Table S1. Significantly enriched consensus sequences in the promoter regions of At1g16300 (*GAPCp2*) and At1g79530 (*GAPCP1*). The analysis was done using the promomer tool (http://www.bar.utoronto.ca/)

Gene	Sequence	p-Values	Present in:
At1g16300	AATC	0.034	AGAMOUS
	ACAG	0.032	AGAMOUS
	AGAA	0.017	AGL2 (AGAMOUS-like 2)
	AGAG	0.032	AGAMOUS
	AGCC	0.020	AGL2 (AGAMOUS-like 2)
	ATCC	0.012	AGAMOUS
	ATCG	0.024	AGAMOUS
	CAGA	0.004	Arabidopsis cab2 gene promoter,MYC recognition site found in the promoters of the dehydration-responsive gene rd22 and many other genes in Arabidopsis
	CATC	0.020	AGAMOUS
	CCAT	0.019	AGAMOUS
	CGCG	0.035	Arabidopsis histone H4
	CTGG	0.014	AGAMOUS
	GAAG	0.030	AGL2 (AGAMOUS-like 2)
	GACC	0.043	AGL2 (AGAMOUS-like 2)
	GACG	0.020	glutathione S-transferase gene (GST6)
	GCCA	0.004	AGAMOUS
	GGCC	0.007	IDRS (Iron-Dependent Regulatory Sequence)
	GGCT	0.047	glutathione S-transferase gene (GST6)
	TCAG	0.043	AGAMOUS
	TCCA	0.035	AGAMOUS
	TGGC	0.021	AGAMOUS
At1g79530	CAGT	0.036	ATMYB1 and ATMYB2, both isolated from Arabidopsis; ATMYB2 is involved in regulation of genes that are responsive to water stress
	GGCC	0.019	IDRS (Iron-Dependent Regulatory Sequence)
	GGGC	0.034	glutathione S-transferase gene (GST6)
	TTCC	0.017	AGAMOUS

Table S2. Metabolite levels in flower buds of wild type (WT), *gapcp1gapcp2*, *gapcp1gapcp2* transformed with *GAPCp1* or *GAPCp2* cDNA under the control of the 35S promoter (*p35S::GAPCp1c; p35S::GAPCp2c*) and *gapcp1gapcp2* transformed with a genomic *GAPCp1* construct (*pGAPCp1::GAPCp1geno*).

Data are normalized to the mean response calculated for the WT. Values are represented as the mean ± SE of seven to ten independent determinations from 3 different transgenic lines. Values in brackets are absolute values. Values in brackets are absolute values (µmol g FW^{-1}). * Absolute value not quantified.Those values that are significantly different to WT are set in bold type, $p< 0.05$. For simplicity *g* stands for *gapcp* and *G* stands for *GAPCp*.

