-nucleotide exchange factor 11	257504_at
A12g42640	0.9680	AHA8_HA8_H(+)-ATPase 8	252820_at
A11g69940	0.9680	ATPPME1_PPME1_Pectin lyase-like superfamily protein	250606_s_
A12g58050	0.9680	GDPDL6_SVL4_SHV3-like 4	247843_at
A12g01270	0.9670	Pectate lyase family protein	259269_at
A12g39880	0.9670	unknown protein	249429_at
A12g05930	0.9670	GLP8_germin-like protein 8	258748_at
A12g61720	0.9670	Protein of unknown function (DUF1216)	247512_at
A12g62170	0.9670	VGDH2_VANGUARD 1 homolog 2	251258_at
A12g01610	0.9670	Protein of unknown function, DUF538	251107_at
A12g05330	0.9670	AGD13_ARF-GAP domain 13	255232_at
A12g35010	0.9660	BGAL11_beta-galactosidase 11	253226_at
A12g55560	0.9660	sks14_SKU5_similar 14	265127_at
A12g02970	0.9660	EXL6_EXORDIUM like 6	258605_at
A11g04700	0.9660	PBI domain-containing protein tyrosine kinase	264602_at
A12g46210	0.9660	AtSLD2_SLD2_Fatty acid/sphingolipid desaturase	266592_at
A11g24620	0.9650	EF hand calcium-binding protein family	257405_at
A12g37990	0.9650	AGL18_AGAMOUS-like 18	251623_at
A12g28810	0.9650	Protein of unknown function (DUF1216)	256580_s_
A12g03800	0.9650	ATSYYP13_SYYP13_syntaxin of plants 131	259338_at
A12g42880	0.9650	Leucine-rich repeat protein kinase family protein	252771_at
A12g20580	0.9640	COBL10_COBLA-like protein 10 precursor	257082_at
A12g16730	0.9640	BGAL13_glycosyl hydrolase family 35 protein	265404_at
A12g62230	0.9640	DAF1_F-box family protein	251252_at
A12g10660	0.9640	calmodulin-binding protein-related	246013_at
A12g19310	0.9640	PLC-like phosphodiesterases superfamily protein	258012_at
A12g40990	0.9640	DHHC-type zinc finger family protein	257358_at
A12g13065	0.9640	SRF4_STRUBBELIG-receptor family 4	257850_at
A12g21570	0.9640	unknown protein	258168_at
A12g07430	0.9640	Pectin lyase-like superfamily protein	250631_at

<i>At2g43230</i>	0.9630	Protein kinase superfamily protein]	266453_at
<i>At4g35180</i>	0.9630	LHT7_LYS/HIS transporter 7]	253181_at
<i>At1g35490</i>	0.9630	bZIP family transcription factor]	262022_at
<i>At4g27580</i>	0.9630	unknown protein	253831_at
<i>At2g20700</i>	0.9620	LLG2_LORELEI-LIKE-GPI ANCHORED PROTEIN 2]	265430_at
<i>At4g30140</i>	0.9620	CDEF1_GDSL-like Lipase/Acylhydrolase superfamily protein]	253660_at
<i>At1g25240</i>	0.9620	ENTH/VHS/GAT family protein]	245636_at
<i>At3g13390</i>	0.9620	sks11_SKU5 similar 11]	256955_at
<i>At1g76370</i>	0.9610	Protein kinase superfamily protein]	259886_at
<i>At5g56640</i>	0.9610	MIOX5_myoinositol oxygenase 5]	247981_at
<i>At5g23270</i>	0.9610	ATSTP11_STP11_sugar transporter 11]	249852_at
<i>At1g74000</i>	0.9610	SS3_strictosidine synthase 3]	260335_at
<i>At5g7620</i>	0.9600	RNA-binding (RRM/RBD/RNP motifs) family protein]	248755_at
<i>At1g55370</i>	0.9600	sks12_SKU5 similar 12]	265080_at
<i>At1g91290</i>	0.9600	ATSYPI24_SYPI24_syntaxin of plants 124]	264760_at
<i>At4g39110</i>	0.9600	Malectin/receptor-like protein kinase family protein]	252933_at
<i>At3g01620</i>	0.9590	beta-1,4-N-acetylglucosaminyltransferase family protein]	257523_at
<i>At1g04540</i>	0.9590	Calcium-dependent lipid-binding (CaLB domain) family protein]	264601_at
<i>At5g19580</i>	0.9590	glyoxal oxidase-related protein]	245946_at
<i>At4g24640</i>	0.9590	APPB1_Plant invertase/pectin methyltransferase inhibitor superfamily protein]	254123_at
<i>At3g20530</i>	0.9590	Protein kinase superfamily protein]	257090_at
<i>At1g29140</i>	0.9590	Pollen Ole e 1 allergen and extensin family protein]	260888_at
<i>At5g64510</i>	0.9580	TIN1_unknown protein	247293_at
<i>At4g28280</i>	0.9580	LLG3_LORELEI-LIKE-GPI ANCHORED PROTEIN 3]	253807_at
<i>At2g33460</i>	0.9570	RIC1_ROP-interactive CRIB motif-containing protein 1]	255837_at
<i>At3g16040</i>	0.9570	Translation machinery associated TMA7]	258337_at
<i>At2g46360</i>	0.9570	unknown protein	263781_at
<i>At4g25780</i>	0.9570	CAP (Cysteine-rich secretory proteins) superfamily protein]	254024_at
<i>At2g18180</i>	0.9570	Sec14p-like phosphatidylinositol transfer family protein]	263062_at
<i>At5g24240</i>	0.9560	Phosphatidylinositol 3- and 4-kinase (Ubiquitin family protein]	249780_at
<i>At5g39420</i>	0.9560	cdc2cAt_CDC2C]	249448_at
<i>At5g18910</i>	0.9560	Protein kinase superfamily protein]	249950_at
<i>At3g17060</i>	0.9560	Pectin lyase-like superfamily protein]	257886_at
<i>At2g26410</i>	0.9560	lq4_IQ-domain 4]	245036_at
<i>At2g18470</i>	0.9560	AtPERK4_PERK4_rolin-rich extensin-like receptor kinase 4]	265923_at
<i>At3g20190</i>	0.9560	Leucine-rich repeat protein kinase family protein]	257119_at
<i>At4g07960</i>	0.9560	ATCSLC12_CSLC12_CSLC12_Cellulose-synthase-like C12]	255175_at
<i>At2g36450</i>	0.9550	Plant invertase/pectin methyltransferase inhibitor superfamily]	245053_at
<i>At5g62750</i>	0.9550	unknown protein	247402_at
<i>At2g07040</i>	0.9550	ATPRK2A_PRK2A_Leucine-rich repeat protein kinase family protein]	266494_at
<i>At1g02790</i>	0.9550	PGA4_polygalacturonase 4]	262122_at
<i>At2g33870</i>	0.9550	ArRABA1h_RAB GTPase homolog A1H]	267447_at
<i>At5g27980</i>	0.9550	Seed maturation protein]	246761_at
<i>At2g26490</i>	0.9550	Transducin/WD40 repeat-like superfamily protein]	245057_at
<i>At1g10660</i>	0.9550	unknown protein	257477_at
<i>At4g39610</i>	0.9550	Protein of unknown function, DUF617]	252881_at
<i>At1g17540</i>	0.9550	Protein kinase protein with adenine nucleotide alpha hydrolases-like domain]	260737_at
<i>At3g56600</i>	0.9540	Protein kinase superfamily protein]	251697_at
<i>At1g66210</i>	0.9540	Subtilisin-like serine endopeptidase family protein]	259820_at
<i>At3g52600</i>	0.9540	AtcwINV2_CWINV2_cell wall invertase 2]	252052_at
<i>At5g61980</i>	0.9540	AGD1_ARF-GAP domain 1]	247503_at
<i>At2g33100</i>	0.9530	ATCSLD1_CSLD1_CSLD1_cellulose synthase-like D1]	245159_at
<i>At1g47280</i>	0.9530	unknown protein	261687_at
<i>At5g57690</i>	0.9530	ATDGK4_DGK4_diaclyglycerol kinase 4]	247873_at
<i>At2g26850</i>	0.9530	F-box family protein]	266850_at
<i>At2g32460</i>	0.9530	ATM1_ATMYB101_MYB101_myb domain protein 101]	267087_at
<i>At1g19500</i>	0.9530	unknown protein	260661_at
<i>At3g13400</i>	0.9530	sks13_SKU5 similar 13]	256966_at
<i>At1g28270</i>	0.9520	RALFL4_raf-like 4]	245658_at
<i>At1g64628</i>	0.9520	CPuORF57_conserved peptide upstream open reading frame 57]	261974_at
<i>At2g21990</i>	0.9520	Protein of unknown function, DUF617]	257433_at
<i>At1g30550</i>	0.9510	ENTH/ANTH/VHS superfamily protein]	263166_at
<i>At3g09530</i>	0.9510	ATEX070H3_EXO70H3_exocyst subunit exo70 family protein H3]	258753_at
<i>At5g45880</i>	0.9510	Pollen Ole e 1 allergen and extensin family protein]	248926_at
<i>At5g56750</i>	0.9510	NDL1_N-MYC downregulated-like 1]	247979_at
<i>At4g10010</i>	0.9500	Protein kinase superfamily protein]	255006_at
<i>At1g49490</i>	0.9500	Leucine-rich repeat (LRR) family protein]	262393_at
<i>At2g23900</i>	0.9500	Pectin lyase-like superfamily protein]	266558_at
<i>At1g70540</i>	0.9500	EDA24_Plant invertase/pectin methyltransferase inhibitor superfamily protein]	260306_at
<i>At2g03410</i>	0.9500	Mo25 family protein]	265705_at
<i>At3g06830</i>	0.9500	Plant invertase/pectin methyltransferase inhibitor superfamily]	258523_at
<i>At1g01460</i>	0.9490	ATPIPK11_PIPK11_Phosphatidylinositol-4-phosphate 5-kinase, core]	259425_at
<i>At4g24580</i>	0.9490	REN1_Rho GTPase activation protein (RhoGAP) with PH domain]	254173_at
<i>At4g04980</i>	0.9490	unknown protein	255251_at
<i>At3g43860</i>	0.9490	AtGH9A4_GH9A4_glycosyl hydrolase 9A4]	252710_at
<i>At5g14890</i>	0.9490	NHL domain-containing protein]	246592_at
<i>At3g61230</i>	0.9480	PLIM2c_GATA type zinc finger transcription factor family protein]	251361_at
<i>At1g15350</i>	0.9480	unknown protein	262599_at
<i>At2g46260</i>	0.9480	BTB/POZ/Kelch-associated protein]	266580_at
<i>At5g59370</i>	0.9480	ACT4_actin 4]	247736_at
<i>At1g01310</i>	0.9480	CAP (Cysteine-rich secretory proteins) superfamily protein]	261045_at
<i>At1g10740</i>	0.9480	alpha/beta-Hydrolases superfamily protein]	262786_at
<i>At4g03620</i>	0.9470	myosin heavy chain-related]	255386_at
<i>At2g44560</i>	0.9470	AtGH9B11_GH9B11_glycosyl hydrolase 9B11]	267398_at
<i>At2g02020</i>	0.9470	Protein kinase protein with adenine nucleotide alpha hydrolases-like domain]	257120_at
