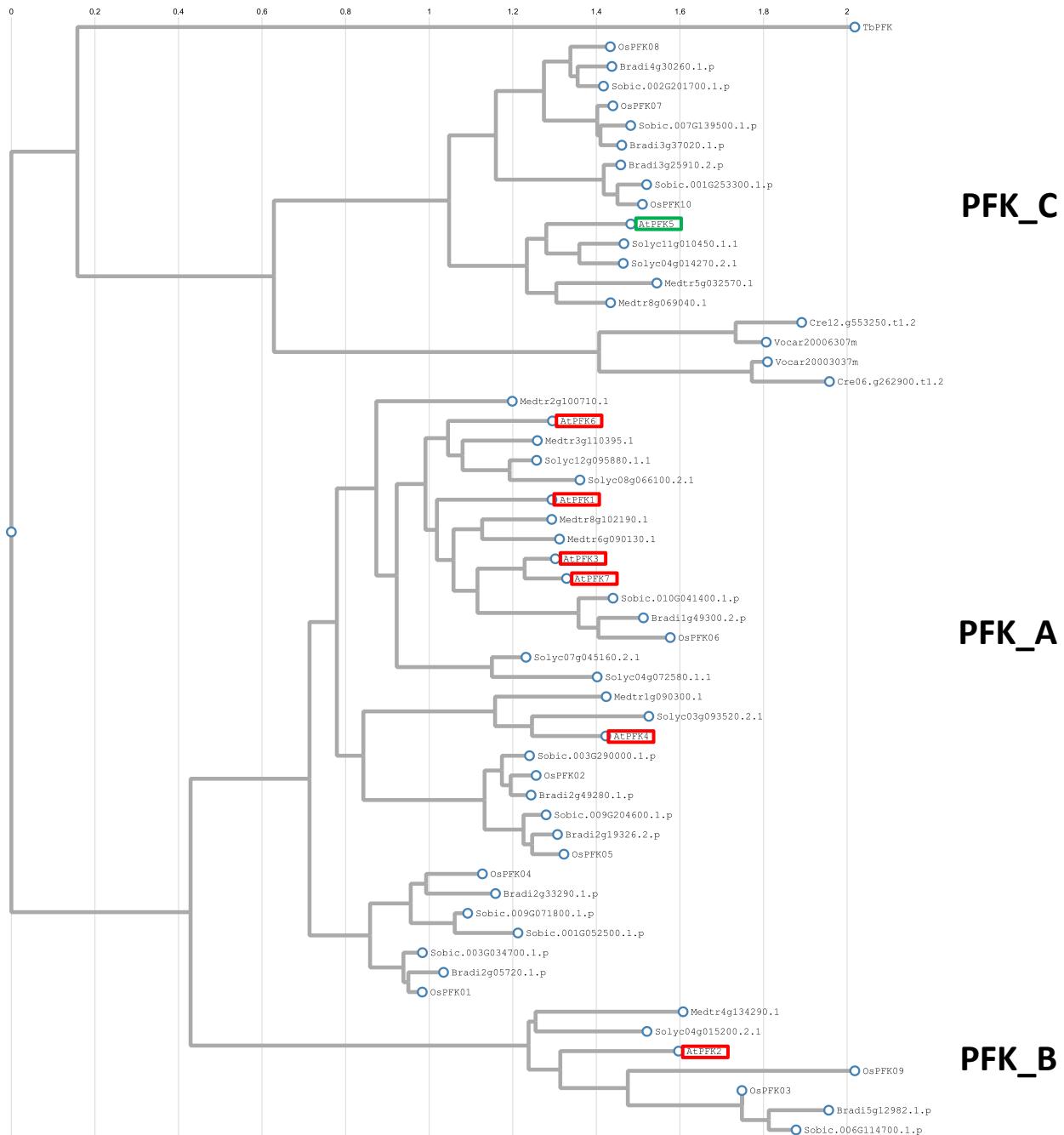


The phosphofructokinase isoform AtPfk5 is a novel target of plastidic thioredoxin-f-dependent redox regulation

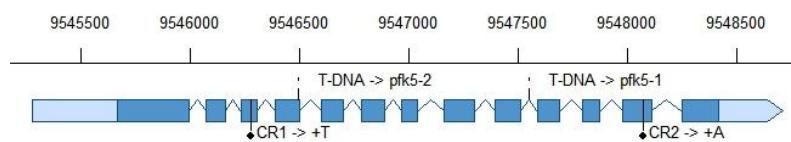
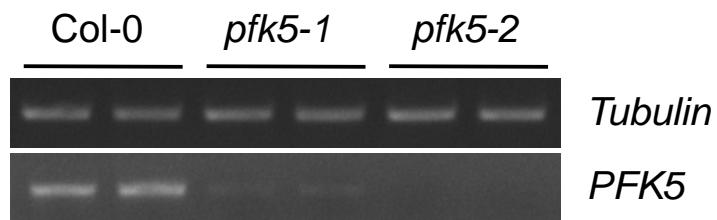
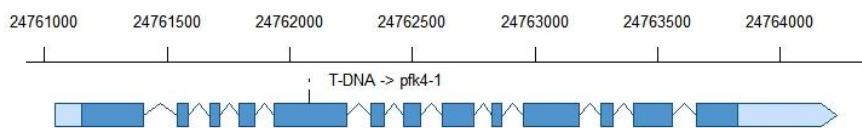
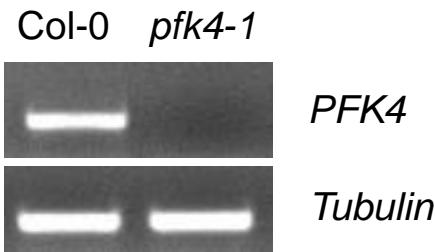
Natalia Hess, Simon Richter, Michael Liebthal, Karl-Josef Dietz, Angelika Mustroph

SUPPLEMENTARY DATA

Supplementary Figures



Supplementary Figure S1: Phylogeny of plant phosphofructokinase isoenzymes. PFK protein sequences were obtained from Phytozome and aligned using ClustalW using the platform <https://www.genome.jp/tools-bin/clustalw#clustalw.aln>. The phylogenetic tree was constructed with function "build" of ETE3 v3.1.1 (Huerta-Cepas et al., 2016) as implemented on the GenomeNet (<https://www.genome.jp/tools/ete/>). Species are abbreviated as follows: At, *Arabidopsis thaliana*; Bradi, *Brachypodium distachyon*; Cre, *Chlamydomonas reinhardtii*; Medtr, *Medicago truncatula*; Os, *Oryza sativa*; Sobic, *Sorghum bicolor*; Soly, *Solanum lycopersicum*; Tb, *Trypanosoma brucei*; Vocar, *Volvox carteri*. Protein IDs are found in Supplementary Table S1b. PFKs from *Arabidopsis* are highlighted in red, the target isoform of this study, AtPFK5, is highlighted in green.

A**B****C****D**

Supplementary Figure S2: Genotype characterization of T-DNA and CRISPR mutants for AtPfk4 and AtPfk5. **(A, C)** Gene models for *AtPfk5* and *AtPfk4*, including site of mutations. **(B, D)** Transcript levels of *AtPfk5* and *AtPfk4* in wildtype Col-0 and T-DNA insertion mutant seedlings. Tubulin was used as the reference.

Supplementary Figure S3 (continued over the next pages): Alignment of plant phosphofructokinase isoenzymes, which is the basis for the phylogenetic tree presented in Supplementary Fig. S1. Cys residues are in red font, and conserved motifs are marked with asterisks above the alignment.

Solyc04g014270.2.1	1	-----MESLSPAIGQKAIFPSTTGYT-----DHDLFLDSVKVRTERNFNRACRRLRIRVQ	50
Solyc11g010450.1.1	1	-----MESLSPAIGSNFIRPTTTISG-----ENELLISSVKSIKLPPVARRKMRMVRVAQ	50
AtPfk5	1	-----MDALSQAIISSGIVSPYKNNSSSSLVPSHGLTSILLRKSRSPVNSSRSRVSRASE	55
Medtr5g032570.1	1	-----MNTHVITPNLNNTLLLHHHHHHVHGTLNSSHRYSKTNHRLFHSFKVSNNNVR	50
Medtr8g069040.1	1	-----MASISHAITTTTNPYFNLPHQQTTPSSILTLSHNSRRVFKNVGVF	46
OsPfk07	1	-----MAVSLKSSGSFCST-PFQWLHSTRDRILYGYSHSNAKECTCKKTKRPAPL	49
Bradi3g37020.1.p	1	-----MAVALKTIGSFCONT-QQQCLHSTRDRILYGYSHSNTKECKSKNAKRPAPl	49
Sobic.007G139500.1.p	1	-----MASALKTNGSFESTQQQQFLQSTTDQFLHGSSHLNFKHCKSKKTIKAPL	50
Sobic.002G201700.1.p	1	-----MTLSGMAVAFKASTSSTTQQHWP-SPTKDRCQYGFTQLSRQKYRKKAAL	49
Bradi4g30260.1.p	1	-----MSSSPAMIAFKASTSYFTAQQICGHSTWDQCONGFTHLNERKSRSRKGSAAL	51
OsPfk08	1	-----MTFSGMDIALKASTHSSTSQQWHLHSTRYRCQYGLGSTHLNGRKRSRPMVL	50
OsPfk10	1	-----MALKSPVDFAGSITSGQKDPCCFGVPGCN-PRCVRYNKKSR-CRLV	45
Sobic.001G253300.1.p	1	-----MALAPMDYAGSISSGQKYLGRFGVPTSSRLRWVGYDTSR-TYLV	45
Bradi3g25910.2.p	1	-----MATASPVDYAGPITSQQRRLSCFVHSCNHLCNAYEKKSRSDQVL	47
Cre06.g262900.tl.2	1	-----MRLQRHAAAGLGATKHRTDTLARLPCQSTRGRAALQVACVATPHSA	46
Vocar20003037m	1	-----MRLQRLARTNASLGGQRRLCVGPGPCRASPGRTRMQVSCVAETSET	46
Cre12.g553250.tl.2	1	-----MLLQRHAPGFTKVPSRQCCKPSVPI	24
Vocar20006307m	1	-----MRLQQRQVIGRSLPVCVPCVTRCRKL	26
Medtr6g090130.1	1		1
Medtr8g102190.1	1		1
AtPfk3	1		1
AtPfk7	1		1
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Bradi4g49300.2.p	1	-----MASPRTTDAATDPAPTPAPIAVPSLRARLPHAHHHLLDRDTPRRPAWWSER	54
OsPfk06	1	-----MASPPTASASASEAAESGRRSAPGPIDVPSPRDHLHHLLDRDTPRVVHVEGTTM	55
AtPfk1	1		1
Solyc08g066100.2.1	1		1
Solyc12g095880.1.1	1		1
Medtr3g110395.1	1		1
AtPfk6	1		1
Solyc04g072580.1.1	1		1
Solyc07g045160.2.1	1		1
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Bradi2g05720.1.p	1	-----MESVVVAPAAAAQGAVAVAEEQQQKKKKLDQKTEL	35
OsPfk04	1	-----MEAATVVAAPIPAAADAAKALEKKLLDEL	30
Bradi2g33290.1.p	1	-----MEAATVVAAPIPAAADAAKALEKKLLDEL	24
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Sobic.009G071800.1.p	1	-----METATVVVAPAPVITSQPPQHKIMEL	26
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Bradi2g49280.1.p	1	-MASHIILPKEEEEEE-----EGLGVAVEADHDSPPEPP--RYQAEPVKALPFSAT	57
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Sobic.009G204600.1.p	1	-MASHIILPPDDADENHNHQAEEEEREELGRDEDADDEEHG-HGHPPALPPKAALPFSAT	68
Bradi2g19326.2.p	1	-MASHIILPPDEEQQRDDEEDGQQ-----SASEHAPLPFSAM	48
OsPfk05	1	-MASHIILPPDDDEQRRLEEEEDDPWARSGPPP-----AAPEHAMKAALPFSAT	62
AtPfk4	1	-----MEASISFLGSTKPNIISLFNPSSNVLPRLDFPLPALKLKVKSVLPRI	46
Solyc03g093520.2.1	1	-----MEFSILYNSSSLRFPQNDFLPLHNRSTLGSFHTFSIKKLASKSIST	49
Medtr1g090300.1	1	-----MDLSSSSSVYTSFSSLKTPPSFSLSSSSSSRQNSLQLLLRLSHLPQRALFLRN	55
Sobic.006G114700.1.p	1		MDP 3
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AtPfk2	1		1
Medtr4g134290.1	1		1
Solyc04g015200.2.1	1		1
OsPfk09	1		1
TbPfk	1		1
Clustal Consensus	1		1