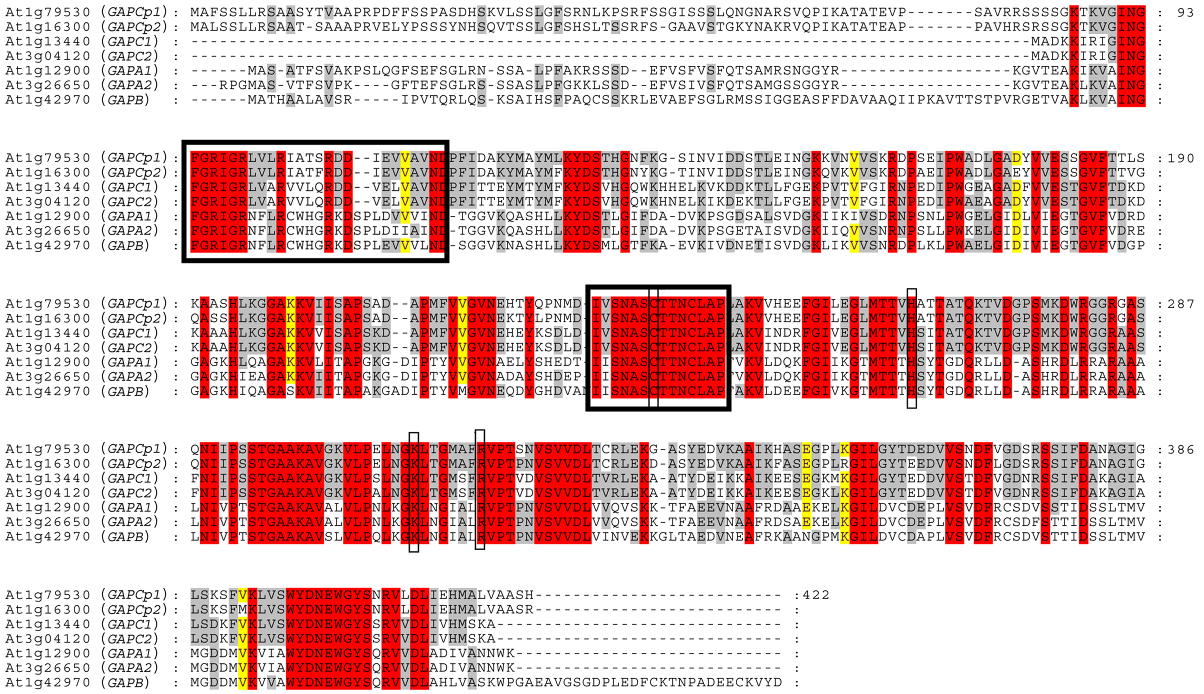
	WT	*g1g2*	*g1g2 p35S::G1c*	*g1g2 p35S::G2c*	*g1g2 pG1::G1geno*
Amino acids					
Alanine, beta-	1.00 ± 0.05 (0.11)	**1.25 ± 0.09**	1.13 ± 0.05	1.32 ± 0.15	0.94 ± 0.07
Asparagine	1.00 ± 0.32 (1.66)	0.64 ± 0.21	0.78 ± 0.08	0.70 ± 0.07	0.94 ± 0.13
Glutamic acid	1.00 ± 0.05 (4.75)	0.95 ± 0.06	**0.81 ± 0.05**	0.86 ± 0.07	0.88 ± 0.07
Glutamine	1.00 ± 0.17 (18.26)	2.09 ± 0.78	**2.07 ± 0.32**	**1.96 ± 0.37**	1.67 ± 0.32
Glycine	1.00 ± 0.14 (1.23)	1.21 ± 0.19	0.65 ± 0.19	0.61 ± 0.22	0.57 ± 0.20
Isoleucine	1.00 ± 0.12 (0.13)	**2.09 ± 0.35**	1.64 ± 0.28	**1.60 ± 0.23**	1.47 ± 0.20
Proline	1.00 ± 0.09 (5.36)	1.20 ± 0.21	1.30 ± 0.16	**1.66 ± 0.22**	1.39 ± 0.20
Serine	1.00 ± 0.15 (2.49)	1.68 ± 0.30	**1.66 ± 0.22**	**1.58 ± 0.16**	1.29 ± 0.14
Threonic acid	1.00 ± 0.04 (0.15)	1.09 ± 0.04	1.09 ± 0.06	**1.25 ± 0.05**	1.08 ± 0.03
Tryptophan	1.00 ± 0.15 (0.03)	**2.50 ± 0.41**	**2.03 ± 0.37**	**2.01 ± 0.11**	**1.95 ± 0.29**
Organic acids					
Ascorbic acid	1.00 ± 0.18 (0.01)	12.77 ± 5.58	0.75 ± 0.17	0.98 ± 0.12	0.86 ± 0.28
Aspartic acid	1.00 ± 0.23 (3.86)	0.74 ± 0.13	0.94 ± 0.07	0.92 ± 0.05	0.88 ± 0.05
Benzoic acid, 4-hydroxy-	1.00 ± 0.09 (*)	1.13 ± 0.10	1.16 ± 0.05	1.15 ± 0.06	1.16 ± 0.07
Butyric acid, 4-amino-	1.00 ± 0.08 (1.11)	0.87 ± 0.15	1.04 ± 0.16	0.92 ± 0.18	1.32 ± 0.28
Citric acid	1.00 ± 0.03 (2.95)	**1.22 ± 0.07**	0.95 ± 0.05	1.07 ± 0.07	0.98 ± 0.04
Dehydroascorbic acid	1.00 ± 0.16 (0.07)	**2.34 ± 0.38**	0.94 ± 0.18	0.95 ± 0.22	0.88 ± 0.12
Fumaric acid	1.00 ± 0.04 (4.61)	0.77 ± 0.12	**0.80 ± 0.04**	1.01 ± 0.09	0.97 ± 0.04