<i>At3g01040</i>	0.9470	GALT13_galacturonosyltransferase 13]	259321_at
<i>At2g23540</i>	0.9470	AtPERK12_IG11_PERK12_Protein kinase superfamily protein]	265178_at
<i>At1g69050</i>	0.9470	unknown protein	259370_at
<i>At3g19020</i>	0.9460	Leucine-rich repeat (LRR) family protein]	256945_at
<i>At1g50610</i>	0.9460	Leucine-rich repeat protein kinase family protein]	261875_at
<i>At5g54095</i>	0.9460	unknown protein	248194_at
<i>At2g22180</i>	0.9450	hydroxyproline-rich glycoprotein family protein]	263453_at
<i>At3g21700</i>	0.9450	ATSGP2_SGP2_Ras-related small GTP-binding family protein]	257951_at
<i>At5g35090</i>	0.9450	unknown protein	246646_at
<i>At2g02970</i>	0.9450	GDA1/CD39 nucleoside phosphatase family protein]	266744_at
<i>At1g79860</i>	0.9450	ATROPGEF12_MEE64_ROPGEF12_RHO guanyl-nucleotide exchange factor 12]	260161_at
<i>At3g29060</i>	0.9450	EXS (ERD1/XPR1/SYG1) family protein]	257106_at
<i>At5g42490</i>	0.9450	ATP binding microtubule motor family protein]	249194_at
<i>At3g29180</i>	0.9450	Protein of unknown function (DUF1336)]	256747_at
<i>At1g01980</i>	0.9440	FAD-binding Berberine family protein]	261623_at
<i>At3g22750</i>	0.9440	Protein kinase superfamily protein]	258323_at
<i>At3g24715</i>	0.9440	Protein kinase superfamily protein with octicosapeptide/Phox/Bem1p domain]	257618_at
<i>At2g07180</i>	0.9440	Protein kinase superfamily protein]	266428_at
<i>At5g16540</i>	0.9440	ZFN3_zinc finger nuclease 3]	250128_at
<i>At1g79910</i>	0.9430	Regulator of Vps4 activity in the MVB pathway protein]	260158_at
<i>At1g31240</i>	0.9430	Plant self-incompatibility protein S1 family]	265133_s_
<i>At1g64300</i>	0.9430	Protein kinase family protein]	259740_at
<i>At3g7980</i>	0.9430	O-fucosyltransferase family protein]	266100_at
<i>At5g42340</i>	0.9430	PUB15_Plant U-Box 15]	249250_at
<i>At4g27350</i>	0.9430	Protein of unknown function (DUF1223)]	253919_at
<i>At4g20890</i>	0.9420	TUB9_tubulin beta-9 chain]	254446_at
<i>At2g41860</i>	0.9420	CPK14_calcium-dependent protein kinase 14]	267531_at
<i>At1g67290</i>	0.9420	GLOX1_glyoxal oxidase-related protein]	264993_at
<i>At5g12950</i>	0.9420	Putative glycosyl hydrolase of unknown function (DUF1680)]	250268_s_
<i>At1g11770</i>	0.9420	FAD-binding Berberine family protein]	262817_at
<i>At1g67480</i>	0.9420	Galactose oxidase/kelch repeat superfamily protein]	264229_at
<i>At1g23350</i>	0.9420	Plant invertase/pectin methyltransferase inhibitor superfamily protein]	263043_at
<i>At3g54240</i>	0.9410	alpha/beta-Hydrolases superfamily protein]	251874_at
<i>At1g64740</i>	0.9410	TUA1_alpha-1 tubulin]	262885_at
<i>At3g59830</i>	0.9410	Integrin-linked protein kinase family]	251433_at
<i>At2g05850</i>	0.9400	scpl38_serine carboxypeptidase-like 38]	266029_at
<i>At1g61563</i>	0.9390	RALFL8_raf-like 8]	265007_s_
<i>At3g52000</i>	0.9390	scpl36_serine carboxypeptidase-like 36]	252085_s_
<i>At4g03290</i>	0.9380	EF hand calcium-binding protein family]	255423_at
<i>At1g61860</i>	0.9380	Protein kinase superfamily protein]	264284_at
<i>At3g28830</i>	0.9380	Protein of unknown function (DUF1216)]	256581_at
<i>At1g78940</i>	0.9380	Protein kinase protein with adenine nucleotide alpha hydrolases-like domain]	264139_at

<i>A15g20390</i>	0.9380	Glycosyl hydrolase superfamily protein]	246123_at
<i>A1g28550</i>	0.9380	AtRABA1i_RABA1i__RAB GTPase homolog A11]	262742_at
<i>A15g58170</i>	0.9370	GDPLD7_SVL5__SHV3-like 5]	247804_at
<i>A13g07880</i>	0.9370	SCN1__Immunoglobulin E-set superfamily protein]	258637_at
<i>A15g13990</i>	0.9370	ATEX070C2_EXO70C2__exocyst subunit exo70 family protein C2]	250204_at
<i>A1g13890</i>	0.9360	SNAP30__soluble N-ethylmaleimide-sensitive factor adaptor protein 30]	259451_at
<i>A13g11690</i>	0.9360	unknown protein	259103_at
<i>A1g63930</i>	0.9360	ROH1__from the Czech 'roh' meaning 'corner']	260320_at
<i>A15g65530</i>	0.9360	Protein kinase superfamily protein]	247170_at
<i>A12g21540</i>	0.9360	ATSFH3_SFHH3__SEC14-like 3]	263765_at
<i>A15g60740</i>	0.9360	ABCG28__ABC transporter family protein]	247613_at
<i>A1g06700</i>	0.9360	Protein kinase superfamily protein]	260835_at
<i>A12g28640</i>	0.9360	ATEX070H5_EXO70H5__exocyst subunit exo70 family protein H5]	263440_at
<i>A1g13640</i>	0.9360	MRH1__Leucine-rich repeat protein kinase family protein]	254633_at
<i>A1g54280</i>	0.9360	ATPase E1-E2 type family protein]	262998_at
<i>A1g30710</i>	0.9350	FAD-binding Berberine family protein]	263215_at
<i>A15g26150</i>	0.9350	protein kinase family protein]	246877_at
<i>A13g05150</i>	0.9350	Major facilitator superfamily protein]	259351_at
<i>A1g60740</i>	0.9350] Thioredoxin superfamily protein]	264923_s_
<i>A15g58380</i>	0.9350	CIPK10_PKS2_SIP1_SNRK3.8__SOS3-interacting protein 1]	247820_at
<i>A15g41780</i>	0.9350	myosin heavy chain-related]	249270_at
<i>A15g39400</i>	0.9350	ATPTEN1_PTEN1__Calcium/lipid-binding (CaLB) phosphatase]	249447_at
<i>A12g47030</i>	0.9350] VGDH1__Plant invertase/pectin methyltransferase inhibitor superfamily]	266750_s_
<i>A12g17890</i>	0.9350	CPK16__calcium-dependent protein kinase 16]	264813_at
<i>A4g25590</i>	0.9340	ADF7__actin depolymerizing factor 7]	245232_at
<i>A13g47440</i>	0.9340	TIP5;1__tonoplast intrinsic protein 5;1]	252440_at
<i>A4g35700</i>	0.9340	DAZ3__zinc finger (C2H2 type) family protein]	253153_at
<i>A12g40620</i>	0.9330	Basic-leucine zipper (bZIP) transcription factor family protein]	255878_at
<i>A1g02000</i>	0.9330	GAE2__UDP-D-glucuronate 4-epimerase 2]	261624_at
<i>A1g44120</i>	0.9330	Armadillo/beta-catenin-like repeat	245741_at
<i>A4g24630</i>	0.9320	DHHC-type zinc finger family protein]	254142_at
<i>A15g07420</i>	0.9320	Pectin lyase-like superfamily protein]	250608_at
<i>A15g10260</i>	0.9320	AtRABH1e_RABH1e__RAB GTPase homolog H1E]	250479_at
<i>A4g13240</i>	0.9320	ATROPGEF9_ROPGEF9__RHO guanyl-nucleotide exchange factor 9]	254757_at
<i>A13g12620</i>	0.9310	Protein phosphatase 2C family protein]	256279_at
<i>A13g07960</i>	0.9310	PIPSK6__Phosphatidylinositol-4-phosphate 5-kinase family protein]	258690_at
<i>A1g12450</i>	0.9310	SNARE associated Golgi protein family]	259530_at
<i>A1g01575</i>	0.9310	serine protease inhibitor, Kazal-type family protein]	255536_at
<i>A12g38180</i>	0.9310	ATCHX8_CHX08_CHX8__Cation/hydrogen exchanger family protein]	266160_at
<i>A12g39890</i>	0.9310	ATPROT1_PROT1__proline transporter 1]	267358_at
<i>A15g09430</i>	0.9300	alpha/beta-Hydrolases superfamily protein]	245880_at
<i>A12g31830</i>	0.9300	endonuclease/exonuclease/phosphatase family protein]	263489_at
<i>A13g18750</i>	0.9300	ATWNK6_WNK6_ZIK5__with no lysine (K) kinase 6]	257801_at
<i>A13g59290</i>	0.9290	ENTH/VHS family protein]	251468_at
<i>A15g01700</i>	0.9290	Protein phosphatase 2C family protein]	251103_at
<i>A12g47340</i>	0.9290	Plant invertase/pectin methyltransferase inhibitor superfamily protein]	260577_at
<i>A12g34440</i>	0.9290	AGL29__AGAMOUS-like 29]	266994_at
<i>A15g61360</i>	0.9290	unknown protein	247547_at
<i>A15g36260</i>	0.9280	Eukaryotic aspartyl protease family protein]	246616_at
<i>A13g13660</i>	0.9280	Disease resistance-responsive (dirigent-like protein) family protein]	256782_at
<i>A13g19970</i>	0.9270	alpha/beta-Hydrolases superfamily protein]	256627_at
<i>A1g16760</i>	0.9270	Protein kinase protein with adenine nucleotide alpha hydrolases-like domain]	255765_at
<i>A4g38230</i>	0.9270	ATCPK26_CPK26__calcium-dependent protein kinase 26]	253034_at
<i>A13g07850</i>	0.9260] Pectin lyase-like superfamily protein]	258645_s_
<i>A1g64320</i>	0.9260	myosin heavy chain-related]	257508_at
<i>A13g28790</i>	0.9250	Protein of unknown function (DUF1216)]	256588_at
<i>A13g02555</i>	0.9250	unknown protein	258493_at
<i>A15g05070</i>	0.9250	DHHC-type zinc finger family protein]	250806_at
<i>A13g57140</i>	0.9250	SDP1-LIKE__sugar-dependent 1-like]	251654_at
<i>A1g44160</i>	0.9250	HSP40/DnaJ peptide-binding protein]	245737_at
<i>A1g44170</i>	0.9240	ATP binding microtubule motor family protein]	254205_at
<i>A15g12180</i>	0.9240	CPK17__calcium-dependent protein kinase 17]	250308_at
<i>A12g46520</i>	0.9240	ACT12__actin-12]	252531_at
<i>A1g58120</i>	0.9240	unknown protein	246392_at
<i>A15g52360</i>	0.9240	ADF10__actin depolymerizing factor 10]	248367_at