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Solycl1g010450.1.1	51	SSNFVVPPNN-TDFNDPDWKVKYEREFEARFNIPHITDLPDAVSYPSTF CLKMRTP VTEDFAQGYPSEEE	119
AtPFK5	56	IQHSKTSASSIDLSDPDWKLYKEKDFEQRFSIPIHITDVLPAEAIRSTF CLKMRS -TEDFVGGYPSDEE	124
Medtr5g032570.1	51	VFSELKSQNKNIDYNPDFDWKDKFKEDFEARFLPHITDIFPDASSMRSTF CLKMRA PITRDFHGNYDSGEE	120
Medtr8g069040.1	47	AEHRNSSTSIDFNDPDFDWKFKFQQDFESRFLPHITDIFPDSPPIPSTF CLMRMRT PIGKDIPGHYTLDDE	116
OsPFK07	50	CVKATSTKV EFLDFNDFSDPSWKQKFQEDWDKRNFLPRITDIYDLK-PRPTTFSLKKNRSAGDENG--TPMDK	116
Bradi3g37020.1.p	50	CVKATSTKV EFLDFNDFSDPSWKQKFQEDWDERFLNPLRITDIYDLK-PRPTTFSLKKNRSAGDENG--TPMDK	117
Sobic.007G139500.1.p	51	CVRATSSKV EFLDFHDESWKQKFQEDWERRFLNPLSITDIYDLK-PRPTTFSLKKNRILTGDEN----VDM	114
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Bradi4g30260.1.p	52	HVRAISRNLLDLSDFSDPSWKQKYQEDWMRFLPHITDIFDLK-PRLTTSFLKKNRTELGDNNG--SSPDM	118
OsPFK08	51	SVRAVSGSKSLDLSDFSDPSWKEKYQEDWNRRFLPHITDIFDLK-PRLTTSFLKKNRTEDGGS----LSADK	114
OsPFK10	46	TRAISVDRPQLDFSFNSNDWKKQFQEDFDRRFLPHLKDVIDVE-PRPTTFSLKS-RTELENVNG--SMOGS	111
Sobic.001G253300.1.p	46	ARAISVDPQQLDFSFNSNDWKKQFQEDFDNRFLPHLRDVIDVE-PRPTTFSLKS-RTELENVNG--TMQES	111
Bradi3g25910.2.p	48	IRAISVDRPQLDFSFNSNDWKKQFQEDFDNRFLPHLRDVIDVE-PRPTTFSLKS-RTELENVNG--PFDES	113
Cre06.g262900.t1.2	47	DSQKGAPKATATPSGQVYSSPYGAGRVLTPSPPGS1DDDDVLELKLNRLNRYLVPRDSEFIVDNN----Q	110
Vocar20003037m	47	AKQGPSSPPTLS-SGAYVTNSFGAGRVRSDS---LDEEDVLELKLNRLNRYLVPRDSEFIVDNN----H	105
Cre12.g553250.t1.2	25	ARQP RSSC CARATPG ADLTNYVIEPV-----SFGE DAVLE CPEMRSKLVVRPSE FVTHNN-----F	81
Vocar20006307m	27	ITVPRARPTPAATSGADLTNTSYIIEPV-----SFGE DAVLE CPEMRSKLVVRPSE FVHN-----F	83
Medtr6g090130.1	1	-----MGLTEPKVVTGAGYVLEDVPHLSDYIPDLP-----TYPNEQLQDNPA---YSVV	46
Medtr8g102190.1	1	-----MGSSPNSKPKIVRGASAGYILEDVPHLTDYIPELP-----TYSNEQLQDNPA---YSVV	49
AtPFK3	1	-----MSTVESSKP KI INGS CYV LEDVPHLSDYLPGLP-----TYPNEQLQDNPA---YSVV	49
AtPFK7	1	-----MSSPRSNKPVINGP GGY ILQDVP H LDPDLP-----TYPNEQLQDNPA---YSVV	49
Sobic.010G041400.1.p	56	RNRRG-----GAMDGA AAAAKLVS GEAGY LEDVPHVSDYLPDLP-----TYPNEQLQDNPA---YSVV	109
Bradi1g49300.2.p	55	TREAM-----DGTAAKPETKLVAGEAGYVLEDVPHLSDYLPDLP-----TYSNEQLQDNPA---YSVV	108
OsPFK06	56	QRQRGEAAGDAGAAAAKPEVKLVTGDDGYVLEDVPHV CDY LPDLP-----TYSNEQLQDNPA---YSVC	116
AtPFK1	1	-----MSSSVPN S DRKIVTGPAGYILEDVPHVSDDFDPH-----TYPNEQLQDNAA---YSVV	50
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Medtr3g110395.1	1	-----MASSESNSQMKVVHCDAGYILEDVPHLSDYVNP-----TYPNEQLRSNPA---YSVV	50
AtPFK6	1	-----MASNGVDEQIKLVEGAGYVLEDVPHLSDYILDLP-----TYPNEQLQSNAA---YSVV	50
Solytc04g072580.1.1	1	-----MGSVLD S ALHNLNKIVMGDNGYVFEDVPHLSDYIPS-----TYPNEQLKKNPS---YSVV	55
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OsPFK01	24	RKAAPAAPSTSMAAKWAMKKLVGGDAGYVLEDVPHLTDYLPPELP-----TYPNEQLQDNPA---YSVV	84
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Bradi2g05720.1.p	36	PLVAALKAPAPASP C KWAMKKLVGGDAGYVLEDVPHLTDYMPPELP-----TYPNEQLQDNPA---YSVV	96
OsPFK04	31	PPFPAPAKKAAKVVAAPKKLAGGAGGYVLEDVPHLTDYLPNLP-----SFPNEQLQNHPA---YSVV	91
Bradi2g33290.1.p	25	LDLKVM S ADPAVQAPARKT KKL SGAGGGYVLEDVPHLKDYLPH-----SYPNEQLQNHPA---YSVV	85
Sobic.001G052500.1.p	26	KFSFAPVAKSSPATKAEPDKKKLTGGCGGYVLEDVPHLTDYLP ELK -----SYPNEQLQDHPA---YSVV	86
Sobic.009G071800.1.p	27	KPAFAAVAKPSPARAKPAKKLAGGCCGGYVLEDVPHLTDYLP ELK -----SYPNEQLQDHPA---YSVV	87
Medtr2g100710.1	1	-----MVDSSSTSHVEANTHVSDFLLEDVPHLSDYIPDLP-----TYPNEQLQDNPS---YSVV	49
OsPFK02	59	NLRALRNASAMS LP DDAA Y AKLEEGDYGYLLDDVPHFTDYLSDLP-----TFPNEQLQDHPA---YSTV	119
Bradi2g49280.1.p	58	NLRALRNASAVSLRDDDAD F KVLEEGDYGYVLLDDVPHLTDYLP-----TFPNEQLQDHPA---YSTV	118
Sobic.003G290000.1.p	69	NLRALRNASTMALHDDDAAFVKIEEGDFGYVLLDDVPHLTDYLPDLP-----TFPNEQLQDHPA---YSTV	129
Sobic.009G204600.1.p	69	NLRALRNASSVSLAD--AAYVKISEGDGYVLLDDVPHFTDYL DIP -----TYPNEQLQDHPA---YSTV	127
Bradi2g19326.2.p	49	NLRALRNASVSLAD--AAYAKISEGDGYVLLDDVPHLADYLPDIP-----TYPNEQLQDHPA---YSTV	107
OsPFK05	63	NLRALRNASSVSLAD--AAYVKISEGDGYVLLDDVPHLADYLPDAP-----TYPNEQLQDHPA---YSTV	121
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Solytc03g093520.2.1	50	IWRRLPLVRRRNAQTATESNAS G D K H G EDDFIVE D VPHLTHFLP DLP -----SYTNEQLKKSQA---YAIV	110
Medtr1g090300.1	56	PILPPFFSRQNRLPLAPVVRVS N QSEN D G F LL D EVPHL T FLP N LP-----SYPNEQLQT SQA ---YSIV	116
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Bradi5g12982.1.p	1	----MDPTTPSSGDHTASTPTNTTV T LP L PI L RD V PLPAADP-----IPNEISSRPC---FHPP	53
OsPFK03	1	-----	1
AtPFK2	1	-----MAAETSI R KLPSL S GLR R -----RNLEDNPY---FHPS	32
Medtr4g134290.1	1	----MDGSSSSSSSSLE D VNL F EPI K L K D L PHLNHYISN-----LKTFPNEQLDQNPY---FHTP	56
Solytc04g015200.2.1	1	-----MSNSPPSIS I SNVOLQHISHLTNYNS-----QIKTHTNELAVNP F -----FR F	44
OsPFK09	1	-----MDDDGETP M PSLE H KL P LAGAAIP-----N I ARHPL---YHPS	38
TbPFK	1	-----MAVESRSRV T SLK V KAHRA M LN S V T QEDLK V DR L PG-----ADYPNE S KKYSS-----	48
Clustal Consensus	1	-----	1