Gluconic acid	1.00 ± 0.07 (*)	1.20 ± 0.25	0.86 ± 0.15	1.20 ± 0.21	0.80 ± 0.15
Glutaric acid, 2-oxo-	1.00 ± 0.05 (0.06)	1.09 ± 0.06	1.17 ± 0.07	1.13 ± 0.07	1.11 ± 0.03
Glyceric acid,	1.00 ± 0.09 (0.14)	1.24 ± 0.11	1.10 ± 0.11	**1.30 ± 0.07**	**1.60 ± 0.05**
Isocitric acid	1.00 ± 0.03 (2.84)	1.03 ± 0.11	1.09 ± 0.12	0.96 ± 0.12	0.91 ± 0.11
Malic acid	1.00 ± 0.03 (12.49)	1.12 ± 0.06	**0.91 ± 0.03**	1.01 ± 0.06	0.99 ± 0.04
Nicotinic acid	1.00 ± 0.05 (0.04)	1.13 ± 0.13	1.06 ± 0.08	1.21 ± 0.11	**1.21 ± 0.08**
Octadecanoic acid	1.00 ± 0.03 (*)	1.25 ± 0.15	0.98 ± 0.07	1.02 ± 0.09	0.99 ± 0.05
Succinic acid	1.00 ± 0.06 (1.45)	1.17 ± 0.15	0.96 ± 0.08	1.14 ± 0.06	0.98 ± 0.02
Sugars and sugar alcohols					
Cellobiose	1.00 ± 0.09 (*)	**2.53 ± 0.48**	**1.69 ± 0.14**	**1.79 ± 0.25**	**1.66 ± 0.16**
Erythritol	1.00 ± 0.05 (*)	1.00 ± 0.09	1.00 ± 0.05	1.04 ± 0.02	1.03 ± 0.04
Fructosa	1.00 ± 0.05 (1.79)	1.02 ± 0.06	1.02 ± 0.07	**1.21 ± 0.08**	**1.56 ± 0.11**
Glucosa	1.00 ± 0.04 (2.90)	1.50 ± 0.30	1.11 ± 0.07	**1.32 ± 0.07**	**1.38 ± 0.10**
Inositol, myo-	1.00 ± 0.04 (0.96)	**2.05 ± 0.25**	**1.48 ± 0.10**	**1.78 ± 0.11**	**1.21 ± 0.07**
Rafinose	1.00 ± 0.00 (0.01)	**6.50 ± 0.85**	**2.03 ± 0.04**	**4.72 ± 0.09**	**1.76 ± 0.03**
Sucrose	1.00 ± 0.04 (5.25)	**1.14 ± 0.05**	1.14 ± 0.10	1.04 ± 0.09	0.96 ± 0.04
Trehalose	1.00 ± 0.09 (0.16)	**4.68 ± 0.45**	**2.64 ± 0.26**	**3.92 ± 0.55**	**1.37 ± 0.05**
Xylose	1.00 ± 0.09 (0.08)	0.99 ± 0.07	1.05 ± 0.09	1.03 ± 0.05	**1.30 ± 0.04**
Other metabolites					