<i>A1g54290</i>	0.9230	Translation initiation factor SUI1 family protein]	262959_at
<i>A13g05820</i>	0.9230	A/N-Invh_H_At-A/N-Invh_H_INVH__invertase H]	258732_at
<i>A13g51770</i>	0.9230	ATEOL1_ETO1__tetratricopeptide repeat (TPR)-containing protein]	246298_at
<i>A15g28680</i>	0.9230	ANX2__Malectin/receptor-like protein kinase family protein]	246106_at
<i>A15g12390</i>	0.9220	FIS1B__Tetratricopeptide repeat (TPR)-like superfamily protein]	245178_at
<i>A13g23170</i>	0.9220	unknown protein	257925_at
<i>A13g57690</i>	0.9220	AGP23_ATAGP23__arabinogalactan protein 23]	251590_at
<i>A4g26400</i>	0.9220	RING/U-box superfamily protein]	253958_at
<i>A15g25340</i>	0.9220	Ubiquitin-like superfamily protein]	246918_at
<i>A12g19770</i>	0.9210	PRF5__profilin 5]	266697_at
<i>A15g13150</i>	0.9210	ATEX070C1_EXO70C1__exocyst subunit exo70 family protein C1]	245979_at
<i>A15g27870</i>	0.9210	Plant invertase/pectin methyltransferase inhibitor superfamily]	246751_at
<i>A4g25900</i>	0.9210	Galactose mutarotase-like superfamily protein]	254040_at
<i>A15g54780</i>	0.9210	Ypt/Rab-GAP domain of gyp1p superfamily protein]	248129_at
<i>A12g33320</i>	0.9200	Calcium-dependent lipid-binding (CaLB domain) family protein]	255849_at
<i>A4g18790</i>	0.9200	ATNRAMP5_NRAMPS__NRAMP metal ion transporter family protein]	254640_at
<i>263366_at</i>	0.9190	unknown protein	263366_at
<i>A1g54920</i>	0.9190	Protein of unknown function (DUF1216)]	256323_at
<i>A13g28980</i>	0.9190	unknown protein	258058_at
<i>A1g75370</i>	0.9190	unknown protein	262696_at
<i>A4g49870</i>	0.9190	TLD-domain containing nucleolar protein]	252867_at
<i>A13g62660</i>	0.9190	GATL7__galacturonosyltransferase-like 7]	251225_at
<i>A4g20160</i>	0.9180	unknown protein	254507_at
<i>A13g05140</i>	0.9170	RBK2__ROP binding protein kinases 2]	259350_at
<i>A15g21050</i>	0.9170	unknown protein	246188_at
<i>A1g53320</i>	0.9160	AtTLPT7_TLPT7__hubby like protein 7]	260588_at
<i>A1g07330</i>	0.9150	unknown protein	257489_at
<i>A4g21420</i>	0.9150	unknown protein	254411_at
<i>A4g20870</i>	0.9150	ATFAH2_FAH2__fatty acid hydroxylase 2]	254448_at
<i>A13g04630</i>	0.9140	WDL1__WVD2-like 1]	258796_at
<i>A13g11740</i>	0.9140	Protein of unknown function (DUF567)]	258781_at
<i>A1g79640</i>	0.9140	Protein kinase superfamily protein]	261401_at
<i>A13g18810</i>	0.9140	AtPERK6_PERK6__Protein kinase superfamily protein]	257804_at
<i>A1g14290</i>	0.9140	SBH2__sphingoid base hydroxylase 2]	261492_at
<i>A13g11850</i>	0.9140	Protein of unknown function, DUF593]	258777_at
<i>255489_at</i>	0.9140	unknown protein	255489_at
<i>A15g45810</i>	0.9130	CIPK19_SnRK3.5__CBL-interacting protein kinase 19]	248909_at
<i>A15g45840</i>	0.9130	Leucine-rich repeat protein kinase family protein]	248916_at
<i>A12g15880</i>	0.9130	Leucine-rich repeat (LRR) family protein]	265536_at
<i>A13g09760</i>	0.9120	RING/U-box superfamily protein]	258718_at
<i>A1g05960</i>	0.9120	ARM repeat superfamily protein]	260961_at
<i>A13g01250</i>	0.9120	unknown protein	259265_at
<i>A15g01960</i>	0.9120	AML1_ML1__MEI2-like protein 1]	247506_at
<i>A4g16745</i>	0.9110	Exostosis family protein]	245314_at
<i>A13g19360</i>	0.9110	CPK34__calcium-dependent protein kinase 34]	246065_at
<i>A12g34770</i>	0.9100	ATFAH1_FAH1__fatty acid hydroxylase 1]	267318_at
<i>A1g077730</i>	0.9100	Pleckstrin homology (PH) domain superfamily protein]	259676_at
<i>A15g27000</i>	0.9100	ATK4_KATD__kinesin 4]	246802_at
<i>A15g16480</i>	0.9100	PFA-DSP5__Phosphotyrosine protein phosphatases superfamily protein]	250124_at
<i>A13g24530</i>	0.9100	AAA-type ATPase family protein / ankyrin repeat family protein]	258134_at
<i>A1g74490</i>	0.9090	Protein kinase superfamily protein]	260213_at
<i>A4g00350</i>	0.9090	MATE efflux family protein]	255717_at
<i>A15g02570</i>	0.9090	Histone superfamily protein]	250997_at
<i>A1g79660</i>	0.9080	unknown protein	261356_at
<i>A4g39180</i>	0.9080	ATSEC14_SEC14__Sec14p-like phosphatidylinositol transfer family protein]	252937_at
<i>A13g54690</i>	0.9080	SETH3__Sugar isomerase (SIS) family protein]	251855_at
<i>A13g05990</i>	0.9070	Leucine-rich repeat (LRR) family protein]	258557_at
<i>A12g38910</i>	0.9070	CPK20__calcium-dependent protein kinase 20]	266199_at
<i>A12g21480</i>	0.9070	Malectin/receptor-like protein kinase family protein]	263748_at
<i>A15g32440</i>	0.9070	Ubiquitin system component Cue protein]	246171_at
<i>A15g17400</i>	0.9070	ER-ANT1__endoplasmic reticulum-adenine nucleotide transporter 1]	246427_at
<i>A15g04460</i>	0.9060	RING/U-box superfamily protein]	250888_at

<i>At2g40090</i>	0.9060	ATATH9_ATH9_ABC2 homolog 9]	265721_at
<i>At2g29050</i>	0.9060	ATRBL1_RBL1_RHOMBOD-like 1]	266774_at
<i>At5g51030</i>	0.9050	NAD(P)-binding Rossmann-fold superfamily protein]	248484_at
<i>At5g57320</i>	0.9050	VLN5_villin, putative]	247928_at
<i>At3g24620</i>	0.9050	ATROPGEF8_ROPGEF8_RHO guanyl-nucleotide exchange factor 8]	258129_at
<i>At3g28490</i>	0.9050	Oxoglutarate/iron-dependent oxygenase]	257870_at
<i>At2g19880</i>	0.9040	Nucleotide-diphospho-sugar transferases superfamily protein]	266703_at
<i>At1g79400</i>	0.9040	ATCHX2_CHX2_cation/H+ exchanger 2]	262936_at
<i>At2g18280</i>	0.9040	AtILP2_TLP2_tubby like protein 2]	265321_at
<i>At4g40020</i>	0.9040	Myosin heavy chain-related protein]	252873_at
<i>At2g35210</i>	0.9040	AGD10_MEE28_RPA_root and pollen arfgap]	266548_at
<i>At3g08730</i>	0.9040	ATPK1_ATPK6_ATSGK1_PK1_PK6_S6K1__protein-serine kinase 1]	258677_at
<i>At1g75160</i>	0.9040	Protein of unknown function (DUF620)]	256506_at
<i>At4g27880</i>	0.9030	Protein with RING/U-box and TRAF-like domains]	253838_at
<i>At2g37670</i>	0.9030	Transducin/WD40 repeat-like superfamily protein]	267160_at
<i>At1g74010</i>	0.9030	Calcium-dependent phosphotriesterase superfamily protein]	260386_at
<i>At1g11990</i>	0.9030	O-fucosyltransferase family protein]	264387_at
<i>At2g33270</i>	0.9030	ACHT3_atypical CYS_HIS rich thioredoxin 3]	255847_at
<i>At1g08135</i>	0.9030	ATCHX6B_CHX6B_cation/H+ exchanger 6B]	261816_at
<i>At5g14870</i>	0.9020	ATCNGC18_CNGC18_cyclic nucleotide-gated channel 18]	246590_at
<i>At5g54130</i>	0.9020	Calcium-binding endonuclease/exonuclease/phosphatase family]	248190_at
<i>At4g13560</i>	0.9020	UNE15_Late embryogenesis abundant protein (LEA) family protein]	254716_at
<i>At2g03060</i>	0.9020	AGL30_AGAMOUS-like 30]	266793_at
<i>At3g55180</i>	0.9020	alpha/beta-Hydrolases superfamily protein]	251835_at
<i>At5g57830</i>	0.9020	Protein of unknown function, DUF593]	247885_at
<i>At4g25150</i>	0.9000	HAD superfamily, subfamily IIIB acid phosphatase]	254096_at
<i>At4g33230</i>	0.9000	Plant invertase/pectin methyltransferase inhibitor superfamily]	253370_at
<i>At1g12070</i>	0.9000	Immunoglobulin E-set superfamily protein]	264395_at
<i>At1g50810</i>	0.9000		265491_s_
<i>At4g13450</i>	0.9000	Adenine nucleotide alpha hydrolases-like superfamily protein]	254775_at
<i>At3g03430</i>	0.8990	Calcium-binding EF-hand family protein]	259044_at
<i>At3g04360</i>	0.8980	Calcium-dependent lipid-binding (CaLB domain) family protein]	258591_at
<i>At1g22110</i>	0.8980	structural constituent of ribosome]	255950_at
<i>At1g61770</i>	0.8980	Chaperone DnaJ-domain superfamily protein]	264427_at
<i>At3g60330</i>	0.8970	AHA7_HA7_H(+)-ATPase 7]	251405_at
<i>At3g2460</i>	0.8970	hydroxyproline-rich glycoprotein family protein]	252046_at
<i>At3g10540</i>	0.8970	3-phosphoinositide-dependent protein kinase]	258064_at
<i>At3g38760</i>	0.8970	Late embryogenesis abundant protein (LEA) family protein]	249536_at
<i>At4g34940</i>	0.8970	ARO1_armadillo repeat only 1]	253214_at
<i>At2g41210</i>	0.8970	PIPSK5_phosphatidylinositol-4-phosphate 5-kinase 5]	267081_at
<i>At2g46300</i>	0.8960	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family]	266607_at
<i>At3g28630</i>	0.8960	Protein of unknown function (DUF569)]	256992_at
<i>At2g48150</i>	0.8960	ATGPX4_GPX4_glutathione peroxidase 4]	262350_at
<i>At4g20380</i>	0.8950	LSD1 zinc finger family protein]	254477_at
<i>At1g24110</i>	0.8950	Peroxidase superfamily protein]	264863_at
<i>At1g49290</i>	0.8950	unknown protein	257469_at
<i>At4g18395</i>	0.8950	unknown protein	254627_at
<i>At5g22000</i>	0.8940	RHF2A_RING-H2 group F2A]	245684_at