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AtPFK5	125	WHGYINNNDRVLLKVISYSSPTSAGA-----
Medtr5g032570_1	121	WNGYISNDRVLTKTIVHSSPTSAGA-----
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OsPFK07	117	WNGYVNNSDDRALLKVIKYSSPNSAGA-----
Bradi3g37020_1.p	118	WNGYVNDDDRALLKVIKYSSPTSAGA-----
Sobic.007G139500_1.p	115	WNGYVNDDDRALLKVIKYSSPTSAGA-----
Sobic.002G201700_1.p	117	WNGYVNKSDDRALLKVIKYASPTSAGA-----
Bradi4g30260_1.p	119	WNGYVNKKDRALLKVIKYASPTSAGS-----
OsPFK08	115	WNGYVNKKDRALLKVIKYASPTSAGA-----
OsPFK10	112	WNGYVNDDDRALLKVIKFASPTSAGA-----
Sobic.001G253300_1.p	112	WNGYVNDDDRALLKVIKFASPTSAGA-----
Bradi3g25910_2.p	114	WNGYVNDDDRALLKVIKFASPTSAGA-----
Cre006_g262900_t1.2	111	GGGFVGDRDRIRLHTVEFESTESAGS-----
Vocar20003037m	106	GGGFVGDRDRIRLHTVEFESAESAGS-----
Cre12_g553250_t1.2	82	GGGFVSDQDRVALNSMRFAFASDPSAGASRSRNFPHGKGGINVLEASMDQLNMTLPPWAI
Vocar20006307m	84	GGGFVSDNDRVALNSMRFAAESAGASRTSGEGQ-AKSSVNLEASMDQLNMTLPPWAI
Medtr6g090130_1	47	KQYFVHVDVTVPQKVJVKHDSP-----
Medtr8g102190_1	50	KQYFVHIDDSVPQKIIANKHDSP-----
AtPFK3	50	KQYFVADDASPVQKIVVHKDGP-----
AtPFK7	50	KQYFVHADDSPEVKVVHKDGP-----
Sobic.010G041400_1.p	110	KQYFVNPPDTVCQKIVVHKDGP-----
Bradi1g49300_2.p	109	KQYFVNPPDTVCQKIVVHKGGA-----
OsPFK06	117	RQYFVNPPDTVCQKAIVVHKDGP-----
AtPFK1	51	KQYFVDEDDTVQPKIVVHPDSP-----
Solyc08g066100_2.1	50	KQYFVDMDDTVQPKIVVHKDSQ-----
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Medtr3g110395_1	51	KQYFVHMDDTVPQKVJVKHDGP-----
AtPFK6	51	RQYFVDEDDTVQEKIVVHKDGP-----
Solyc04g072580_1.1	56	NQYFVDEDDTVAQNIVVVRKNSP-----
Solyc07g045160_2.1	53	KQYFVNEDDTVAEKVVVHKNSP-----
OsPFK01	85	KQYFVNEDDTVTQKIVVHKTS-----
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Bradi2g05720_1.p	97	KQYFVNNTDDTVTQKIVVHKTS-----
OsPFK04	92	KQYFVNADDTVAKKIVVHKNSA-----
Bradi2g33290_1.p	86	KQYFVNPGDTVSKKIVVHESSA-----
Sobic.001G052500_1.p	87	KQYFVKPDETVAKKVVVHKSSA-----
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Medtr2g100710_1	50	KQYYVHPPDTVAQQIVVHKNSP-----
OsPFK02	120	KQYFVNADDTVPEKVVVQKDSP-----
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Sobic.009G204600_1.p	128	KQYFVNEDDTVPQKVVVQKNSR-----
Bradi2g19326_2.p	108	KQYFVNEDDTVPQKVVVQKNSR-----
OsPFK05	122	KQYFVNEDDTVPQKVVVQKNSR-----
AtPFK4	101	KRTFVSSEDVVAQNIVVQKGSK-----
Solyc03g093520_2.1	111	KKTFVSPEDMVAKELIIVQKDSP-----
Medtr1g090300_1	117	KNTFVSPEDVVAQTIIVQKNSP-----
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OsPFK03	1	-----
AtPFK2	33	NGFYITPSDVILAQVAYDHS-----
Medtr4g134290_1	56	-----
Solyc04g015200_2.1	45	PGFFITSSDIVLRHNVLDSLGT-----
OsPFK09	39	PSFFISPTDVVLRDILFASPASAAG-----
TbPFK	49	RTEFRDKTDYIMYNPRPRDEPSEN-----
Clustal Consensus	1	-----

1

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OsPFK08	167 PAEVKAAIVTCGGLC C PGLNDVIRQIVITLEIYGVKN--IVGIPFGYGFKEK-GLKEMPLSRKVVENINL	233
OsPFK10	164 PQYVKRAGIVTCGGLC C PGLNDVIRQIVITLEIYGVKN--IVGIPFGYGFKEK-GLKEMPLSRKVVENINL	230
Sobic_001G253300_1.p	164 PQYVKRAGIVTCGGLC C PGLNDVIRQIVITLEIYGVKN--IVGIPFGYGFKEK-GLKEMPLSRKVVENINL	230
Bradi3g25910_2.p	166 PQSVKRAGIVTCGGLC C PGLNDVIRQIVITLEIYGVKN--IVGIPFGYGFKEK-GLKEMPLSRKVVENINL	232
Cre06_g262900_t1.2	171 PKQVSAAVVT CGGLC PGLNDVQVNQIVYTLDYGVPEDNILGIRYGLGFGYER-DAKPIITLTKYVDGIHL	239
Vocar20003037m	166 PKQVSAAVVT CGGLC PGLNDVQVNQIVYTLDYGVPEDNILGIRYGLGFGYER-DAKPIITLTKYVDGIHL	234
Cre12_g553250_t1.2	152 PSQTAAIVTCGGLC C PGLNDVQGLVNKLTDYGVPEGKILGIKYGFYDP-QVKPIVLSKRVVDCIQL	220
Vocar20006307m	153 PQQVTAIAIVTCGGLC C PGLNDVQGLVNKLTDYGVPEGKILGIKYGFYDP-SVKPVVLTKRVVDCIQL	221
Medtr6g090130_1	86 SDEIQAIVTCGGLC C PGLNTVIREIV CSL HMYGVT-RVLGIEGGYGRGYA---RNITLTTPSSVNNIHK	151
Medtr8g102190_1	89 SDEVKAIVTCGGLC C PGLNTVIREIV CSL HMYGVK-KVLGISGGYGRGYA---HNTISLTPKTVNNDIHK	154
AtPFK3	89 SDEVKAIVTCGGLC C PGLNTVIREIV CSL HMYGVK-RILGIDGGYGRGYA---KNTVSLDSKVVNDIHK	154
AtPFK7	89 SDEVKAIVTCGGLC C PGLNTVIREIV CSL HMYGVK-RILGIDGGYGRGYA---KNTIPLNSKVVNDIHK	154
Sobic_010G041400_1.p	149 PDEVKAIVTCGGLC C PGLNTVIREIV CSL SDMYGVT-KILGIQGGYGRGYA---RNITLTTPKSVNNDIHK	214
Bradi1g49300_2.p	148 SDEVKAIVTCGGLC C PGLNTVIREIV CSL SDMYGVT-KILGIQGGYGRGYA---CNTINLTTPKSVNNDIHK	213
OsPFK06	156 SDEVKAIVTCGGLC C PGLNTVIREIV CSL YDMYGVS-RVLGIDGGYGRGYA---CNTIDLSPKSVNNDIHK	221
AtPFK1	90 SDDVRAIVTCGGLC C PGLNTVIREIV CSL YMYGVK-RILGIDGGYGRGYA---RNTHLDLKTVNNDIHK	155
Solyc08g066100_2.1	89 SDDVRAIVTCGGLC C PGLNTVIREIV CSL YMYGVD-KVLGIEGGYGRGYA---KNTINLTPKLVVNNDIHK	154
Solyc12g095880_1.1	89 SDDVRAIVTCGGLC C PGLNTVIREIV CSL YMYGVS-KVFGIDGGYGRGYA---KNTINLTPKLVVNNDIHK	154
Medtr3g110395_1	90 SDDVRAIVTCGGLC C PGLNTVIREIV CSL YMYGVD-KVFGIDGGYGRGYA---KNTINLTPKLVVNNDIHK	155
AtPFK6	90 PSDVRAIVTCGGLC C PGLNTVIREIV CSL HFMYGVT-EVICVDC G FGRGYFS---KNTVALTPKTVDIHK	155
Solyc04g072580_1.1	95 ADDVNAIVTCGGLC C PGLNTVIREIV CSL YSMYGVA-RVMGIDGGYGRGYFS---KNTIPLTPNVVNNDIHK	160
Solyc07g045160_2.1	92 PDDVNAIVTCGGLC C PGLNTVIREIV CSL YMYGVS-RVMGIDGGYGRGYFS---KNTIPLTPKVVNNDIHK	157
OsPFK01	124 SDEVNAIAIVTCGGLC C PGLNTVIREIV CSL YDMYGVT-SVVGIECCYKGFY---RNTPALTPKSVNNDIHK	189
Sobic_003G034700_1.p	126 SDEVNAIAIVTCGGLC C PGLNTVIREIV CSL YDMYGVT-SVVGIECCYKGFY---RNTPALTPKSVNNDIHK	191
Bradi2g05720_1.p	136 SDEVNAIAIVTCGGLC C PGLNTVIREIV CSL CDMYGVT-SVVGIECCYKGFY---RNTPALTPKSVNNDIHK	201
OsPFK04	131 PDEVNAIVTCGGLC C PGLNTVIREIV CSL HDMYGVT-SVVGIECCYKGFY---RNTPALTPRSVNNDIHK	196
Bradi2g33290_1.p	125 PGEVVAIAIVTCGGLC C PGLNTVIREIV CSL HDMYGVG-SVVGIECCYKGFY---RNTPALTPRSVNNDIHK	190
Sobic_001G052500_1.p	126 SDEVNAIAIVTCGGLC C PGLNTVIREIV CSL HDMYGVG-SIHGIECCYKGFY---RNTPALTPRSVNNDIHK	191
Sobic_009G071800_1.p	127 PDEVNAIAIVTCGGLC C PGLNTVIREIV CSL HDMYGVG-SIYGIECCYKGFY---RNTPALTPRSVNNDIHK	192
Medtr2g100710_1	89 SEEVKAIVTCGGLC C PGLNTVIREIV CSL YMYGVQ-KVLGIGGGYGRGYFS---RNTPALTPKIVVNNDIHK	154
OsPFK02	159 SEDVKAIVTCGGLC C PGLNTVIREIV CSL SHMYNVN-DIFGQONQYKGFY---SNYLPMTPKSVVNNDIHK	224
Bradi2g49280_1.p	158 PEDVKAIVTCGGLC C PGLNTVIREIV CSL SHMYNVN-DVFGQONQYKGFY---SNYLPMTPKSVVNNDIHK	223
Sobic_003G290000_1.p	169 SEEVKAIVTCGGLC C PGLNTVIREIV CSL SHMYNVS-NVFGQONQYKGFY---SNYLPMTPKSVVNNDIHK	234
Sobic_009G204600_1.p	167 TDEVKAIVTCGGLC C PGLNTVIREIV CSL SHMYNVS-SIFGQONQYKGFY---SNYLPMTPKSVVNNDIHK	232
Bradi2g19326_2.p	147 SDEVKAIVTCGGLC C PGLNTVIREIV CSL SHMYNVN-KIYQGONQYKGFY---SNYLAUTPKTVVNNDIHK	212
OsPFK05	161 SDEVKAIVTCGGLC C PGLNTVIREIV CSL LAHMNVN-KIYQGONQYKGFY---SNYLTLTPKSVDDIHK	226
AtPFK4	140 SDEVKAIVTCGGLC C PGLNTVIREIV CSL NNMYGVN-NILGIGQYGRGYFS---KNTMNLTPKVVNNDIHK	205
Solyc03g093520_2.1	150 PEEVKAAIVTCGGLC C PGLNTVIREIV CSL KNMYGVD-DVLGIOGGYSGFY---KNTLNLTTKVVVNNDIHK	215
Medtr1g090300_1	156 AEEVKAIVTCGGLC C PGLNTVIREIV CSL KNMYGV-EILGIEEYKGFY---KNTMRLTPKVVDIHK	221
Sobic_006G114700_1.p	113 PAAARAAIVTCGGLC C PGLNTVIREIV CSL WELYGVR-HVFGVAAGYGFYGT-DEDHVRLDPAAVDDWHK	180
Bradi5g12982_1.p	96 PARARAAIVTCGGLC C PGLNTVIREIV CSL WELYGVR-DVFGVAAGYGFYGA-DVDHVRLDPAAVDDWHK	163
OsPFK03	1 ----- 1	1
AtPFK2	74 PSAVKAAIVTCGGLC C PGLNTVIREIV CSL WELYGVR-EIYGIPASYGFY---SMKAVLDPKAVIDWHK	139
Medtr4g134290_1	91 PSDVRAIVTCGGLC C PGLNTVIREIV CSL WELYGVR-OIFGITAGYGFYSS-STQPVOLNPNIHVHWHT	158
Solyc04g015200_2.1	89 PTVVRAIAIVTCGGLC C PGLNTVIREIV CSL WELYGVR-EIFGKAGYGFYSS-YDPVRLNPKMVDDWHK	154
OsPFK09	87 PATVRAAI F TCGGLC C PGLNTVIREIV CSL SELYGVRGGVFVRNGYGRGYFS---DEVVPLDPAAVEHWHK	153
TbPFK	95 PTETTIGIVTCGGLC C PGLNDVIRSI L TGINVYNVK-RVIGFRG G WGLSKKGQSQTAELHRGRVNTIHK	163
Clustal Consensus	1 ----- 1	1