Fructose-6-phosphate	1.00 ± 0.06 (0.01)	0.96 ± 0.16	1.04 ± 0.06	1.03 ± 0.05	1.10 ± 0.04
Glucose-6-phosphate	1.00 ± 0.07 (0.01)	0.89 ± 0.14	1.03 ± 0.05	1.00 ± 0.03	1.06 ± 0.04
Glycerol	1.00 ± 0.03 (3.98)	1.03 ± 0.11	1.15 ± 0.05	1.15 ± 0.10	1.24 ± 0.13
Glycerol-3-phosphate	1.00 ± 0.04 (*)	1.29 ± 0.21	1.07 ± 0.09	1.25 ± 0.11	1.16 ± 0.07
Phosphoric acid	1.00 ± 0.06 (36.14)	0.87 ± 0.12	**1.47 ± 0.07**	**1.51 ± 0.07**	**1.48 ± 0.11**
Putrescine	1.00 ± 0.09 (0.01)	1.66 ± 0.44	1.00 ± 0.14	0.89 ± 0.16	0.77 ± 0.13
Tyramine	1.00 ± 0.02 (*)	**1.20 ± 0.03**	1.21 ± 0.05	1.19 ± 0.09	0.88 ± 0.07

Table S3. Primers used in this work

gene	Primer Name	Sequence
	Primers for Mutant genotyping	
At1g16300(GAPCp2)	LP3	TCTTCCAATTCGACCAAAACC
At1g16300(GAPCp2)	RP3	TCCTCGTGTCGAGCTTTATCC
At1g79530(GAPCp1)	At1g79530FBProm	GGCTTATCGGGTTATGCCAATCAGGG
At1g79530(GAPCp1)	At1g79530R3Ex	CGAACTGCAGATGGCACTTCTGTAGCCG
At1g79530(GAPCp1)	LP1	TTCGTTTCTGATTCTCTTGCG
At1g79530(GAPCp1)	RP1	TCATCCCTTGATGTTGCAATG
T-DNA SAIL	LB1_SAIL	GCCTTTTCAGAAATGGATAAATAGCCTTGCTTCC
T-DNA Salk	LBa1	TGGTTCACGTAGTGGGCCATCG
	Primers for Cloning	
At1g79530(GAPCp1)	PromAt1g79530FHindIII	CCCCAAGCTTCCGAGCTGTGTCAAACTGATTCATGG
At1g79530(GAPCp1)	PromAt1g79530RXhoI	CCGCTCGAGGATTCGGAAGTGGGAGAAACAAAAG
	Primers for site directed mutagenesis	
At1g79530(GAPCp1)	GAPCp1.C236G.F	GATATAGTCTCCAATGCAAGTGGTACCACCAATTGTCTTGC
At1g79530(GAPCp1)	GAPCp1.C236G.R	GCAAGACAATTGGTGGTACCACTTGCATTGGAGACTATATC
At1g79530(GAPCp1)	GAPCp1.H263A.F	GAAGGCTTGATGACAACTGTCGCTGCAACTACAGCTACTCAGAAAAC
At1g79530(GAPCp1)	GAPCp1.H263A.R	GTTTTCTGAGTAGCTGTAGTTGCAGCGACAGTTGTCATCAAGCCTTC
At1g79530(GAPCp1)	GAPCp1.K311A.F	GTTCTTCCAGAACTGAATGGGGCTCTTACGGGAATGGCCTTCCG
At1g79530(GAPCp1)	GAPCp1.K311A.R	CGGAAGGCCATTCCCGTAAGAGCCCCATTCAGTTCTGGAAGAAC
At1g79530(GAPCp1)	GAPCp1.R318E.F	GAAACTTACGGGAATGGCCTTCGAGGTACCAACATCGAATGTTTCTG
At1g79530(GAPCp1)	GAPCp1.R318E.R	CAGAAACATTCGATGTTGGTACCTCGAAGGCCATTCCCGTAAGTTTC
	Primers for Q-RT-PCR	
At1g13440(GAPC2)	JFRTQ	GTCACTGTTTTCGGCATCAGGAACC
At1g13440(GAPC2)	JRRTQ	AGTCCCTCAACAATGCCAAACCTG
At1g16300(GAPCp2)	OL	TCTTCCAATTCGACCAAAACC
At1g16300(GAPCp2)	OR	TCCTCGTGTCGAGCTTTATCC
At1g79530(GAPCp1)	Q1F	GTCGCAACCTGAAGCCATCAAG
At1g79530(GAPCp1)	QR	TCATCCCTTGATGTTGCAATG
At3g04120(GAPC1)	AFRTQ	CCTACGATGAAATCAAAAAGGCTAT
At3g04120(GAPC1)	ARRTQ	GACATGTGGACGATCAAGTCG
At3g51590(LPT12)	At3g51590 For	GTGAGTGCCTTAAACTAGCGGG
At3g51590(LPT12)	At3g51590 Rev	TCACACGGCAGTCGATATACTG
At4g21330(DYT1)	At4g21330 For	CGGATCCAATGATAAAACCTGAAG
At4g21330(DYT1)	At4g21330 Rev	GATCCCATCTCTCTTCTCTGTTATG
At4g28395(ATA7)	At4g28395 For	GTCTGTGCATTGAGATAATGGGA
At4g28395(ATA7)	At4g28395 Rev	CAACGTCGGGATTCTTGGTG
At4g37900(GRP)	At4g37900 For	CAACATCCTTATGGTAAAGCTGTGG
At4g37900(GRP)	At4g37900 Rev	CGGCTGCACTAAAGCCTTCC
At5g22260(MS1)	At5g22260 For	CCGACTTAACCGGTCATCAGG
At5g22260(MS1)	At5g22260 Rev	GCTACCCCATGCAGCAGCC
	Standards for Q-RT-PCR	
At1g13320	At1g13320 For	ACCTGCGGTAATAACTGCATCTA
At1g13320	At1g13320 Rev	CCGAACATCAACATCTGGGTC
At5g15710	At5g15710 For	CTGCTTTACGTCTTGGAATCAAG