<i>At1g18150</i>	0.8940	ATMPK8_MPK8_Protein kinase superfamily protein]	256075_at
<i>At4g15200</i>	0.8940	AFH3_FH3_formin 3]	245537_at
<i>At5g66740</i>	0.8930	Protein of unknown function (DUF620)]	247055_at
<i>At3g10470</i>	0.8930	C2H2-type zinc finger family protein]	258967_at
<i>At1g06890</i>	0.8930	nodulin MtN21/EamA-like transporter family protein]	260818_at
<i>At2g38500</i>	0.8930	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein]	267051_at
<i>At1g67810</i>	0.8920	SUFE2_sulfur E2]	245193_at
<i>At2g29410</i>	0.8920	ATMTPB1_MTPB1_metal tolerance protein B1]	266273_at
<i>At4g27110</i>	0.8920	COBL11_COBRA-like protein 11 precursor]	253924_at
<i>At2g41970</i>	0.8910	Protein kinase superfamily protein]	267582_at
<i>At2g19050</i>	0.8900	GDSL-like Lipase/Acylhydrolase superfamily protein]	267438_at
<i>At4g18700</i>	0.8900	ATWL4_C1PK12_SoRCK3_9_WL4_CBL-interacting protein kinase 12]	254636_at
<i>At5g57460</i>	0.8890	ATTPA_Haloacid dehalogenase-like hydrolase (HAD) superfamily protein]	248404_at
<i>At1g11040</i>	0.8890	HSP40[Dna] peptidyl-binding protein]	260478_at
<i>At1g68610</i>	0.8890	PCR11_PLANT CADMIUM RESISTANCE 11]	262282_at
<i>At4g33970</i>	0.8890	Leucine-rich repeat (LRR) family protein]	253318_at
<i>At3g22290</i>	0.8880	Endoplasmic reticulum vesicle transporter protein]	258448_at
<i>At3g55190</i>	0.8880	alpha/beta-Hydrolases superfamily protein]	251836_at
<i>At4g15980</i>	0.8880	Plant invertase/pectin methyltransferase inhibitor superfamily]	245468_at
<i>At3g61580</i>	0.8880	AtSLD1_SLD1_Fatty acid/sphingolipid desaturase]	251323_at
<i>At3g14595</i>	0.8870	Ribosomal protein L18ae family]	258092_at
<i>At4g32630</i>	0.8870	ArfGap/RecO-like zinc finger domain-containing protein]	253447_at
<i>At2g30690</i>	0.8870	Protein of unknown function, DUF593]	267575_at
<i>At2g20430</i>	0.8870	RIC6_ROP-interactive CRIB motif-containing protein 6]	257397_at
<i>At1g06970</i>	0.8860	ATCHX14_CHX14_cation/hydrogen exchanger 14]	256051_at
<i>At4g28000</i>	0.8860	P-loop containing nucleoside triphosphate hydrolases superfamily protein]	253846_at
<i>At1g03457</i>	0.8860	RNA-binding (RRM/RBD/RNP motifs) family protein]	264822_at
<i>At1g47270</i>	0.8850	AtILP6_TLP6_tubby like protein 6]	260502_at
<i>At1g04600</i>	0.8840	ATXIA_XIA_myosin XI A]	264599_at
<i>At3g52620</i>	0.8840	unknown protein	252061_at
<i>At2g37010</i>	0.8840	ATNAP12_NAP12_non-intrinsic ABC protein 12]	263889_at
<i>At1g65240</i>	0.8830	Eukaryotic aspartyl protease family protein]	263108_at
<i>At3g20300</i>	0.8830	Protein of unknown function (DUF3537)]	257672_at
<i>At5g20810</i>	0.8830	SAUR-like auxin-responsive protein family	245997_at
<i>At5g04390</i>	0.8830	C2H2-type zinc finger family protein]	245705_at
<i>At4g38190</i>	0.8820	ATCSLD4_CSLD4_cellulose synthase like D4]	253031_at
<i>At5g54310</i>	0.8820	AGD5_NEF_ARF-GAP domain 5]	248180_at
<i>At2g55110</i>	0.8820	GAE4_UDP-D-glucuronate 4-epimerase 4]	245123_at
<i>At3g00010</i>	0.8810	farric reductase-like transmembrane component family protein]	247647_at
<i>At3g16380</i>	0.8810	PAB6_poly(A) binding protein 6]	259377_at
<i>At3g08990</i>	0.8800	Yippee family putative zinc-binding protein]	257522_at
<i>At2g25600</i>	0.8800	AKT6_SPIK_Shaker pollen inward K+ channel]	265903_at
<i>At3g56800</i>	0.8800	ACAM-3_CAM3_calmodulin 3]	246290_at
<i>At3g60570</i>	0.8790	ATEXPB5_ATHXP BETA 1.3_EXPB5_expansin B5]	251397_at
<i>At5g47470</i>	0.8780	Nodulin MtN21/EamA-like transporter family protein]	248804_at
<i>At4g26650</i>	0.8770	RNA-binding (RRM/RBD/RNP motifs) family protein]	253926_at
<i>At1g22200</i>	0.8770	Endoplasmic reticulum vesicle transporter protein]	255925_at
<i>At2g46490</i>	0.8770	unknown protein	265451_at
<i>At2g25880</i>	0.8770	AtAUR2_AUR2_ataurora2]	266655_at
<i>At3g52080</i>	0.8760	chx28_cation/hydrogen exchanger 28]	252087_at
<i>At2g13620</i>	0.8760	ATCHX15_CHX15_CHX15_cation/hydrogen exchanger 15]	263720_at
<i>At2g03840</i>	0.8760	TET13_tetraspanin13]	263361_at
<i>At1g05020</i>	0.8750	ENTH/ANTH/VHS superfamily protein]	265213_at
<i>At5g15470</i>	0.8750	GAUT14_galacturonosyltransferase 14]	246555_at
<i>At4g30770</i>	0.8740	Putative membrane lipoprotein]	253587_at
<i>260342_at</i>	0.8740		260342_at
<i>At3g01630</i>	0.8740	Major facilitator superfamily protein]	259177_at
<i>At5g24940</i>	0.8740	Protein phosphatase 2C family protein]	246971_at
<i>At1g06750</i>	0.8730	P-loop containing nucleoside triphosphate hydrolases superfamily protein]	260828_at
<i>At4g34750</i>	0.8730	SAUR-like auxin-responsive protein family	253253_at
<i>At2g68660</i>	0.8730	APP3_PP3_pyrophosphorylase 3]	266765_at
<i>At2g03980</i>	0.8730	GDSL-like Lipase/Acylhydrolase superfamily protein]	263482_at
<i>At5g02180</i>	0.8730	Transmembrane amino acid transporter family protein]	251024_at
<i>At3g51150</i>	0.8720	ATP binding microtubule motor family protein]	252143_at
<i>At2g19000</i>	0.8720	unknown protein	267443_at
<i>At2g39700</i>	0.8720	ATEXP4_ATEXP4_ATHXP ALPHA 1.6_EXPA4_expansin A4]	267590_at
<i>At1g11250</i>	0.8720	ATSYPI25_SYP125_syntaxin of plants 125]	262511_at
<i>At4g00110</i>	0.8710	GAE3_UDP-D-glucuronate 4-epimerase 3]	255696_at
<i>At3g57480</i>	0.8700	zinc finger (C2H2 type, AN1-like) family protein]	251634_at
<i>At1g26840</i>	0.8690	ATORC6_ORC6_origin recognition complex protein 6]	263681_at
<i>At1g15920</i>	0.8690	Polynucleotidyl transferase, ribonuclease H-like superfamily protein]	261841_at
<i>At3g48450</i>	0.8690	RP1-interacting protein 4 (RIN4) family protein]	252364_at
<i>At5g64690</i>	0.8690	neurofilament triplet H protein-related]	247242_at
<i>At1g01500</i>	0.8680	Erythronate-4-phosphate dehydrogenase family protein]	259436_at
<i>At5g40155</i>	0.8680	Defensin-like (DEFL) family protein]	249402_at
<i>At5g59030</i>	0.8680	COPT1_copper transporter 1]	247745_at
<i>At1g51260</i>	0.8680	LPAT3_lyso-phosphatidyl acyltransferase 3]	265134_at
<i>At4g15200</i>	0.8680		
<i>At3g12600</i>	0.8680	atnud16_NUDT16_nudix hydrolase homolog 16]	256240_at

<i>At4g15530</i>	0.8670	PPDK_pyruvate orthophosphate dikinase]	245528_at
<i>At5g39650</i>	0.8670	DAU2_Protein of unknown function (DUF679)]	249468_at
<i>At5g25430</i>	0.8660	HCO3- transporter family]	246942_at
<i>At5g58950</i>	0.8660	Protein kinase superfamily protein]	247750_at
<i>At2g38400</i>	0.8650	AGT3_alanine:glyoxylate aminotransferase 3]	267035_at
<i>At2g31800</i>	0.8650	Integrin-linked protein kinase family]	263461_at
<i>At5g37060</i>	0.8650	ATCHX24_CHX24_cation/H+ exchanger 24]	249649_at
<i>At1g29750</i>	0.8650	RKF1_receptor-like kinase in flowers 1]	255995_at
<i>At3g03090</i>	0.8640	AtVGT1_VGT1_vacuolar glucose transporter 1]	258869_at
<i>At3g56960</i>	0.8640	PIP5K4_phosphatidylinositol monophosphate 5 kinase 4]	251711_at
<i>265829_at</i>	0.8640		265829_at
<i>At3g44070</i>	0.8640	Glycosyl hydrolase family 35 protein]	252663_at
<i>At1g17483</i>	0.8640	alpha/beta-Hydrolases superfamily protein]	245423_at
<i>At4g27840</i>	0.8640	SNARE-like superfamily protein]	253836_at
<i>At3g10090</i>	0.8630	TPR13_Tetratricopeptide repeat (TPR)-like superfamily protein]	250466_at
<i>At1g74780</i>	0.8630	Nodulin-like / Major Facilitator Superfamily protein]	262216_at
<i>At3g61710</i>	0.8620	unknown protein	247539_at
<i>At5g54130</i>	0.8620		
<i>At3g12160</i>	0.8610	ATRABA4D_RABA4D_RAB GTPase homolog A4D]	256261_at
<i>At5g40730</i>	0.8600	AGP24_ATAGP24_arabinogalactan protein 24]	249375_at
<i>At1g20630</i>	0.8600	CAT1_catalase 1]	259517_at
<i>At1g63220</i>	0.8590	Calcium-dependent lipid-binding (CaLB domain) family protein]	260083_at
<i>At5g57200</i>	0.8590	ENTH/ANTH/VHS superfamily protein]	247941_at
<i>At3g24760</i>	0.8580	Galactose oxidase/kelch repeat superfamily protein]	257596_at
<i>At1g33770</i>	0.8580	Protein kinase superfamily protein]	261983_at
<i>At4g39670</i>	0.8570	Glycolipid transfer protein (GLTP) family protein]	252908_at
<i>At1g15470</i>	0.8560	Transducin/WD40 repeat-like superfamily protein]	262597_at
<i>At1g64610</i>	0.8560	Transducin/WD40 repeat-like superfamily protein]	261973_at
<i>At2g37620</i>	0.8550	AAc1_ACT1_actin 1]	267175_s_
<i>At1g28960</i>	0.8550	ATNUDT15_ATNUDX15_NUDX15_nudix hydrolase homolog 15]	262746_at