Solyc04g014270.2.1	240	SGGSILGVSRGGPKVSDIVDSI	QERGINNMLFVLGGNGTHAGANAIHDE	CRKRR-IAAVVGVPKTIDNDI	308	
Solycl1g010450.1.1	239	SGGSILGVSRGGPKVSDIVDSI	QERGINNMLFVLGGNGTHAGANAIHDE	CRKRR-MQAVAVVGVPKTIDNDI	307	
AtPFK5	244	SGGSILGVSRGGPSVSEIVDS	SMERGERINNMLFVLGGNGTHAGANAIHDE	CRKRR-IVAVVGVPKTIDNDI	312	
Medtr5g032570.1	240	SGGSILGVSRGGPGVSEIVDS	SLEERGINNMLFVLGGNGTHAGANAIHDE	CRKRR-IVSVIGVPKTIDNDI	308	
Medtr8g069040.1	236	SGGSILGVSRGGPGVSDIVDS	LEDRGINNMLFVLGGNGTHAGANAIHDE	CRKRR-LKVSVIGVPKTIDNDI	304	
OsPFK07	236	AGGSILGVSRGGAKTSEIVDSI	QARRIDMLFVLGGNGTHAGANAIHDE	CRKRR-LKSVVVAVPKTIDNDI	304	
Bradi3g37020.1.p	237	AGGSILGVSRGGAKTSEIVDSI	QARRIDMLFVLGGNGTHAGANAIHDE	CRKRR-LKSVVVAVPKTIDNDI	305	
Sobic.007G139500.1.p	234	NGGSILGVSRGGAKTSEIVDSI	QARRIDMLFVLGGNGTHAGANAIHDE	CRKRR-LKSVVVAVPKTIDNDI	302	
Sobic.002G201700.1.p	236	SGGSILGVSRGGAKTSEIVDSI	QARRIDMLFVLGGNGTHAGANAIHDE	CRKRR-LKSVVVAVPKTIDNDI	304	
Bradi4g30260.1.p	238	SGGSILGVSRGGAKTSEIVDSI	QARRIDMLFVLGGNGSHAGAKAIHDE	CRKRR-LKSVVVAVPKTIDNDI	306	
OsPFK08	234	SGGSILGVSRGGAKTSEIVDSI	QARRIDMLFVI	GGNGTHAGANAIHDE	CRKRR-LKSVVVAVPKTIDNDI	302
OsPFK10	231	AGGSILGVSRGGANISDIVDSI	QARRIDMLFVLGGNGTHAGANLIHDE	CRKRR-LKSVIVGVVPKTIDNDI	299	
Sobic.001G253300.1.p	231	AGGSILGVSRGGANISDIVDSI	QARRIDMLFVLGGNGTHAGANAIHDE	CRKRR-LQSVIVCVPKTIDNDI	299	
Bradi3g25910.2.p	233	SGGSILGVSRGGASDIVDSI	QARRIDMLFVLGGNGTHAGANAIHDE	CRKRR-LKSVIVGVVPKTIDNDI	301	
Cre06_g262900.t1.2	240	KGGTMIGTSRGGANVKEIVRI	IDLWGLNMVFVVGNGGNAANAIHSE	CEAQG-VCCSVVGVPKSIDNDI	308	
Vocar20003037m	235	KGGTMIGTSRGGANVKEIVRI	IDLWGLNMVFVVGNGGNAANAIHSE	CEAQG-VVC	TVVGVGPKSIDNDI	303
Cre12_g553250.t1.2	221	QGGTIGTSRGGANIREIVKRI	DMWGI	DMLFVVGNGGNAANAINAMCRQHD-VPC	CSVVGVPKSIDNDI	289
Vocar20006307m	222	QGGTIGTSRGGANIREIVKRI	DMWGI	DMLFVVGNGGNAANAINAMCRQHD-VPC	TVVGVPKSIDNDI	290
Medtr6g090130.1	152	RGGTIGTSRGGHDTNKIVDSI	QDRGINQVYII	GGDGCTQRGASVIFEEVRRRG-LKCAVVGIPKTIDNDI	220	
Medtr8g102190.1	155	RGGTIGTSRGGHDTTKIVDSI	QDRGINQVYII	GGDGCTQRGAYRIFEEIRNRG-LKVAVVGIPKTIDNDI	223	
AtPFK3	155	RGGTIGTSRGGHDTTKIVDSI	QDRGINQVYII	GGDGCTQRGASVIFEEIRRRG-LKVAVIGIPKTIDNDI	223	
AtPFK7	155	RGGTIGTSRGGHDTNKIVDSI	QDRGINQVYII	GGDGCTQRGASVIFEEIRRRR-LKVAVVGIPKTIDNDI	223	
Sobic.010G041400.1.p	215	RGGTIGTSRGGHDTVKIVDSI	QDRGINQVYII	GGDGCTQRGAGVIFEEVRRRG-LKSVVAGIPKTIDNDI	283	
Bradi4g49300.2.p	214	RGGTIGTSRGGHDTMKIVDSI	QDRVINQVYII	GGDGCSQRGARVIFEEVRRRG-LKVAVAGIPKTIDNDI	282	
OsPFK06	222	RGGTIVLGTTSRGGHDTMKIVDSI	QDRGINQVYII	GGDGCTQRGAGVIFEEIRRRG-LKVAVAGIPKTIDNDI	290	
AtPFK1	156	SGGTIGTSRGGHNTTKIVDSI	QDRGINQVYII	GGDGCSQKGAAIFIEEIRRRG-LKVAVAGIPKTIDNDI	224	
Solyc08g066100.2.1	155	RGGTIGTSRGGHDTKKIVDSI	QDHGINQVYII	GGDGCTTLKGAIIYEIEIRRRG-LKVAVAGIPKTIDNDI	223	
Solycl2g095880.1.1	155	RGGTIGTSRGGHDTTKIVDSI	QDRGINQVYII	GGDGCTQKGAAVIYEIEIRRDR-LKVIVAGIPKTIDNDI	223	
Medtr3g110395.1	156	RGGTIGTSRGGHDTGKIVDSI	QDRGINQVYII	GGDGCTQKGAAVIIYEIEVRRRG-LKVAIAGIPKTIDNDI	224	
AtPFK6	156	RGGTIGTSRGGHDTGKIVDSI	QDRGINQVYII	GGDGCTQKGAAVIIYEIEVRRRG-LKVAVAGIPKTIDNDI	224	
Solyc04g072580.1.1	161	RGGTIGTSRGGHVTKKIVDSI	QDRGINQVYII	GGDGCTQKGASLIFEEITRRG-LNVVVVGIPKTIDNDI	229	
Solycl07g045160.2.1	158	RGGTIGTSRGGHVTKKIVDSI	QDRGINQVYII	GGDGCTQRGAAVIFEEIRRRG-LNVAVAGIPKTIDNDI	226	
OsPFK01	190	RGGTIVLGTTSRGGHDTGKIVDSI	QDRGINQVYII	GGDGCTQKGASVIIYEIEVRRRG-LKCSVVGVPKTIDNDI	258	
Sobic.003G034700.1.p	192	RGGTIVLGTTSRGGHDTAKIVDSI	QDRGINQVYII	GGDGCTQKGASVIIYEIEVRRRG-LKCSVVGIPKTIDNDI	260	
Bradi2g05720.1.p	202	RGGTIVLGTTSRGGHDTAKIVDSI	QDRGINQVYII	GGDGCTQQGASVIIYEIEVRRRG-LKCSVVGVPKTIDNDI	270	
OsPFK04	197	RGGTIVLGTTSRGGQDTGKIVDSI	QDRGINQVYII	GGDGCTQKGAAATIYEIEVRRRG-LKCAVVGIPKTIDNDI	265	
Bradi2g33290.1.p	191	RGGTIVLRA\$RGGQDTAKIVDSI	QDRGINQVYII	GGDGCTQKGAAQVHEIEVRRRG-LKCAVVGVPKTIDNDI	259	
Sobic.001G052500.1.p	192	RGGTIGTSRGGQDTAKIVDSI	QDRGFTNQVYIV	GGDGCSQKGAAASIHEIEVRRRG-LKCAVVGVPKTIDNDI	260	
Sobic.009G071800.1.p	193	RGGTIVLGTTSRGGQDTAKIVDSI	QDRGVINQVYII	GGDGCTQKGAAASIHEIEVRRRG-LKCAVVGVPKTIDNDI	261	
Medtr2g100710.1	155	RGGTIVLGT\$YGGHDTSKIVDSI	QDRGINQVYII	GGDGCTQNEAAMIFFEIRRRD-LKVAVVGIPKTIDNDI	223	
OsPFK02	225	RGGTIVLGTTSRGGHDTKIVDSI	QDRGINQVYII	GGDGCTQKGAEIYEIEIRRRG-LKVAVAGWPKTIDNDI	293	
Bradi2g49280.1.p	224	RGGTIVLGTTSRGGHDTKIVDSI	QDRGINQVYII	GGDGCTQKGAEIYEIEIRRRG-LKVAVAGIPKTIDNDI	292	
Sobic.003G290000.1.p	235	RGGTIVLGTTSRGGHDTKKIVDSI	QDRGINQVYII	GGDGCTQKGAEIYEIEVERRG-LQAVAVSGIPKTIDNDI	303	
Sobic.009G204600.1.p	233	RGGTIVLGTTSRGGHDTKKIVDSI	QDRGINQVYII	GGDGCTQKGAEIYEIEIRRRG-LHVAVAGIPKTIDNDI	301	
Bradi2g19326.2.p	213	RGGTIVLGTTSRGGHDTKKIVDSI	QDRGINQVYII	GGDGCTQKGAEIYEIEIRRRG-LKVSVAGIPKTIDNDI	281	
OsPFK05	227	RGGTIVLGTTSRGGHDTKKIVDSI	QDRGINQVYII	GGDGCTQKGAEIYEIEIRRRG-LKVSVAGIPKTIDNDI	295	
AtPFK4	206	RGGTFLQTSRGGHDTAKIVDSI	QDRGINQVYII	GGDGCTQKGAEIYEIEVERRG-LQAVAVSGIPKTIDNDI	274	
Solyc03g093520.2.1	216	RGGTFLQTSRGGHDTKKIVDSI	QDRGINQVYII	GGDGCTQKGAAAIYEIEVEKRG-IKVAVAGIPKTIDNDI	284	
Medtr4g090300.1	222	IGGTFLRTTSRGGHDTKIVDSI	IEDRGINQVYII	GGDGCTQKGAAARIYEIEVEKRR-LOVAVAGIPKTIDNDI	290	
Sobic.006G114700.1.p	181	KGGTIVLKTTRGGFDLGKIVDGI	VARGYTOIYAIGCB	TMRGAVAI	FQEFKRRC-LNISITGIPKTIDNDI	249
Bradi5g12982.1.p	164	KGGTALKTTRGGFDLKIVDGI	VARGYTOVAYAI	GGDGCTMGRGAVAI	FQEFKRRC-LHISITGIPKTIDNDI	232
OsPFK03	1	-----	-----	-MRGAVAII	FNEFKRRC-LNISITGIPKTIDNDI	31
AtPFK2	140	KGGTIVLATSRGGFHQJKIVDAI	HNLGYNQVYII	GGDGCTMGRGAVEI	FKEIISIRK-LEVGITVIPKTIDNDV	208
Medtr4g134290.1	159	KGGTFLQTSRGGFDLICKIVDAI	QNQAFNQVYII	GGDGCTMGRGAVKI	FNEIKORK-LNVAVVGIPKTIDNDV	227
Solyc04g015200.2.1	155	RGGTIVLETTSRGGFDLKKIVDAI	ODHGFNOLYI	GGDGCTMGRGAVEI	FEELKEK-LYISVVGIPKTIDNDV	223
OsPFK09	154	AGGAALGTSRGGFDLARIVDAI	ERHGFNQVYAVGGDG	TMRGAARI	IHFEVRRGRGLAVAVAGIPKTIDNDV	223
TbPFK	164	YGGTIGTSRGPQDPKEMVDTLERLGVNILFTV	GGDGCTQRGALVI	ISCEAKRREG-VDISVFGV	PKTIDNDL	232
Clustal Consensus	1	*	:	:	:	:
		*	:	:	:	***:
			*	:	:	14