At5g15710	At5g15710 Rev	GGACAGATGCATCAAATCTTGG
At5g55840	At5g55840 For	GATGATATTGCAGTTTGTCACCGT
At5g55840	At5g55840 Rev	CACTGTCTTGCTTGTCTTGTTCTG



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At1g79530 (GAPCp1): MAFSSLLRSAASYTVAAPRPDFFSSPASDHSKVLSSLGFSRNLKPSRFSSGISSSLQNGNARSVQPIKATATEVP-------SAVRRSSSSGKTKVGING : 93
At1g16300 (GAPCp2): MALSSLLRSAAT-SAAAPRVELYPSSSYNHSQVTSSLGFSHSLTSSRFS-GAAVSTGKYNAKRVQPIKATATEAP-------PAVHRSRSSGKTKVGING :
At1g13440 (GAPC1)  : ----------------------------------------------------------------------------------------MADKKIRIGING :
At3g04120 (GAPC2)  : ----------------------------------------------------------------------------------------MADKKIRIGING :
At1g12900 (GAPA1)  : ------MAS-ATFSVAKPSLQGFSEFSGLRN-SSA-LPFAKRSSSD--EFVSFVSFQTSAMRSNGGYR------------------KGVTEAKIKVAING :
At3g26650 (GAPA2)  : ---RPGMAS-VTFSVPK----GFTEFSGLRS-SSASLPFGKKLSSD--EFVSIVSFQTSAMGSSGGYR------------------KGVTEAKLKVAING :
At1g42970 (GAPB)   : ------MATHAALAVSR-----IPVTQRLQS-KSAIHSFPAQCSSKRLEVAEFSGLRMSSIGGEASFFDAVAAQIIPKAVTTSTPVRGETVAKLKVAING :

At1g79530 (GAPCp1): FGRIGRLVLRIATSRDD--IEVVAVNDPFIDAKYMAYMLKYDSTHGNFKG-SINVIDDSTLEINGKKVNVVSKRDPSEIPWADLGADYVVESSGVFTTLS :190
At1g16300 (GAPCp2): FGRIGRLVLRIATFRDD--IEVVAVNDPFIDAKYMAYMFKYDSTHGNYKG-TINVIDDSTLEINGKQVKVVSKRDPAEIPWADLGAEYVVESSGVFTTVG :
At1g13440 (GAPC1)  : FGRIGRLVARVVLQRDD--VELVAVNDPFITTEYMTYMFKYDSVHGQWKHHELKVKDDKTLLFGEKPVTVFGIRNPEDIPWGEAGADFVVESTGVFTDKD :
At3g04120 (GAPC2)  : FGRIGRLVARVVLQRDD--VELVAVNDPFITTEYMTYMFKYDSVHGQWKHNELKIKDEKTLLFGEKPVTVFGIRNPEDIPWAEAGADYVVESTGVFTDKD :
At1g12900 (GAPA1)  : FGRIGRNFLRCWHGRKDSPLDVVVINDTGGVKQASHLLKYDSTLGIFDA-DVKPSGDSALSVDGKIIKIVSDRNPSNLPWGELGIDLVIEGTGVFVDRD :
At3g26650 (GAPA2)  : FGRIGRNFLRCWHGRKDSPLDIIAINDTGGVKQASHLLKYDSTLGIFDA-DVKPSGETAISVDGKIIQVVSNRNPSLLPWKELGIDIVIEGTGVFVDRE :
At1g42970 (GAPB)   : FGRIGRNFLRCWHGRKDSPLEVVVLND-SGGVKNASHLLKYDSMLGTFKA-EVKIVDNETISVDGKLIKVVSNRDPLKLPWAELGIDIVIEGTGVFVDGP :