<i>At5g41730</i>	0.8550	Protein kinase family protein]	249263_at
<i>At4g31230</i>	0.8550	Protein kinase protein with adenine nucleotide alpha hydrolases-like domain]	253567_at
<i>At1g79450</i>	0.8550	ALIS5_ALA-interacting subunit 5]	262942_at
<i>At1g10620</i>	0.8550	AtPERK11_PERK11_Protein kinase superfamily protein]	261830_at
<i>At5g33360</i>	0.8540	TRAF-like superfamily protein]	248256_at
<i>At5g35980</i>	0.8530	serine-rich protein-related]	248038_at
<i>At1g07623</i>	0.8530	F-box family protein]	260197_at
<i>At5g41310</i>	0.8510	P-loop nucleoside triphosphate hydrolases superfamily protein	249296_at
<i>At1g17290</i>	0.8510	AlaAT1_alanine aminotransferase]	260847_s_
<i>At5g03760</i>	0.8500	CSLA9_RAT4_Nucleotide-diphospho-sugar transferases superfamily protein]	250892_at
<i>At1g79250</i>	0.8490	AGC17_AGC kinase 1.7]	264127_at
<i>At5g23670</i>	0.8490	LCB2_long chain base2]	249799_at
<i>At4g02380</i>	0.8480	AtLEA5_SAG21_senescence-associated gene 21]	255479_at
<i>At3g50310</i>	0.8480	MAPKKK20_MKKK20_mitogen-activated protein kinase kinase kinase 20]	252212_at
<i>252225_at</i>	0.8480		252225_at
<i>At5g10500</i>	0.8480	Kinase interacting (KIP1-like) family protein]	250427_at
<i>At5g20460</i>	0.8470	unknown protein	246080_at
<i>At2g19400</i>	0.8470	AGC (cAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein]	267281_at
<i>At1g14560</i>	0.8470	Mitochondrial substrate carrier family protein]	260777_at
<i>At3g04690</i>	0.8460	ANX1_Maleicn/receptor-like protein kinase family protein]	258843_at
<i>At5g24880</i>	0.8460	BEST Arabidopsis thaliana protein match is: calmodulin-binding protein-related	246969_at
<i>At2g43790</i>	0.8460	ATMAPK6_ATMPK6_MAPK6_MPK6_MAP kinase 6]	260571_at
<i>At1g04985</i>	0.8450	unknown protein; Has 37 Blast hits to 37 proteins in 11 species: Archae - 0; Bacteria - 0; Mi	261179_at
<i>At1g15880</i>	0.8450	atgosl1_GOS11_golgi snare 11]	259498_at
<i>At4g33850</i>	0.8440		253312_s_
<i>At4g14810</i>	0.8440	unknown protein	245579_at
<i>At2g28440</i>	0.8440	proline-rich family protein]	265275_at
<i>At1g19780</i>	0.8430	ATCNGC8_CNGC8_CNGC8_cyclic nucleotide gated channel 8]	261142_at
<i>At3g06150</i>	0.8420	unknown protein	256396_at
<i>At4g20880</i>	0.8410	ethylene-responsive nuclear protein / ethylene-regulated nuclear protein (ERT2)]	254434_at
<i>At1g18410</i>	0.8410	P-loop containing nucleoside triphosphate hydrolases superfamily protein]	261716_at
<i>At1g02400</i>	0.8410	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein]	264269_at
<i>At5g65160</i>	0.8410	TPR14_tetratricopeptide repeat (TPR)-containing protein]	247229_at
<i>At2g03720</i>	0.8400	CAT4_cationic amino acid transporter 4]	259337_at
<i>At1g26480</i>	0.8390	GF14_IOTA_GRF12_general regulatory factor 12]	261015_at
<i>At1g19110</i>	0.8390	inter-alpha-trypsin inhibitor heavy chain-related]	259470_at
<i>At2g37070</i>	0.8380	unknown protein	265465_at
<i>At1g49270</i>	0.8380	AtPERK7_PERK7_Protein kinase superfamily protein]	262389_at
<i>At5g02390</i>	0.8380	DAU1_Protein of unknown function (DUF3741)]	251047_at
<i>At5g03690</i>	0.8380	Aldolase superfamily protein]	250917_at
<i>At2g04410</i>	0.8370	RPM1-interacting protein 4 (RIN4) family protein]	263856_at
<i>At2g29040</i>	0.8370	Exostosin family protein]	266773_at
<i>At1g47380</i>	0.8370	Protein phosphatase 2C family protein]	261688_at
<i>At4g00720</i>	0.8360	ASKTHETA_ATSK32_SK32_shaggy-like protein kinase 32]	255635_at
<i>At3g44920</i>	0.8360	ATCHX11_CHX11_cation/H+ exchanger 11]	246338_s_
<i>At4g31020</i>	0.8360	alpha/beta-Hydrolases superfamily protein]	253573_at
<i>At4g35790</i>	0.8350	ATPLDDELTA_PLDDELTA_phospholipase D delta]	253120_at
<i>At3g47080</i>	0.8350	Tetratricopeptide repeat (TPR)-like superfamily protein]	252467_at
<i>At5g48270</i>	0.8350	Plant protein of unknown function (DUF868)]	248711_at
<i>At2g13570</i>	0.8340	NF-YB7_nuclear factor Y, subunit B7]	263718_at
<i>At4g17790</i>	0.8340	SNARE associated Golgi protein family]	245361_at
<i>At4g19120</i>	0.8340	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein]	254563_at
<i>At2g18080</i>	0.8340	EDA2_Serine carboxypeptidase S28 family protein]	265811_at
<i>At1g03620</i>	0.8330	ELMO/CED-12 family protein]	264815_at
<i>At3g16350</i>	0.8330	Homeodomain-like superfamily protein]	259379_at
<i>At2g47490</i>	0.8320	ATNDT1_NDT1_NAD+ transporter 1]	245152_at
<i>At2g02960</i>	0.8310	RING/FYVE/PHD zinc finger superfamily protein]	266791_at
<i>At5g01690</i>	0.8300	ATCHX27_CHX27_cation/H+ exchanger 27]	251102_at
<i>At1g27700</i>	0.8300	Syntaxin/t-SNARE family protein]	261649_at
<i>At3g06560</i>	0.8300	PAPS3_poly(A) polymerase 3]	258564_at
<i>At3g51030</i>	0.8300	ATTRX_H1_ATTRX1_TRX1_thioredoxin H-type 1]	252119_at
<i>At1g51410</i>	0.8300	NAD(P)-binding Rossmann-fold superfamily protein]	260518_at
<i>At1g18750</i>	0.8290	AGL65_AGAMOUS-like 65]	261423_at
<i>At4g37280</i>	0.8290	MRG family protein]	246234_at
<i>At5g53520</i>	0.8290	ATOPT8_OPT8_oligopeptide transporter 8]	248275_at
<i>At5g45820</i>	0.8280	CIPK20_PKS18_SnRK3.6_CBL-interacting protein kinase 20]	248910_at
<i>At1g22460</i>	0.8280	O-fucosyltransferase family protein]	261929_at
<i>At2g01450</i>	0.8270	ATMPK17_MPK17_MAP kinase 17]	266348_at
<i>At3g02440</i>	0.8270	TBL20_TRICHOME BIREFRINGENCE-LIKE 20]	258479_at
<i>At4g03110</i>	0.8270	AtRBP-DR1_RBP-DR1_RNA-binding protein-defense related 1]	255411_at
<i>At5g09550</i>	0.8270	GDP dissociation inhibitor family protein / Rab GTPase activator family protein]	250514_at
<i>At2g24320</i>	0.8270	alpha/beta-Hydrolases superfamily protein]	265690_at
<i>At1g22130</i>	0.8270	AGL104_AGAMOUS-like 104]	255952_at
<i>At5g25530</i>	0.8270	DNAJ heat shock family protein]	246894_at
<i>At3g23900</i>	0.8260	ATHMT-1_HMT-1_Homocysteine S-methyltransferase family protein]	258075_at
<i>At5g10740</i>	0.8250	Protein phosphatase 2C family protein]	250400_at
<i>At5g01800</i>	0.8250	saposin B domain-containing protein]	251074_at
<i>At3g36660</i>	0.8250	PABY_poy(A) binding protein 7]	265205_at
<i>At3g01260</i>	0.8240	Remorin family protein]	251306_at
<i>At1g77980</i>	0.8240	AGL66_AGAMOUS-like 66]	262179_at
<i>At5g16100</i>	0.8240	unknown protein	246491_at
<i>At3g35410</i>	0.8230	ATSOS2_CIPK24_SNRK3.11_SOS2_Protein kinase superfamily protein]	246614_at
<i>At2g45610</i>	0.8230	alpha/beta-Hydrolases superfamily protein]	267527_at
<i>At1g09600</i>	0.8230	Protein kinase superfamily protein]	264558_at
<i>At5g18150</i>	0.8230	Methyltransferase-related protein]	250018_at
<i>At5g47180</i>	0.8230	Plant VAMP (vesicle-associated membrane protein) family protein]	248796_at
<i>At3g48010</i>	0.8220	ATCNGC16_CNGC16_cyclic nucleotide-gated channel 16]	252399_at
<i>At2g19330</i>	0.8220	PIRL6_plant intracellular ras group-related LRR 6]	267322_at
<i>At3g59350</i>	0.8220	Protein kinase superfamily protein]	251494_at
<i>At5g57740</i>	0.8210	XBAT32_XB3 ortholog 2 in Arabidopsis thaliana]	247877_at
<i>At1g03610</i>	0.8190	Protein of unknown function (DUF789)]	264836_at
<i>At5g64920</i>	0.8180	CIP8_COP1-interacting protein 8]	247219_at
<i>At4g09950</i>	0.8180	P-loop containing nucleoside triphosphate hydrolases superfamily protein]	255003_at
<i>At5g10950</i>	0.8180	Tudor/PWWP/MBT superfamily protein]	250395_at
<i>At2g42380</i>	0.8180	BZIP34_Basic-leucine zipper (bZIP) transcription factor family protein]	265877_at
<i>At1g74220</i>	0.8180	unknown protein	260246_at
<i>At1g74320</i>	0.8170	Protein kinase superfamily protein]	260244_at

<i>At3g06483</i>	0.8160	ATPDHK_PDK_pyruvate dehydrogenase kinase]	258902_at
<i>At5g16110</i>	0.8150	unknown protein	246506_at
<i>At1g73480</i>	0.8140	alpha/beta-Hydrolases superfamily protein]	245734_at
<i>At1g19890</i>	0.8140	ATMGH3_MGH3_male-gamete-specific histone H3]	255815_at
<i>At1g72460</i>	0.8130	Leucine-rich repeat protein kinase family protein]	260424_at
<i>At2g22340</i>	0.8130	unknown protein	264051_at
<i>At5g06560</i>	0.8120	Protein of unknown function, DUF593]	250692_at
<i>At3g54930</i>	0.8120	Protein phosphatase 2A regulatory B subunit family protein]	251865_at
<i>At2g29620</i>	0.8110	unknown protein	266674_at
<i>At5g61350</i>	0.8100	Protein kinase superfamily protein]	247581_at