Solyc04g014270.2.1	309	MLMDKT FGF DTAVEEAQRAINSAYIEAHSAYRGIGEVKLMGRSSGFIAMQASLASGQIDI	CLIP	VEFNL	378
Solycl1g010450.1.1	308	MLMDKT FGF DTAVEEAQRAINSAYIEAHSAYHGTGVKLMGRSSGFIAMQASLASGQIDI	CLIP	VEFNL	377
AtPFK5	313	LHMDKT FGF DTAVEEAQRAINSAYIEAHSAYHGIGVKLMGRSSGFIAMQASLASGQIDI	CLIP	VEFNL	382
Medtr5g032570.1	309	LLMDKT FGF DTAVEEAQRAINSAYIEAHSAYHGIGVKLMGRSSGFIAMQASLSSGQVDI	CLIP	VEFDL	378
Medtr8g069040.1	305	LLMDKT FGF DTAVEEAQRAINSAYIEAHSAYHGIGVKLMGRSSGFIAMQASLSSGQVDI	CLIP	VEFNL	374
OsPFK07	305	LLMDKT FGF DTAVEEAQRAINSAYIEAHSAYHGIGVKLMGRSSGFIAMQASLSSGQVDI	CLIP	VEFNL	374
Bradi3g37020.1.p	306	PLMDKT FGF DTAVEEAQRAINSAYIEAHSAYHGIGVKLMGRSSGFIAMQASLSSGQVDI	CLIP	VEFNL	375
Sobic.007G139500.1.p	303	LLMDKT FGF DTAVEEAQRAINSAYIEAHSAYHGIGVKLMGRSSGFIAMQASLSSGQVDI	CLIP	VEFNL	372
Sobic.002G201700.1.p	305	LFMDKT FGF DTAVEEAQRAINSAYIEAHSAYHGIGVKLMGRSSGFIAMQASLSSGQVDI	CLIP	VEFNL	374
Bradi4g30260.1.p	307	LFMDKT FGF DTAVEEAQRAINSAYIEAHSAYHGVVKLMGRSTGFIAMQASLSSGQVDI	CLIP	EISFNL	376
OsPFK08	303	LFMDKT FGF DTAVEEAQRAINSAYIEAHSAYHGIGVKLMGRSSGFIAMQASLSSGQVDI	CLIP	VEFNL	372
OsPFK10	300	LLMDKT FGF DTAVEEAQRAINSAYIEAHSAYHGIGVKLMGRSSGFIITMHSASLSSGQVDI	CLIP	VEFNL	369
Sobic.001G253300.1.p	300	LLMDKT FGF DTAVEEAQRAINSAYIEAHSAYHGIGVKLMGRSSGFIITMHSASLSSGQVDI	CLIP	VEFNL	369
Bradi3g25910.2.p	302	LLMDKT FGF DTAVEEAQRAINSAYIEAHSAYHGIGVKLMGRSSGFIITMHSASLSSGQVDI	CLIP	VEFNL	371
Cre06_g262900.t1.2	309	LIIDKC FGF ETAVQEAQRAALLAAKVEAGSARNGLGVVKLMGRQSGFIAMQAMASGVADV	CLIP	EIPFRM	378
Vocar20003037m	304	LIIDKC FGF ETAVQEAQRAALLAAKVEAGSARNGLGVVKLMGRQSGFIAMQAMASGVADV	CLIP	EIPFRM	373
Cre12_g553250.t1.2	290	LIIDKC FGF DTAVEEESQRALMAAKVEASSARKGIGVKLMGRQSGFIAMQAMASGVVDDA	CLIP	VNFKL	359
Vocar20006307m	291	LIIDKC FGF DTAVEEESQRALLAKEAASSARKGIGVKLMGRQSGFIAMQAMASGVVDDA	CLIP	VNFKL	360
Medtr6g090130.1	221	PIIDKSFGFDTAVEEAQRAINAHAVEAESFENGIGGVVKLMGRYSGFIAMYATLASRDVD	CC	CLIPESPFYL	290
Medtr8g102190.1	224	PVIDKSFGFDTAVEEAQRAINAHAVEAESVENGIGGVVKLMGRYSGFIAMYATLANRDVD	CC	CLIPETPPFL	293
AtPFK3	224	PVIDKSFGFDTAVEEAQRAINAHAVEAESIENGIGGVVKLMGRYSGFIAMYATLASRDVD	CC	CLIPESPFYL	293
AtPFK7	224	PVIDKSFGFDTAVEEAQRAINAHAVEAESVENINGIGGVVKLMGRYSGFIAMYATLASRDVD	CC	CLIPESPFYL	293
Sobic.010G041400.1.p	284	PVIDKSFGFDTAVEEAQRAINAHAVEAEVSAENGIGGVVKLMGRHSGFIATHYATLASRDVD	CC	CLIPESPFYL	353
Bradi4g49300.2.p	283	PVIDKSFGFDSAVEEAQRAINAHAVEAEESAENGIGGVVKLMGRYSGFIHYATLASRDVD	CC	CLIPESPFYL	352
OsPFK06	291	PVIDRSFGFDTAVEEAQRAINAHAVEAEAGSANGIGGVVKLMGRHSGFIHYATLASRDVD	CC	CLIPESPFYL	360
AtPFK1	225	PIIDRSFGFDTAVEEAQRAINAHAVEATSFENGIGGVVKLMGRSGFIAMYATLASRDVD	CC	CLIPESPFYL	294
Solyc08g066100.2.1	224	PIIDKSFGFDTAVEEAQRAINAHAVEAEQSAENGIGGVVKLMGRYSGFIAMYATLASRDVD	CC	CLIPESPFYL	293
Solycl2g095880.1.1	224	PVIDKSFGFDTAVEEAQRAINAHAVEAESEAENGIGGVVKLMGRYSGFIAMYATLASRDVD	CC	CLIPESPFYL	293
Medtr3g110395.1	225	PVIDRSFGFDTAVEEAQRAINAHAVEAESVENGIGGVVKLMGRYSGFIAMYATLASRDVD	CC	CLIPESPFYL	294
AtPFK6	225	PVIDKSFGFDTAVEEAQRAINAHAVEATSVENGIGGVVKLMGRYSGFIAMYATLASRDVD	CC	CLIPESPFYL	294
Solyc04g072580.1.1	230	PVIDKSFGFDSAVEEAQRAISAHHVEATSFENGIGGVVKLMGRDSGFIAMYATLASRDVD	CC	CLIPESPFYL	299
Solycl07g045160.2.1	227	PVIDKSFGFDSAVEEAQRAISAHHVEATSFENGIGGVVKLMGRDSGFIAMYATLASRDVD	CC	CLIPESPFYL	296
OsPFK01	259	AVIDKSFGFDTAVEEAQRAINAHAVEAESEAENGIGGVVKLMGRNSGFIAMYATLASRDVD	CC	CLIPESPFYL	328
Sobic.003G034700.1.p	261	AVIDKSFGFDTAVEEAQRAIDAHHVEAC G ENGIGGVVKLMGRNSGFIAMYATLASRDVD	CC	CLIPESPFYL	330
Bradi2g05720.1.p	271	AVIDKSFGFDTAVEEAQRAINAHAVEAESEAENGIGGVVKLMGRNSGFIAMYATLASRDVD	CC	CLIPESPFYL	340
OsPFK04	266	AVIDRSFGFDTAVEEAQRAINAHAVEAESEAENGIVVKLMGRNSGFIAMYATLASRDVD	CC	CLIPESPFYL	335
Bradi2g33290.1.p	260	AVIDKSFGFDTAVEEAQRAIDAHHVEAESEAENGIGGVVKLMGRNSGFIAMYATLASRDVD	CC	CLIPESPFYL	329
Sobic.001G052500.1.p	261	AVIDKSFGFDTAVEEAQRAIDAHHVEAE C GENGIGGVVKLMGRNSGFIAMYATLASRDVD	CC	CLIPESPFYL	330
Sobic.009G071800.1.p	262	AVIDKSFGFDTAVEEAQRAINAHAVEAESEAENGIGGVVKLMGRNSGFIAMYATLASRDVD	CC	CLIPESPFYL	331
Medtr2g100710.1	224	PVIDKS I GFDTAVEEAQRAINSAHVEAESEAENGIGGVVKLMGRCSGFIAMYATLASRDVD	CC	CLIPESPFYL	293
OsPFK02	294	AVIDKSFGFDSAVEEAQRAIDAHHVEASSAENGIGGVVKLMGRYSGFIAMYATLASRDVD	CC	CLIPESPFYL	363
Bradi2g49280.1.p	293	AVIDKSFGFDTAVEEAQRAIDAHHVEASSAENGIGGVVKLMGRYSGFIAMYATLASRDVD	CC	CLIPESPFYL	362
Sobic.003G290000.1.p	304	AVIDKSFGFDTAVEEAQRAINAHAVEAESEAENGIGGVVKLMGRYSGFIAMYATLASRDVD	CC	CLIPESPFYL	373
Sobic.009G204600.1.p	302	AIIDKSFGFDTAVEEAQRAIDSAAHVEAC S AENGIGGVVKLMGRYSGFIAMYATLASRDVD	CC	CLIPESPFYL	371
Bradi2g19326.2.p	282	AIIDKSFGFDSAVEEAQRAIDSAAHVEAC S AENGIGGVVKLMGRYSGFIAMYATLASRDVD	CC	CLIPESPFYM	351
OsPFK05	296	AIIDKSFGFDTAVEEAQRAIDSAAHVEAC S AENGIGGVVKLMGRYSGFIAMYATLASRDVD	CC	CLIPESPFYM	365
AtPFK4	275	AVIDKSFGFDTAVEEAQRAINAHAHV E ESVENGVGVVKLMGRYSGFIAMIATLANRDVD	CC	CLIPESPFYL	344
Solyc03g093520.2.1	285	AVIDKSFGFDTAVEEAQRAINAHAHV E ESVQNVGVGVVKLMGRYSGFIAMIATGNRDVD	CC	CLIPESPFYL	354
Medtr4g090300.1	291	AVIDKSFGFDTAVEEAQRAINAHAHV E VNSVENGVGVVKLMGRYSGFIAMIATLASRDVD	CC	CLIPESPFYL	360
Sobic.006G114700.1.p	250	GIIDRSFGFTAVEAQQAIDAHHVEAVSAVNGIGGVVKLMGRSTGHALHTLSSRVDC C CLIP	VEFHL	319	
Bradi5g12982.1.p	233	GIIDRSFGFTAVEAQQAINAHAHV E AVSAVNGIGGVVKLMGRSTGHALHTLSSRVDC C CLIP	VEFHV	302	
OsPFK03	32	GIIDRSFGFTAVEAQQAIDAHHVEAVSAVNGIGGVVKLMGRSTGHALHTLSSRVDC C CLIP	VEFHV	101	
AtPFK2	209	GIIDRSFGFTAVEAQQAISAHHVEAESAVNGIGGVVKLMGRSTGHALHTLSSRVDC C CLIP	EMDFYL	278	
Medtr4g134290.1	228	GIIDRSFGFTAVEMAQQAISAHHVEAESAVNGIGGVVKLMGRSTGHALVLHSTLSSRVDC C CLIP	ELDFYL	297	
Solyc04g015200.2.1	224	GIIDRSFGFTAVEMAQQAINAHHVEAESAVNGIGGVVKLMGRSTGHALHTLSSRVDC C CLIP	EIDFYL	293	
OsPFK09	224	GVVDRSFGFTAVEAQQAIAAGHVEAESANGVGIGVKLMGRSAGHALHTLSSRVDC C CLIP	EEDFYL	293	
TbPFK	233	SFSHRD F GTAVEKAOAIRAAYAEAVSANYGVGVVKLMGRDSGFIIAOAVASAQANI C CLIP	ENPISE	302	
Clustal Consensus	14	.. :**.:**: :.*: : . * :*. **:***** :*. : : .. : **:*** :			49