At1g79530 (GAPCp1): KAASHLKGGAKKVIISAPSAD--APMFVVGVNEHTYQPNMD-IVSNASCTTNCLAPLAKVVHEEFGILEGLMTTVHATTATQKTVDGPSMKDWRGGRGAS :287
At1g16300 (GAPCp2): QASSHLKGGAKKVIISAPSAD--APMFVVGVNEKTYLPNMD-IVSNASCTTNCLAPLAKVVHEEFGILEGLMTTVHATTATQKTVDGPSMKDWRGGRGAS :
At1g13440 (GAPC1)  : KAAAHLKGGAKKVVISAPSKD--APMFVVGVNEHEYKSDLD-IVSNASCTTNCLAPLAKVINDRFGIVEGLMTTVHSITATQKTVDGPSMKDWRGGRAAS :
At3g04120 (GAPC2)  : KAAAHLKGGAKKVVISAPSKD--APMFVVGVNEHEYKSDLD-IVSNASCTTNCLAPLAKVINDRFGIVEGLMTTVHSITATQKTVDGPSMKDWRGGRAAS :
At1g12900 (GAPA1)  : GAGKHLQAGAKKVLITAPGKG-DIPTYVVGVNAELYSHEDT-IISNASCTTNCLAPTVKVLDQKFGIIKGTMTTTHSYTGDQRLLD-ASHRDLRRARAAA :
At3g26650 (GAPA2)  : GAGKHIEAGAKKVIITAPGKG-DIPTYVVGVNADAYSHDEP-IISNASCTTNCLAPTVKVLDQKFGIIKGTMTTTHSYTGDQRLLD-ASHRDLRRARAAA :
At1g42970 (GAPB)   : GAGKHIQAGASKVIITAPAKGADIPTYVMGVNEQDYGHDVANIISNASCTTNCLAPTAKVLDEEFGIVKGTMTTTHSYTGDQRLLD-ASHRDLRRARAAA :

At1g79530 (GAPCp1): QNIIPSSTGAAKAVGKVLPELNGKLTGMAFRVPTSNVSVVDLTCRLEKG-ASYEDVKAAIKHASEGPLKGILGYTDEDVVSNDFVGDSRSSIFDANAGIG :386
At1g16300 (GAPCp2): QNIIPSSTGAAKAVGKVLPELNGKLTGMAFRVPTPNVSVVDLTCRLEKD-ASYEDVKAAIKFASEGPLRGILGYTEEDVVSNDFLGDSRSSIFDANAGIG :
At1g13440 (GAPC1)  : FNIIPSSTGAAKAVGKVLPSLNGKLTGMSFRVPTVDVSVVDLTVRLEKA-ATYDEIKKAIKEESEGKMKGILGYTEDDVVSTDFVGDNRSSIFDAKAGIA :
At3g04120 (GAPC2)  : FNIIPSSTGAAKAVGKVLPALNGKLTGMSFRVPTVDVSVVDLTVRLEKA-ATYDEIKKAIKEESEGKLKGILGYTEDDVVSTDFVGDNRSSIFDAKAGIA :
At1g12900 (GAPA1)  : LNIVPTSTGAAKAVALVLPNLKGKLNGIALRVPTPNVSVVDLVVQVSKK-TFAEEVNAAFRDAAEKELKGILDVCDEPLVSVDFRCSDVSSTIDSSLTMV :
At3g26650 (GAPA2)  : LNIVPTSTGAAKAVALVLPNLKGKLNGIALRVPTPNVSVVDLVVQVSKK-TFAEEVNAAFRDSAEKELKGILDVCDEPLVSVDFRCSDFSTTIDSSLTMV :
At1g42970 (GAPB)   : LNIVPTSTGAAKAVSLVLPQLKGKLNGIALRVPTPNVSVVDLVINVEKKGLTAEDVNEAFRKAANGPMKGILDVCDAPLVSVDFRCSDVSTTIDSSLTMV :

At1g79530 (GAPCp1): LSKSFVKLVSWYDNEWGYSNRVLDLIEHMALVAASH-------------------------- :422
At1g16300 (GAPCp2): LSKSFMKLVSWYDNEWGYSNRVLDLIEHMALVAASR-------------------------- :
At1g13440 (GAPC1)  : LSDKFVKLVSWYDNEWGYSSRVVDLIVHMSKA------------------------------ :
At3g04120 (GAPC2)  : LSDKFVKLVSWYDNEWGYSSRVVDLIVHMSKA------------------------------ :
At1g12900 (GAPA1)  : MGDDMVKVIAWYDNEWGYSQRVVDLADIVANNWK---------------------------- :
At3g26650 (GAPA2)  : MGDDMVKVIAWYDNEWGYSQRVVDLADIVANNWK---------------------------- :
At1g42970 (GAPB)   : MGDDMVKVVAWYDNEWGYSQRVVDLAHLVASKWPGAEAVGSGDPLEDFCKTNPADEECKVYD :
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Supplemental Figure 1. Amino acid alignment of GAPCps with other members of the GAPDH family in Arabidopsis.