<i>At3g39680</i>	0.8100	unknown protein	251477_at
<i>At3g12690</i>	0.8100	AGC1.5_AGC kinase 1.5]	257696_at
<i>At1g70170</i>	0.8070	MMP_matrix metalloproteinase]	264716_at
<i>At2g39420</i>	0.8070	alpha/beta-Hydrolases superfamily protein]	266977_at
<i>At2g19010</i>	0.8060	GDSL-like Lipase/Acylhydrolase superfamily protein]	267466_at
<i>At1g73630</i>	0.8050	EF hand calcium-binding protein family]	260076_at
<i>At1g18530</i>	0.8040	EF hand calcium-binding protein family]	255772_at
<i>At3g60780</i>	0.8040	Protein of unknown function (DUF1442)]	251339_at
<i>At5g56160</i>	0.8030	Sec14p-like phosphatidylinositol transfer family protein]	247995_at
<i>At1g62450</i>	0.8030	Immunoglobulin E-set superfamily protein]	265115_at
<i>At3g35390</i>	0.8020	Leucine-rich repeat protein kinase family protein]	246609_at
<i>At5g20690</i>	0.8020	Leucine-rich repeat protein kinase family protein]	245992_at
<i>At2g16030</i>	0.8010	[S-adenosyl-L-methionine-dependent methyltransferases superfamily protein]	253929_s_
<i>At3g12110</i>	0.8010	ACT11_actin-11]	256275_at
<i>At1g16360</i>	0.8010	LEM3 (ligand-effect modulator 3) family protein / CDC50 family protein]	262755_at
<i>At1g13900</i>	0.8010	Purple acid phosphatases superfamily protein]	259420_at
<i>At5g46840</i>	0.8010	RNA-binding (RRM/RBD/RNP motifs) family protein]	248869_at
<i>At5g18650</i>	0.8010	CHY-type/CTCHY-type/RING-type Zinc finger protein]	250000_at

Supplementary Table S4. Detailed information about pollen development-related genes that are co-expressed with ASK β .

At_Locus	R-value to Bait	Gene Name	Gene description	Conserved Motifs
<i>At3g21180</i>	0.9830	<i>ACA9</i>	One of the type IIB calcium pump isoforms. encodes an autoinhibited Ca(2+)-ATPase that contains an N-terminal calmodulin binding autoinhibitory domain.	Motif 1, 2, 3, 6
<i>At1g24520</i>	0.9770	<i>BCP1</i>	HOMOLOG OF BRASSICA CAMPESTRIS POLLEN PROTEIN 1. Male fertility gene acting on tapetum and microspore	Motif 1, 2, 3, 6
<i>At4g05330</i>	0.9670	<i>AGD13</i>	A member of ARF GAP domain (AGD). A thaliana has 15 members, grouped into four classes.	Motif 1, 2, 3
<i>At3g57390</i>	0.9650	<i>AGL18</i>	Encodes a MADS-box containing protein likely to be a transcription factor that is expressed in endosperm and developing gametophytes. The protein sequence is most similar to that of AGL15.	Motif 1, 2, 3, 6
<i>At3g62230</i>	0.9640	<i>DAF1</i>	DUO1-ACTIVATED F-BOX 1. Target promoter of the male germline-specific transcription factor DUO1.	Motif 1, 2, 3, 5, 6
<i>At5g64510</i>	0.9580	<i>TIN1</i>	Encodes Tunicamycin Induced 1(TIN1), a plant-specific ER stress-inducible protein. TIN1 mutation affects pollen surface morphology. Transcriptionally induced by treatment with the N-linked glycosylation inhibitor tunicamycin.	Motif 1, 2, 3
<i>At2g32460</i>	0.9530	<i>MYB101</i>	Member of the R2R3 factor gene family.	Motif 1, 2, 3, 4, 6
<i>At3g01040</i>	0.9470	<i>GAUT13</i>	GALACTURONOSYLTRANSFERASE 13, Encodes a protein with putative galacturonosyltransferase activity.	Motif 1, 2, 3, 4, 6
<i>At2g02970</i>	0.9450	<i>APY6</i>	Encodes a putative apyrase involved in pollen exine pattern formation and anther dehiscence.	Motif 1, 3, 6
<i>At5g39400</i>	0.9350	<i>ATPTEN1</i>	PHOSPHATASE AND TENSIN HOMOLOG DELETED ON CHROMOSOME TEN 1	Motif 1, 2, 3, 6
<i>At3g47440</i>	0.9340	<i>TIP5;1</i>	Encodes ATIP5;1, functions as water and urea channels in pollen. Target promoter of the male germline-specific transcription factor DUO1.	Motif 1, 2, 3, 5
<i>At4g35700</i>	0.9340	<i>DAZ3</i>	DUO1-ACTIVATED ZINC FINGER 3. Target promoter of the male germline-specific transcription factor DUO1.	Motif 1, 2, 3, 5
<i>At1g53320</i>	0.9160	<i>ATTLP7</i>	TUBBY LIKE PROTEIN 7, Member of TLP family	Motif 1, 3, 4, 6
<i>At2g35210</i>	0.9040	<i>RPA</i>	ROOT AND POLLEN ARFGAP, A member of ARF GAP domain (AGD), A thaliana has 15 members, grouped into four classes.	Motif 1, 2, 3, 6
<i>At2g03060</i>	0.9020	<i>AGL30</i>	Encodes a member of the MIKC (MADS box, Keratin binding domain, and C terminal domain containing) family of transcriptional regulators. AGL30 is expressed in pollen. It forms heterodimers with other MICK family members.	Motif 1, 2, 3, 4, 6
<i>At5g22000</i>	0.8940	<i>RHF2A</i>	RING-H2 GROUP F2A, encodes a RING-type E3 ubiquitin ligase implicated in gametogenesis. Double mutant analyses with RHF1a suggests that RHF2a may be involved in targeting ICK4KRP6 for degradation following meiosis in order to allow the mitoses associated with megagametogenesis and microgametogenesis to occur. RHF2a is expressed in all four floral whorls and is present at ~8-fold higher levels than RHF1a in inflorescences by RT-PCR analyses.	Motif 1, 2, 3, 6
<i>At3g10470</i>	0.8930	—	C2H2-type zinc finger family protein	Motif 1, 2, 3, 4
<i>At1g68610</i>	0.8890	<i>PCR11</i>	PLANT CADMIUM RESISTANCE 11, Target promoter of the male germline-specific transcription factor DUO1.	Motif 1, 2, 3, 5, 6
<i>At1g47270</i>	0.8850	<i>ATTLP6</i>	TUBBY LIKE PROTEIN 6, Member of TLP family	Motif 1, 2, 3, 6
<i>At5g15470</i>	0.8750	<i>GAUT14</i>	Encodes a protein with putative galacturonosyltransferase activity.	Motif 1, 2, 3, 6
<i>At5g59030</i>	0.8680	<i>COPT1</i>	Encodes a putative copper transport protein that contains copper-binding motif and functionally complements in copper-transport defective yeast strains	Motif 1, 2, 3
<i>At5g39650</i>	0.8670	<i>DAU2</i>	DUO1-ACTIVATED UNKNOWN 2. Target promoter of the male germline-specific transcription factor DUO1.	Motif 1, 2, 3, 5
<i>At5g23670</i>	0.8490	<i>LCB2</i>	LONG CHAIN BASE2, Encodes the LCB2 subunit of serine palmitoyltransferase, an enzyme involved in sphingosine biosynthesis. The protein is localized to the endoplasmic reticulum.	Motif 1, 2, 3, 6
<i>At3g50310</i>	0.8480	<i>MKKK20</i>	MAPKKK20, MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE 20. Encodes a member of MEKK subfamily. Target promoter of the male germline-specific transcription factor DUO1. Involved in osmotic stress response via regulation of MPK6 activity.	Motif 1, 2, 3
<i>At5g02390</i>	0.8380	<i>DAU1</i>	DUO1-ACTIVATED UNKNOWN 1. Target promoter of the male germline-specific transcription factor DUO1.	Motif 1, 2, 3, 6
<i>At2g18080</i>	0.8340	<i>EDA2</i>	EMBRYO SAC DEVELOPMENT ARREST 2	Motif 1, 2, 3, 6
<i>At5g53520</i>	0.8290	<i>ATOPT8</i>	Encodes an oligopeptide transporter. Target promoter of the male germline-specific transcription factor DUO1.	Motif 1, 2, 3, 6
<i>At1g18750</i>	0.8290	<i>AGL65</i>	Encodes a member of the MIKC (MADS box, Keratin binding domain, and C terminal domain containing) family of transcriptional regulators. AGL65 is expressed in pollen. It forms heterodimers with other MICK family members (AGL104). Involved in late stages of pollen development and pollen	Motif 1, 2, 3, 4, 6
<i>At1g22130</i>	0.8270	<i>AGL104</i>	Encodes a member of the MIKC (MADS box, Keratin binding domain, and C terminal domain containing) family of transcriptional regulators. AGL104 is expressed in pollen. It forms heterodimers with other MICK family members (AGL65 and AGL30). Involved in late stages of pollen development	Motif 1, 2, 3, 6
<i>At1g77980</i>	0.8240	<i>AGL66</i>	Encodes a member of the MIKC (MADS box, Keratin binding domain, and C terminal domain containing) family of transcriptional regulators. AGL66 is expressed in pollen. It forms heterodimers with other MICK family members (AGL104). Involved in late stages of pollen development and pollen	Motif 1, 2, 3, 4, 6
<i>At2g42380</i>	0.8180	<i>ATBZIP34</i>	Encodes a member of the BZIP family of transcription factors. Forms heterodimers with the related protein AtbZIP61. Binds to G-boxes in vitro and is localized to the nucleus in onion epidermal cells.	Motif 1, 2, 3, 6
<i>At1g19890</i>	0.8140	<i>ATMGH3</i>	Histone 3.3, male-gamete-specific expression. Direct target promoter of the male germline-specific transcription factor DUO1.	Motif 1, 2, 3, 5, 6

Supplementary Table S6. Putative phosphorylation sites on ASK β co-expressed proteins predicted by Musite. Putative ASK phosphorylation sites and the regions carrying putative priming phosphorylation sites are indicated in red and bold, respectively.