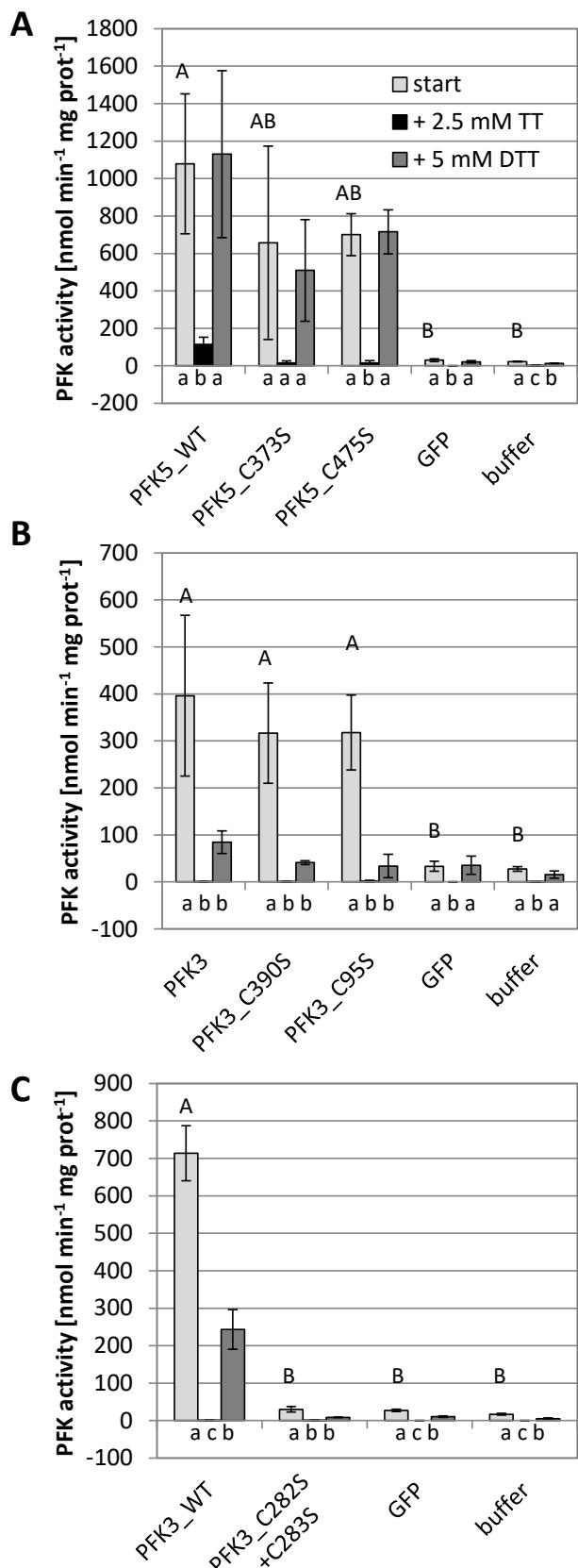
SolyC04g014270.2.1	379	HGPHGVLRHLKYLLTKGSAVVCAEGAG-----QDFLEKTNAKDAS-----GNAVLGDI	GVYI	LQ	433	
SolyC11g010450.1.1	378	HGPHGVLQHHLKYLLTKGSAVICVAEGAG-----QDFLEKTNAKDAS-----GNAVLGDI	GVH	IQ	432	
AtPFK5	383	HGPNGVVKHLKYLIETKGSAVICVAEGAG-----QNFLEKTNAKDAS-----GNAVLGDI	GVYI	Q	437	
Medtr5g032570.1	379	HGPHGVLSHLKYLIESKGSAVVCAEGAG-----QNLQKTNDTDP-----GNAKLGDI	GVYI	Q	433	
Medtr8g069040.1	375	HGPHGVLRHLQYLLEMKGSAVVCAEGAG-----QNLQNTNAKDAS-----GNIVFGD	IGVYI	Q	429	
OsPFK07	375	DGEYGVLRHLLEHLLTKGFCVVCAVABAG-----QELQKSGATDAS-----GNVILSD	DIGVHM	Q	435	
Bradi3g37020.1.p	376	DGEYGVLQHLEHLLLENKGFCVVCAVABAG-----QELQKSGATDAS-----GNVILSD	DIGVHM	Q	430	
Sobic.007G139500.1.p	373	DGEFGVQLQHLEHLLSKGFCVVCAVABAG-----QDLQKSGATDAS-----GNVIFSD	DIGVHM	Q	427	
Sobic.002G201700.1.p	375	DGEHGVLRHLLEHLLNTKGFCVVCAVABAG-----QDLQKSNATDAS-----GNVILSDF	GVHM	Q	429	
Bradi4g30260.1.p	377	DGERGVLAHLEHLLTKGFCVVCAVABAG-----QDLQKSNATDAS-----GNVILSD	DFGVHM	Q	431	
OsPFK08	373	DGEHGVMRHLEHLLLEKKGFCVVCAVABAG-----QDLQKSNATDAS-----GNVILSD	DFGVHM	Q	427	
OsPFK10	370	DGPNGVQLQHLEHLLIETKGFAVICVAEGAG-----QEHLQQSNATDAS-----GNMILG	DIGVHL	H	424	
Sobic.001G253300.1.p	370	DGPNGVLRHLIEHLLIETKGFAVICVAEGAG-----QELLEDGGOLGTDAS-----GNMVLS	DIGVHL	Q	424	
Bradi3g25910.2.p	372	DGPNGVLRHLIEHLLDTKGFAVICIAEGAG-----QEYFQKSNTDAS-----GNMVLS	DIGAHL	Q	426	
Cre06_g262900.t1.2	379	DK---LCEHVESIFEKQGHCVVCVAEGAG-----QDLITAGGTGGTDAS-----GNPILAD	IGIFMR	432		
Vocar20003037m	374	DK---LIAHIAVSFEKQGHCVVCVAEGAG-----QDLILNNG---AAGTVDAS-----GNPILAD	IGIFLR	426		
Cre12_g553250.t1.2	360	DGDNGLLKYLDDGVIKAKGHAVVCAEGAG-----QDILEDGGQIGTDAS-----GNPILKDI	GAFLK	416		
Vocar20006307m	361	NGDQGLLRLYLEGVINKNKGHCVVCAEGAG-----QDILLEDGGOLGTDAS-----GNPILKDI	GAFLK	417		
Medtr6g090130.1	291	EGPGGLYLEYIDRRLKENGHMVIVIAEGAG-----QELLTESLQSGKK-----Q-DASGNKLLQDV	GLWIS	349		
Medtr8g102190.1	294	EGPGGLFYEYTERRLKENGHMVIVIAEGAG-----QELVTESIQSMMH-----QQDASGNKLLQDV	GLWIS	353		
AtPFK3	294	EGERGVLFYEYIEKRLKENGHMVIVIAEGAG-----QDLMSKSMESMTL-----KDAS-GNK	LLKDVG	GLWLS	352	
AtPFK7	294	EGERGVLFYEYIEKRLKDNGHMIVIVIAEGAG-----QDLMKCSMESTP-----DAS-GNK	LLKDVG	GLWLS	351	
Sobic.010G041400.1.p	354	EGERGVLFRYIEKRLKDNGHMIVIVVAEGAG-----QKLIAETMQSIGK-----DAS-GNE	LLLDV	GLWLS	411	
Bradi4g49300.2.p	353	EGERGVLYRYIEKRLKDNGHMIVIVVAEGAG-----QKLFAETMKAMQ-----DAS-GNA	LLLDV	GLWLS	410	
OsPFK06	361	EGERGVLFYRFLYEKRLKENGHMVIVVAEGAG-----QKLINETKESMGK-----DAS-GNS	LLLDV	GLWLS	418	
AtPFK1	295	EGSGGLFPEFIDKRLKESGHMVIVIAEGAG-----QDLLSEMSKESTT-----LKDA	SGN	KLLQD	IGLWIS	354
SolyC08g066100.2.1	294	DGSGGLFPEFVKKRLREBEGHMIVIVIAEGAG-----QELLAENSNAGS-----QDASGNK	LLQDV	GLWVS	353	
SolyC12g095880.1.1	294	EGDGGGLFPEYIEKRLKENGHMVIVIAEGAG-----QELLAEEAHAKN-----EQDASGNK	LLQDV	GLWIS	353	
Medtr3g110395.1	295	EGKGGGLYEFITKRLKESGHMVIVIAEGAG-----QDLLTESMQMD-----QKDASGNK	LLQDV	GLWIS	353	
AtPFK6	295	EGKGGGLYEFIAKRLRENGHMIVIVIAEGAG-----QDLVAES-----IE-----QDASGNK	LLQDV	GLWIS	350	
SolyC04g072580.1.1	300	EGRGGGLFPEYIEQRRLKENGHMVIVVAEGVG-----QDDE-----QVDV	GLWIS	341		
SolyC07g045160.2.1	297	EGSGGLFPEYIEHRLKDNGHMIVIVIAEGAG-----QELVSESLKSTD-----SGNK-----	LLQDV	GLWIS	352	
OsPFK01	329	EGERGVLFYIEFIEKRLKDNGHMIVIVVAEGAG-----QDLIAKSMNFVDT-----QDAS-GNK	LLLDV	GLWLS	387	
Sobic.003G034700.1.p	331	EGERGVLFYIEKRLKDNGHMIVIVVAEGAG-----QDLIAKSMNFVDT-----QDAS-GNK	LLLDV	GLWLS	389	
Bradi2g05720.1.p	341	EGERGVLFYIEKRLKDNGHMIVIVVAEGAG-----QDLIAQSMNFVDT-----QDAS-GNK	LLLDV	GLWLS	399	
OsPFK04	336	EGERGVLFYIEFAEKRRLRENGHMIVIVVAEGAG-----QDVIARSMRLADA-----HDAS-GNK	VLLD	VGWL	C	394
Bradi2g33290.1.p	330	EGERGVLFYIEKRLKDNGHMIVIVVAEGAG-----QDLIAKGMRADT-----HDAS-GNR	HLLD	VGWL	388	
Sobic.001G052500.1.p	331	EGERGVLFYIEFIEKRLRDNGHMIVIVVAEGAG-----QDLVAKGMPFANT-----HDAS-GNK	VLLD	VGWL	389	
Sobic.009G071800.1.p	332	DGKGGLLFEVEKRLRDNGHMIVIVVAEGAG-----QDLIAKSMNFADT-----HDAS-GNK	VLLD	VGWL	390	
Medtr2g100710.1	294	EGERGVLFYIEKRLREQGHMIVIVIAEGAG-----QELIPRNTDSNKN-----KPDAS	PDDLV	QDV	GLWLS	353
OsPFK02	364	EGERGVLFYIEKRLKENNHMVIVVAEGAG-----QDLIAKSIAAADQ-----IDAS-GNK	LLLDV	VGWL	T	422
Bradi2g49280.1.p	363	EGERGVLFYIEERRLKENNHMVIVVAEGAG-----QDLIAKSIAPAADQ-----LDAS-GNK	LLLDV	VGWL	T	421
Sobic.003G290000.1.p	374	EGERGVLFYIEDRRLKENNHMVIVVAEGAG-----QDLIAQSIAPAADQ-----QDAS-GNK	LLLDV	VGWL	T	432
Sobic.009G204600.1.p	372	DGEGGGLLQYVEKRLKENKHMVIVVAEGAG-----QDLIAKSIATSDQ-----QDAS-GNK	LLLDI	VGWL	T	430
Bradi2g19326.2.p	352	DGEGGGLLQYIEKRLKENKHMVIVVAEGAG-----QDIIAKSIPSSDQ-----QDAS-GNK	LLLDI	VGWL	T	410
OsPFK05	366	DGEGGGLLQYVERRLKENKHMVIVVAEGAG-----QDLIAKSLSTSEQ-----QDAS-GNK	LLLDI	VGWL	T	424
AtPFK4	345	EGERGVLFYIEERLKENRHMVIVIAEGAG-----QDYVAQSMRASET-----KDAS-GNR	RLLLD	VGWL	T	403
SolyC03g093520.2.1	355	EGERGVLYEYIEQQLKENRHVLIVLAEGAG-----QEYVAQSMQAFQE-----KDAS-GNR	RLLLD	VGWL	T	413
Medtr4g090300.1	361	EGRGGGFYIEFIEQRRLKENGHMVIVVAEGAG-----QECVASEVNTVDE-----KDAS-GNK	LLLDV	GPWLS	419	
Sobic.006G114700.1.p	320	EGERGVLFYIEFIEKRLKENKHMVIVVAEGAG-----QELIPRT	DDQRE	-----QDESGN	I	378
Bradi5g12982.1.p	303	EGERGVLFYIEYERIKKKGHAVIVVAEGAG-----QDLIPRT	DDQRE	-----QDESGN	I	361
OsPFK03	102	EGERGVLFYIEYERIKQKGHAWVVVAEGAG-----QELIPRT	DDQRE	-----QDESGN	I	160
AtPFK2	279	EGERGVLFYIEFIEKRLKERGHAVLVVAEGAG-----QEMIPRNESQKQE-----RDESGN	AVEFL	DVG	VWFK	337
Medtr4g134290.1	298	EGERGVLFYIEFIEKRLKERGHAVLVVAEGAG-----QDIIPRTESHKEE-----RDESGNP	VFL	DVG	VWLF	356
SolyC04g015200.2.1	294	EGERGVLFYIEFIEKRLKERGHAVLVVAEGAG-----QDIIPRTESQKTE-----KDESGN	VPFL	DVG	GWLF	352
OsPFK09	294	RGAGGLFDYIIRRRIKDNGHAWVVVAEGAG-----QRLIPRTTTTSASGA	CAGADES	GNETFL	DVGAWLK	357
TbPFK	303	QE---VMSLERRFCHSRSCVIIIVAEFG-----QDWGRGSGGYDAS-----GNKKL	IDIGV	ILT	354	
Clustal Consensus	49	:	:	:	**. * .	58

Solyc04g014270.2.1	434	QEVKKYFKE---LGQTADVKYIDPTYMIRA C RANASD G I C TVLGQNAVHGAFAGYSGITVGI C NTHYVV	500
Solycl1g010450.1.1	433	QQIKKYFKE---IGVTTDVKYIDPTYMIRA C RANASD G I C TVLGQNAVHGAFAGYSGITVGI C NTHYVV	499
AtPFK5	438	QETKKYFKE---ISTPIDVKYIDPTYMIRA C RANASD G I C TVLGQNAVHGAFAGYSGITVGI C NTHYAY	504
Medtr5g032570.1	434	QETKNYFKE---NDIHADVKYIDPTYMIRA C RANASD G I C TVLGQNAVHGAFAGYSGITVGI C NTHYAY	500
Medtr8g069040.1	430	QETKKYFKE---IGVHADVKYIDPTYMIRA C RANASD G I C TVLGQNAVHGAFAGYSGISVGI C NTHYAY	496
OsPFK07	436	QKIKMHFKD---IGVPADVKYIDPTYMVR A RANASD A IL C TVLGQNAVHGAFAGFSGITS C C NTHYVV	502
Bradi3g37020.1.p	431	QKIKMHFKG---IGVHADVKYIDPTYMVR A RANASD A IL C TVLGQNAVHGAFAGFSGITS C C NTHYVV	497
Sobic.007G139500.1.p	428	QKIKTHFKD---IGVPADVKYIDPTYMVR A RANASD A IL C TVLGQNAVHGAFAGFSGITS C C NTHYVV	494
Sobic.002G201700.1.p	430	QKIKKHFKD---IGVPADLKYIDPTYMVR A RANASD A IL C TVLGQNAVHGAFAGFSGITS C C NTHYVV	496
Bradi4g30260.1.p	432	QKIKHFKD---IGVLADIKYIDPTYMVR A RANASD A IL C TVLGQNAVHGAFAGFSGITS C C NTHYAY	498
OsPFK08	428	QKIKSHFKD---IGVPADVKYIDPTYMVR A RANASD A IL C TVLGQNAVHGAFAGFSGITS C C NTHYAF	494
OsPFK10	425	QKIKAHFKE---IGVHSdvKYIDPTYMVR A RANASD A IL C TVLGQNAVHGAFAGFSGITTG C C NTHNVY	491
Sobic.001G253300.1.p	425	QKIKSHFKD---IGVHSdIKYIDPTYMVR A RANASD A IL C TVLGQNAVHGAFAGFSGITTG C C NTHNVY	491
Bradi3g25910.2.p	427	QKIKSHFNE---IGVHSdvKYIDPTYMVR A RANASD A IL C TVLGQNAVHGAFAGFSGITTG C C NTHNVY	493
Cre06_g262900.t1.2	433	NEFKKHFKG-----EADIKYIDPSYMI S IRSVP T TSNDR I RY C KVLGQAVHGAFAGFTDVTGLVNTHYVV	496
Vocar20003037m	427	NELKKHFKG-----DADIKYIDPSYMI S IRSVP T TSNDR I RY C KVLGQAVHGAFAGFTDVTGLVNTHYVV	490
Cre12_g553250.t1.2	417	DKFKAYFKF-----DADIKYIDPSYMI S IRSVP T TSNDR I RY C KILAHNAHVHGAFAGFTGITVGLVNTHYVV	479
Vocar20006307m	418	EKFAYFKF-----DADIKYIDPSYMI S IRSVP T TSNDR I RY C KILAHNAHVHGAFAGFTGITVGLVNTHYVV	480
Medtr6g090130.1	350	QSIKDHFAREK-TLPIT-LKYIDPTYMIRAVPSNASDNVY C TLLAQS A VHGAMAGYTGYTSLGVNGRQTY	417
Medtr8g102190.1	354	HKLKDYFAKQK-TMGI T -LKYIDPTYMIRAVPSNASDNVY C TLLAQS A VHGAMAGYTGTFTSGLVHGRQAY	421
AtPFK3	353	QSIKDHFNQKK-MVMN--LKYIDPTYMIRAVPSNASDNVY C TLLAQS A VHGAMAGYTGYISGLVNGRQTY	419
AtPFK7	352	QSIKDHFKKNK-MVMN--LKYIDPTYMIRAVPSNASDNVY C TLLAQS A VHGAMAGYTGYTSLGVNGRQTY	418
Sobic.010G041400.1.p	412	QKINEYFKKNK-MTIN--LKYIDPTYMIRAVPSNASDNVY C TLLAQS A VHGAMAGYTGYTIGQVNGRHC C	478
Bradi4g49300.2.p	411	QKINEHFKKTK-TTIN--LKYIDPTYMIRAVPSNASDNVY C TLLAQS A VHGAMAGYTGYTIGFTVGVNGRHC C	477
OsPFK06	419	QKIKEHFKKIK-TTIN--LKYIDPTYMIRAVPSNASDNVY C TLLAQS A VHGAMAGYTGYTIGFTVGVNGRHC C	485
AtPFK1	355	QRICKDHFAK-K-MTLT--LKYIDPTYMIRAVPSNASDNVY C TLLAQS A VHGAMAGYTGYTIGFTVGVNGRHTY	420
Solytc08g066100.2.1	354	HKIRDHFCKKL-KMPIT-LKYIDPTYMIRAVPSNASDNVY C TLLAQS C VHGAMAGYTGYTSGIVNGRQTY	421
Solycl2g095880.1.1	354	HKIRDHFAKKT-KMPIT-LKYIDPTYMIRAVPSNASDNVY C TLLAQS C VHGAMAGYTGYTSGIVNGRQTY	421
Medtr3g110395.1	354	HKIKDHFAKEN-KM A IV-LKYIDPTYMIRAVPSNASDNVY C TLLAQS A VHGAMAGYTGYTSGIVNGRHTY	421
AtPFK6	351	HKIKEHFKAKH-VMDIT-LKYIDPTYMIRAVPSNASDNVY C TLLAQS A VHGAMAGYTGYTSGIVNGRHTY	418
Solytc04g072580.1.1	342	TRIKEHFSKEK-KMMIN-LKYIDPTYMIRATASN D NMY C TLLAQS A VHGAMAGYTGYTSGIVNGRHTY	409
Solytc07g045160.2.1	353	ERIKEHFSKQK-KMLIN-LKYIDPTYMIRAVPSNASDNVY C TLLAQS A VHGAMAGYTGYTSGIVNGRHTY	420
OsPFK01	388	QKIKDHFKKKR-NFPIT-LKYIDPTYMIRAVRSNASDNVY C TLLAQS A HLGHAMAGYTGYTGFVAPVNGRHY	455
Sobic.003G034700.1.p	390	QKIKDHFKKKP-SFPIT-LKYIDPTYMIRAVRSNASDNVY C TLLAQS A HLGHAMAGYTGYTGFVAPVNGRHY	457
Bradi2g05720.1.p	400	QKIKDHFKKKT-NFPIT-LKYIDPTYMIRAVRSNASDNVY C TLLAQS A HLGHAMAGYTGYTGFVAPVNGRHY	467
OsPFK04	395	AKIKDHFKKKA-NFPIT-LKYIDPTYMIRAVPSNASDNVY C SLLAQS A HLGHAMAGYTGYTGFVAPVNGRHY	462
Bradi2g33290.1.p	389	QKIKEHFKKKT-NLPIT-LKYIDPTYMIRAVPSNASDNVY C TLLAQS A HLGHAMAGYTGYTGFVAPVNGRHY	456
Sobic.001G052500.1.p	390	QKIKEHFKKKP-RFPIT-LKYIDPTYMIRAVPSNASDNVY C TLLAQS A HLGHAMAGYTGYTGFVAPVNGRHY	457
Sobic.009G071800.1.p	391	HKIKEHFKKKP-SFPIT-LKYIDPTYMIRAVPSNASDNVY C TLLAQS A HLGHAMAGYTGYTGFVAPVNGRHY	458
Medtr2g100710.1	354	QKIKDHFRERSK-KIIN--LKYIDPTYMIRAVPSNASDNVY C TLLAQS A VHGAMAGYTGYTGFVAPVNGRNC C	420
OsPFK02	423	HKIKDY C KNKK-MEMT--I K YIDPTYMIRAVPSNASDNVY C TLLAQS A HLGHAMAGYS-FTVGMVNGRHY	488
Bradi2g49280.1.p	422	HKIKDY C KSKK-MEMT--I K YIDPTYMIRAVPSNASDNVY C TLLAQS A HLGHAMAGYS-STVGMVHGRHY	487
Sobic.003G290000.1.p	433	HKIKDY C KSKK-MEMT--I K YIDPTYMIRAVPSNASDNVY C TLLAQS A HLGHAMAGYS-FTVGMVNGRHY	498
Sobic.009G204600.1.p	431	HKIKDY C KSKK-MEMT--I K YIDPTYMIRAVPSNASDNVY C TLLAQS A HLGHAMAGYS-FTVGMVNGRHTY	496
Bradi2g19326.2.p	411	HKIKDHFKSKK-VEMT--I K YIDPTYMIRAVPSNASDNVY C TLLAQS A HLGHAMAGYS-FTVGMVNGRHTY	476
OsPFK05	425	HKIKDHFKSKK-MEMT--I K YIDPTYMIRAVPSNASDNVY C TLLAQS A HLGHAMAGYS-FTVGMVNGRHY	490
AtPFK4	404	QQIKDHFTNRV-KMMIN-MKYIDPTYMIRAVPSNASDNVY C TLLAQS A VHGAMAGYTGYTGFVAPVNGRHTY	471
Solytc03g093520.2.1	414	QQIKDHFTNER-KMTIN-MKYIDPTYMIRAVPSNASDNVY C TLLAQS A VHGAMAGFTGFTVGPVNSRHY	481
Medtr4g090300.1	420	NKIKDHFTKLP-KMVNN-MKYIDPTYMIRAVPSNASDNVY C TLLAQS A VHGAMAGYS-GFTVGPVNSKHAY	487
Sobic.006G114700.1.p	379	SELGRWKWREH-PDELFTVKYIDPTYMIRAVPANA D ONLY C TLLAQS A HGVMAGFTGFTVGPVNGTYSY	447
Bradi5g12982.1.p	362	SEVGRWKWREH-PSELF T VKYIDPTYMIRAVPANA D ONLY C TLLAQS A HGIMAGFTGFTVGPVINGTYSY	430
OsPFK03	161	SELGKWKWREH-PSELF T VKYIDPTYMIRAVPANA D ONLY C TLLAQS A HGIMAGFTGFTVGPVINGNYSY	229
AtPFK2	338	SVLKAWWEREH-PDELFTVKYIDPTYMIRAVPANA D ONLY C TLLAQS A HGVMAGFTGFTVGPVINGNYAY	406
Medtr4g134290.1	357	SELNKWWDRDH-PGEFTVKYIDPTYMIRAVHANA D ONLY C TLLAQS A HGVMAGFTGFTVVAAPINGNYAY	425
Solytc04g015200.2.1	353	SELNKWWDRDH-PNELFTVKYIDPTYMIRAVPANA D ONLY C TLLAQS A HGVMAGFTGFTVVAAPINGNYAY	421
OsPFK09	358	AEMRAWWEEEH-AGEVFTVKYIDPTYMIRAVPANA D ONLY C TLLAQS A HGAMAGYTGFVSGTINGNYAY	426
TbPFK	355	EKVKAFLKANKSRYPDSTVKYIDPSYMI A R C PPS A ND A LF C ATLATIAV F AMAGAT G CIIAMRHNNYIL	424
Clustal Consensus	58	:*****:****: . . * . * . : * : * . : . : . :	79