At Locus	Gene Name	R-value to Bait	Position	Amino acid	Surround sequence	Specificity
AT3G21180	ACA9	0.983	32	S	DMEAGSAKTEEH SD HEELQHDPDDP	97.85%
			28	T	GRHDDMEAGSAK TE EHSDHEELQHD	94.73%
			920	T	ATEPPTDHLMHRT TP VGRREPLITNI	94.59%
			120	T	LAGEQQIAFGSS TP AASTGNFDIDL	94.15%
			376	T	LMASISED TG EETPLQVRLNGLATF	94.05%
			779	S	QVAKKITVMGRS SP NDKLLLVQALR	91.53%
			560	S	HPKDGGEVEIS SG PTKAILSWAYK	91.32%
			372	T	EWGLLMASISED TG EETPLQVRLNG	88.06%
			25	S	SMSGRHDDMEAG SA KTEEHS D HEEL	87.29%
			77	T	ALVLNASRRFRY TL DLNKEEHYDNR	85.11%
AT1G24520	BCP1	0.977	64	T	DQIGTTDDDAAP TP GDGDVAVAGPL	99.56%
			57	T	VEAPVTDDQIG T DDDAAPT PG DGD	99.02%
			32	S	LAAAASSPSP SA SPKAPAASKTDH	98.70%
			28	S	AIIGLAAAASSP SP SASPKAPAAS	97.27%
			56	T	HVEAPVTDDQIG T DDDAAPT PG DG	96.32%
			26	S	FMAIIGLAAA AS SPSPASPKAPA	94.58%
			30	S	IGLAAAASSP SP SASPKAPAASKT	92.45%
			50	T	AASKTDHVEAPV T DDQIGTTDDDA	91.21%
			78	S	GDGDVAVAGPL GS DSSYDNAPT GS A	90.24%
			42	T	SASPKAPAASK TD HVEAPVTDDQI	87.84%
			87	T	PLGSDSSYDNAP TGS ADSAKSGAAA	87.06%
			81	S	DVAVAGPLGSD S YDNAPT GS ADSA	86.75%
			40	S	SPSASPKAPAA SK TDHVEAPVTDD	86.14%
80	S	GDVAVAGPLGSD S YDNAPT GS ADSA	85.68%			
AT4G05330	AGD13	0.967	76	S	ISKVLSVTLDEW S DEEVDSMIEIGG	94.50%
			138	S	LQEFKPSLRIT S GKGSTKSSAFLT	87.84%
AT3G57390	AGL18	0.965	206	S	PQDSSPEADPES SS SEEDENDNEEH	99.44%
			198	S	GPKVLNERPQD SS PEADPESSSSEE	99.40%
			208	S	DSSPEADPESS S SEEDENDNEEHHS	99.15%
			255	S	ELVCDNSGSQV ASD *****	98.33%
			207	S	QDSSPEADPESS S SEEDENDNEEHH	98.06%
			205	S	RPQDSSPEADP ES SSSEEDENDNEE	97.54%
			197	S	SGPKVLNERPQD SS PEADPESSSSE	88.93%
			220	S	SEEDENDNEEHH SD TSLQLGLSSTG	87.48%
20	T	IKKIENINSRQV T FSKRRNGLIKKA	87.26%			
AT3G62230	DAF1	0.964				
AT5G64510	TIN1	0.958	219	T	LLSLAEQLRRAS T DQESPVLSLRIV	99.51%
			420	S	TMSKLP II ESPP SP PFTL*****	98.73%
			242	S	IVGPTSLASTSQ PD NK LK LRLAP	98.15%
			223	S	AEQLRRAS T DQ EP VLSLRIVGPTS	96.41%
			29	S	FTIFPSSALIS SP DANPPYPK AI S	95.06%
			423	T	KL PI IESPP P FTL*****	94.53%
			218	S	GLLSLAEQLRRAS T DQESPVLSLR I	93.71%
			270	S	ELSSMSKDKRSL S TIGANAMTTVLT	93.37%
			126	S	NGLVPMRNK KT SDDVLPV L APFQL	93.21%
			282	T	STIGANAMTTV L TPREFTTMWPITS	92.85%
			240	S	LRIVGPTSLASTSQ SP DNK LK LRL	91.75%
			417	S	GNVTMSKLP II ESPP SP PFTL****	88.94%
			261	S	LKRLAPGLVEL SS MSKDKRSL ST IG	87.29%
AT2G32460	MYB101	0.953	77	T	NHLRPNLKKG S FT P DEEK II DLHA	98.62%
			406	T	HNKYNEPTMV KV TVD DD DELLT S LL	95.68%
			314	S	PSNQRP TH SFSS SP IIDNGVHLEPP	95.43%
			289	S	SLLMGDLEIR SS FP L GLD NS VLEL	92.80%
			186	S	TSSSSSFSS S SQPSKRLRPDPLV	90.58%
			465	T	GNHQGN GR VEPP T VPPSSVDP M AS	90.05%
			310	S	VLELPSNQRP TH SFSS SP IIDNGVH	87.22%
			355	S	LSRGG L FKDVR V SSDLCEVQDKRV	85.94%
239	S	DNNQFGFSV PL SSSSSNEVCNPNH	85.68%			
AT3G01040	GAUT13	0.947	195	S	YSSNAHARRQL SP ELLPVLS D NAY	97.29%
			311	T	GNHIAGANL S ET TP RTFASKLQ S RS	96.46%
			323	S	TPRTFASKLQ SR PKYISLLNHL R I	88.87%
AT2G02970	APY6	0.945	379	T	CSYQHCSIG ST FP K LRGRFLATEN	94.62%
			264	S	SEPMPEFSR T ISFGNVTYNLYSHS	93.16%
			15	S	RSHARSRVKNSS S SKSDMDPIKFQI	90.62%
			16	S	SHARSRVKNSS S SKSDMDPIKFQIR	90.30%
			18	S	ARSRVKNSS S SKSDMDPIKFQIRSG	90.16%
			340	S	HLSGLLAEESR L SDFQAGGNYSQC	89.58%
			13	S	MRRSHARSRVKN S SSSKSDMDPIKF	87.80%
			311	T	NSAVEPTREK I FDPCAPKGYNLDA	86.48%
AT5G39400	ATPTEN1	0.935	299	T	HVNC D SEED E EV T DGEEP H LVVQMD	99.64%
			412	S	FGKFLSR DD LS L S*****	98.64%
			292	S	SPRY Y ISHVNC D SEED E EV T DGEEP	98.22%

			410	S	SKFGKFLSRDDL S L S *****	94.52%
			405	S	FGPACSKFGKFLSRDDL S L S ****	93.26%
			280	S	CRQFKKGYCRSS S PRYYISHVNCDS	93.16%
			14	S	GLKLSRGPVKEK S PLEFTRVHILTY	92.51%
			383	S	ELDKVGGNGRS S IGPDFSLELLFGP	86.48%
AT4G35700	DAZ3	0.934	25	S	ENENFDES DYL W SDEEGDIREIVLG	99.63%
			220	S	TASSAGGLATAS S DGEGLVSSIGRA	98.63%
			261	S	GVGSKRKF DLN R SPPPDGDEENDDK	97.78%
			111	T	VLEALAEASG C TPIGVTTTEGEVV	94.74%
			88	T	EQSASGTGDVSG T PEIKVVGKPRVL	93.83%
			82	T	EATGNTEQSASG T GDVSGTPEIKV	88.03%
			217	T	EVPTASSAGGLAT A SSDGEGLVSSI	86.30%
AT3G47440	TIP5;1	0.934	250	T	VVVVVEDDRG S TGDAIGV*****	97.56%
			249	S	NVVVVEDDRG S TGDAIGV*****	97.21%
			248	S	DNVVVVEDDRG S TGDAIGV****	90.82%
AT1G53320	ATTL7	0.916	255	S	RRMVSTLRC P SP S SSSAGLSSDQ	99.01%
			253	S	GPRRMVSTLRC P SP S SSSAGLSS	98.68%
			217	S	GKASRRFASK Q IS P QVPAGNFEVGH	94.61%
			259	S	STLRC P SP S SSSAGLSSDQKPCD	92.61%
			258	S	VSTLRC P SP S SSSAGLSSDQKPC	92.45%
			260	S	TLRC P SP S SSSAGLSSDQKPCDV	92.06%
			247	S	NLLKSRGPRRMV S TLRC P SP S SS	91.47%
			213	S	KPSNGKASRRF A SK Q IS P QVPAGNF	89.16%
			29	S	RFHQGETT A PE S ESIPPSNMAGS	85.70%
			265	S	SPSPSSSAGL S DQKPCDVTKIMK	85.24%
AT2G35210	RPA	0.904	173	S	LKQKEKPDVV P SPRISRSVKKPLG	99.57%
			135	S	KSKAEEELD L PP S PPDSTQVPNGLS	99.27%
			223	S	QKPEESVII Q AT S PVSAKSARSSFS	98.43%
			233	S	ATSPVSAKSAR S FSRFDYADNVQ	94.72%
			235	S	SPVSAKSAR S FSRFDYADNVQNR	93.21%
			336	S	EAKSSLK K FG S SAISSADLFGDGD	93.18%
			252	S	YADNVQNR E DY M SPQVVSHVAPPKS	93.14%
			226	S	EESVII Q AT S PVSAKSARSSFSRF	90.82%
			202	T	GKTGGLGARK L TKSSGTLYDQKPE	89.20%
			236	S	PVSAKSAR S FSRFDYADNVQNR	89.07%
			151	T	STQVPNGL S SI K TSEALKESNTLKQ	88.08%
			264	S	SPQVVSHVAPP K SGFFEEEMNG	88.00%
			229	S	VII Q AT S PVSAK S ARSSFSRFDYA	87.97%
			222	T	DQKPEESVII Q AT S PVSAKSARSS	87.46%
			285	T	EMNGGRFQ K K P ITSSSKLQIQETDE	87.13%
			295	T	PITSSSKLQI Q ET D EARKKFTNAKS	85.35%
AT2G03060	AGL30	0.902	75	T	SMEEVIAK F S Q VT P QERTKRKFESL	98.76%
			358	S	YNDNTNQTR F G S SSSLPCSISMFD	87.88%
			240	S	IPQREVECS A SS S FGSYPGYFGTGK	87.76%
			253	S	FGSYPGYFGTG K SP E MTIPGQETSF	86.97%
			357	S	AYNDNTNQTR F G S SSSLPCSISM	86.42%
AT5G22000	RHF2A	0.894	228	S	TQPPTSS H PR Q V S PSASDSNRPLN	98.50%
			374	S	RGVKETCATG S G S *****	96.29%
			189	S	ASSPP H PP M PS P SPQRDESDTVSN	95.71%
			191	S	SPP H PP M PS P SPQRDESDTVSNLP	95.43%
			375	S	GVKETCATG S G S *****	94.56%
			332	S	LETRENSRP S T A SVSDVSENHTPET	94.16%
			257	S	SEQDRAG P SEL Q SF S ESLKSRLNAV	93.40%
			196	S	PPMPSS P QR D ES T TVSNLPHNALG	91.91%
			243	S	ASDSNSRPL N Q S SP E QDRAGPSEL	91.53%
			10	S	***MEVRV S T T SE G H L T S AAAFVE	90.98%
			330	T	ERLETRENSRP S T A SVSDVSENHTP	90.85%
			242	S	SASDSNSRPL N Q S SP E QDRAGPSE	90.71%
			245	S	DSNSRPL N Q S SP E QDRAGPSELQS	90.41%
			341	T	STASVSDVSEN H T P ETNNEHNRAAA	90.17%
			294	S	RNWKDRL F SR N T S MADLGSEVKREV	89.27%
			162	S	GVRREGHR S R S S Q GH Q Q F MFSSQ	88.44%
			198	T	MPSS P QR D ES T TVSNLPHNALGEG	88.07%
			337	S	NSRPSTASVSDV S ENHTPETNNEHN	87.34%
			358	S	NEHNRAA A AG D EH S VNERGVK E T C A T	86.98%
			179	S	QFMV F SS Q PN A SS P PP H PP M SS S	86.64%
			300	S	LFSRNT S MAD L G S EVKREVSAGIAT	86.63%
			112	T	NPTRNAT I FR H PT L GD F EL Q HL P V G	86.14%
AT3G10470	—	0.893	30	S	LKGK R TK R Q R P Q SP I PF S I P PM S	96.44%
			100	T	SSSS N NNAT L K A T A DEED Q DMAN C L	93.77%
			314	S	AIPATANT A L S L S PM S FD Q M S EG P I	93.38%
			52	T	MSSHE P DA E EE S T S LV S KE K SL N D E	91.83%
			335	S	EG P IQ A P V K R AR S AV S LD L DL N LP	90.60%
AT1G68610	PCR11	0.889	146	T	GNMERHAR L AA S TP S AP L Q A PM S R	98.08%
AT1G47270	ATTL6	0.885	285	S	PISAI Q EG G K I Q S P T E F T N Q G K K K K	95.17%
			235	S	PFNR L PP S M Q V S P W VSSSS S Y N I	87.84%
			45	S	KNKY K AIG R RR G SH I A E PG S SVSS	85.02%
AT5G15470	GAUT14	0.875	194	S	YSSNA H ARR Q LP S PE F LP V LS D N A Y	95.91%

			310	T	GNHVAGANLTETTPRTFASKLQSR	94.70%
			322	S	TPRTFASKLQSRSPKYISLLNHLRI	89.10%
AT5G59030	COPT1	0.868	14	S	DHDHMHGMPRPSSSSSSPSSMMNN	94.18%
			17	S	HMHGMPRPSSSSSSPSSMMNNGSM	90.88%
			19	S	HGMPRPSSSSSSPSSMMNNGSMNE	89.30%
			94	T	EWLAHSSLLRGSTGDSANRAAGLIQ	88.60%
			15	S	HDHMHGMPRPSSSSSSPSSMMNNG	86.76%
AT5G39650	DAU2	0.867	29	S	PPQKPSPPSPSRSPKPVLISSPL	92.87%
			16	T	TEESVIRVYTAATPPQKPSPPSPSR	92.76%
			27	S	ATPPQKPSPPSPSRSPKPVLISSLP	87.83%
			24	S	VYTATPPQKPSPPSPSRSPKPVLI	87.46%
AT5G23670	LCB2	0.849	121	T	NYLGFGSFEYCTPRVIESLKKFSA	89.12%
			216	T	GSATIRVFQHNTPSHLERVLREQI	86.14%
AT3G50310	MAPKKK20	0.848	316	S	DSFTLDSNPSFDSFVERLGLSVGS	99.49%
			313	S	DDWDSFTLDSNPSFDSFVERLGLSV	94.36%
			112	T	GEGLESTVRRHTGSLRGLRHIHA	92.85%
			307	T	KCPFEFDDWDSFTLDSNPSFDSFVE	92.54%
			8	T	*****MEWVRGETIGFGTFSTVSTA	90.98%
			293	S	VVKVKDEDKVLMSPKCPFEFDDWDS	89.85%
			323	S	NPSFDSFVERLGLSVGSIPDWSVG	86.55%
AT5G02390	DAU1	0.838	220	S	NPLYLMSEESSNDSEEFVDNNIQ	99.84%
			280	S	HTKGFSENDDDTSPRRSKACLDALN	99.62%
			175	S	PVQNSKEKDSLSEVGSSDKNSSNG	98.92%
			273	S	WFDPKMRHTKGFSENDDDTSPRRSK	98.87%
			242	S	NIQVDDNTDGSKSDFDEKEFKKKEK	98.85%
			586	S	ETLDQTMDAESEDSPVDAETEQRDI	98.76%
			592	T	MDASEDSPVDAETEQRDIESTLDVE	98.64%
			279	T	RHTKGFSENDDDTSPRRSKACLDAL	98.52%
			218	S	SLNPLYLMSEESSNSDSEEFVDN	98.42%
			222	S	LYLMSEESSNSDSEEFVDNNIQVD	97.81%
			240	S	DNNIQVDDNTDGSKSDFDEKEFKK	97.55%
			255	S	DFDEKEFKKKEKSDDEEAWFDPKMR	97.22%
			237	T	FRVDNNIQVDDNTDGSKSDFDEKEF	96.95%
			310	S	RNFLKVLQDPGSLARHFQSQSF	96.47%
			359	S	FDPVGDVDKIPMPPSIAAEHRADG	96.28%
			80	T	GIPVPKIKLEDKTDVESVQRPKKS	96.12%
			387	S	MNETVLKLGDEDSGGYARKRGKN	96.10%
			571	S	NISEISEDHSQSEHETLDQTMAS	95.92%
			65	S	GTKNEVNNTIPSPDGIPVPKIKLE	95.53%
			613	S	LDVEHETRSLKESSEESPNNVSTVD	95.53%
			179	S	NSKEKDSLSEVGSSDKNSSNGDERN	94.76%
			549	S	FHALKIDDLTVQSIIEEQDGLDNIS	93.70%
			185	S	SLSEVGSSDKNSSNGDERNRVFNKK	93.60%
			479	S	EGTKLKQITRASSLCSGLDRYLQLY	92.86%
			617	S	HETRSLKESSEESPNNVSTVDIDEN	92.23%
			217	S	GSLNPLYLMSEESSNSDSEEFVDN	91.40%
			93	S	DVESVQRPKKPSAVKSKESSNSGE	91.25%
			599	S	PVDAETEQRDIESTLDVEHETRSLK	91.23%
			614	S	DVEHETRSLKESSEESPNNVSTVDI	91.18%
			716	S	TTTGCMFQDPECNRNEEEGGNCNHL	91.03%
			519	S	KSKMELEESALPSKRAPKFLGRILS	90.56%
			390	S	TVLKLGDDESSGGYARKRGKNQVV	90.43%
			583	S	SEHETLDQTMDAESEDSPVDAETEQR	90.30%
			568	S	GLDNISEISEDHSQSEHETLDQTM	90.29%
			579	T	HSQSSEHETLDQTMDAESEDSPVDAE	89.58%
			564	S	EEQDGLDNISEISEDHSQSEHETL	89.54%
			646	T	DISRDLDTETVSTSKQLDEEVLNID	88.90%
			796	S	PYDEQQSFDKVMSTRDLRDDGWMDL	88.60%
			173	S	TYPVQNSKEKDSLSEVGSSDKNSS	87.25%
			201	S	ERNRVFNKKVGISPAVGSNLPLYLM	86.95%
			326	T	RHFQSQSFSSKTMTKAGSFPTHGI	86.53%
			180	S	SKEKDSLSEVGSSDKNSSNGDERNR	86.09%
			54	T	HKRVPVRRTPAGTKNEVNNTIPSSP	86.00%
			101	S	KKPSSAVKSKESSNSGEKTKKKNHP	85.64%
AT2G18080	EDA2	0.834	58	S	NELWFNQTLDHESPNDHRKFRQRY	90.12%
AT1G18750	AGL65	0.829	75	T	CIEEVISKFAQLTPQERTKRKLESL	95.57%
			286	T	GLQQLGEEYSYTPFGTTLGMEEDQ	94.16%
AT5G53520	ATOPT8	0.829	9	S	*****MKDFTDTISESECDEISIVP	98.07%
			11	S	**MKDFTDTISESECDEISIVPQV	97.85%
			35	S	VELTVPKTDDPTSPVTFRMWVVG	96.79%
			30	T	SIVPQVELTVPKTDDPTSPVTFRM	89.56%
			275	S	GLDWSTIASYLGSPPLASPFASANI	87.16%
AT1G22130	AGL104	0.827	124	S	IALQVTNPAAINSDEVELEHEVCRL	94.17%
			323	S	GVTAETQVDHEVSDYETKVPQLSSQ	92.83%
			334	S	VSDYETKVPQLSSQ*****	90.56%
			159	T	LRRYEPDPIRFTMEEYEVSEKQLL	88.41%
			249	S	LSSAMYEPQLQSSSSSNQNNMSEC	87.81%
AT1G77980	AGL66	0.824	124	S	IALQLTNPTAINSDEVELEHEVYKL	94.00%

			74	S	RIEDVFSRYINLSDQERENALVFPD	88.77%
			186	S	LTRVNQRREHILSQDQLSSYEASAL	87.89%
			159	T	LRKYEPDPIRFTIMEEYETCEKQLM	85.04%
<i>AT2G42380</i>	<i>ATBZIP34</i>	0.818	24	S	TQHWPDFSSQKLSPFSTPTATAVAT	97.47%
			28	T	PDFSSQKLSPFSTPTATAVATATTT	96.65%
			97	T	DRFDDEQFMSMFTDDDNLHSNPSHI	94.19%
			303	T	NANHLSATGAGATPAVDIKSSVETE	93.16%
			229	S	SVTSLQAEVSVLSPRVAFLDHQRL	89.08%
			94	S	HQFDRFDDEQFMSMFTDDDNLHSNP	88.97%
			219	T	KLQYISELERSVTSLQAEVSVLSPR	87.90%
			66	S	SASRRGNHRRSISDSIAFLEAPT	87.47%
			64	S	DFSASRRGNHRRSISDSIAFLEAPT	86.89%
			127	T	NVGPTGSSSNTSTPSNSFNDDNKEL	86.54%
<i>AT1G19890</i>	<i>ATMGH3</i>	0.814	12	T	*MARTKQTARKSTGGKGPRKELATK	90.58%