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Solyc04g014270_2.1	501	FPIPEVIISKPRVVDPNNSRMWHR C LTSI G QPDEFI-----	533
Solyc11g010450_1.1	500	FPIPEVIAQPKVVDPNNSRMWHR C LTSI G QPDEFI-----	532
AtPFK5	505	IPIPEVIAYPKSVDPNNSRMWHR C LTSI G QPDEFI-----	537
Medtr5g032570_1	501	FPIPEVISHPQLVDPNNSRMWHR C LTSI G QPDEFI-----	533
Medtr8g069040_1	497	FPIPEVISHPRIVDPNNSRMWHR C LTSI G QPDEFI-----	529
OsPFK07	503	LPITEVITVPKRVPNPNNSRMWHR C LTSI G QPDEFH-----	535
Bradi3g37020_1.p	498	LPITEVITSKRVNPNSRMWHR C LTSI G QPDEFH-----	530
Sobic_007G139500_1.p	495	LPITEVITASKRVPNPNNSRMWHR C LTSI G QPDEFH-----	527
Sobic_002G201700_1.p	497	LPITEVITTPKHVNPNNSRMWHR C LTSI G QPDEFH-----	529
Bradi4g30260_1.p	499	LPITEVITTPKHVNPNNSRMWHR C LTSI G QPDEFD-----	531
OsPFK08	495	LPITEVITKPKRVPNPNNSRMWHR C LTSI G QPDEFH-----	527
OsPFK10	492	LPISEVIKSTRFVDPNNSRMWHR C LTSI G QPDEFH-----	524
Sobic_001G253300_1.p	492	IPIPEVIKSTRFVDPNNSRMWHR C LTSI G QPDEFH-----	524
Bradi3g25910_2.p	494	IPIPEVIKSTRFVDPNNSRMWHR C LTSI G QPDEFH-----	526
Cre06_g262900_t1.2	497	IPIPIIIQAARKVNPKGRRNNRLITAI R QPDMA-----	529
Vocar20003037m	491	IPIPIIIQAPRKVNPKGRRNNRLIAAI R QPDES-----	523
Cre12_g553250_t1.2	480	IPIPVIIQAPRKVDPRKAKANRLLRAAIGQPSFQ-----	512
Vocar20006307m	481	IPIPVIIQAPRKVDPRKAKANRLLRAAIGQPSFT-----	513
Medtr6g090130_1	418	IPFYRITERQNVVITDRMWARLSSTNQPS E MEVKSDEDTKGENSLDELPDH C SEDTSVDEITHNLG	487
Medtr8g102190_1	422	IPFNKRINEGQNTVITDRMWARLSSTNQPS E LIAKTAVEEKKKEEEEEDSFNL-----	475
AtPFK3	420	IPFYRITERQNHVVIIDRMWARLSSTNQPS E LGPKDVF-NKEKPMSALLDDGN C NGVVDPPVTKEIT	488
AtPFK7	419	IPFYRITERQNVVITDRMWARLSSTNQPS E LGPKDTSSEEKKELPETPLDDG-----AVDIPPVTKEV	484
Sobic_010G041400_1.p	479	IPFYRITERQNKRVSIIDRMWARLSSTNQPS E LCNKKVVEEAKEQERAALLDGSPSHRKG-----	539
Bradi1g49300_2.p	478	IPFYRITERQNKVSIDRMWARLSSTNQPS E LCQDVDEAKVEDERTAKLNDGSPSNPKVEDGLASSNS	547
OsPFK06	486	IPFYRITERQNKVSIDRMWARLSSTNQPS E LSKKDVEDAKMEEERASKFFDGPPNPKVEDKVASNGK	555
AtPFK1	421	IPFNRITEQNKVVITDRMWARLSSTNQPS E MKQADKIHSNQLVGEPGTMKW-----	473
Solyc08g066100_2.1	422	IPFNRITEQNKVVITDRMWARLLASTNQPS E LSTNDIVQVHQHSQSQQLNQDENESITGTYLKVLD	491
Solyc12g095880_1.1	422	IPFNRITEQNKVVITDRMWARLSSTNQPS E LRVKDIEEIKKEEQQTQLLDGDNNVHENSGH-----	485
Medtr3g110395_1	422	IPFNRITEKMNKVITDRMWARLSSTNQPS E LRVKDIEEIKKEEQQTQLLDGDNNVHENSGH-----	491
AtPFK6	419	IPFNRITEKMNKVITDRMWARLSSTNQPS E MNPKGTTEFTD-----	462
Solyc04g072580_1.1	410	IPFDRITEQNKVVDITDMMAQLLSSTNQPS E LSTARSDADNEANKDEEPPQLSDEETNQLSFLTRVD	479
Solyc07g045160_2.1	421	IPFNRIIEQNKVVTIDRMWARLSSTNQPS E LRTR-VDIKANKDEEPPQLSDDATTDDNLMEQKIL	488
OsPFK01	456	IPFYRITERQNKVVITDRMWARV C STNQPS E LSHEDVEH1KHDDDE-HHLHNTQLEGEESPVKDSSC	524
Sobic_003G034700_1.p	458	IPFYRITERQNKVVITDRMWARV C STNQPS E LSHEDVENMKHDDDE-HHLHNTQLEGEESPVKDASKC	526
Bradi2g05720_1.p	468	IPFYRITERQNKVVITDRMWARV C STNQPS E LSHEDVENMKHDDDE-QPAK C SPKC	535
OsPFK04	463	IPFYRITERQNKVVITDRMWARV C STNQPS E LSLSTDEVEKAQGD---DEEFIVPLVEGENSLVKAPP	528
Bradi2g33290_1.p	457	IPFYRITERQNKVVITDRMWARV C STNQPS E LSHEDVEKARQD---EEEPHVPLIEGENSLVRTSPMS	522
Sobic_001G052500_1.p	458	IPFYRITERQNKVSIDRMWARV C STNQPS E LTTEEDVEGAGLEEEEFPHMMPLVEGGMQRQLGQCPV	527
Sobic_009G071800_1.p	459	IPFYRITERQNKVVITDRMWARV C STNQPS E LTTHEDVEAGLDEEEP---HMPLVEGEYALVRSPSMC	525
Medtr2g100710_1	421	IPFHLINEGQKRVVITDRMWARLSSTNQPS E VNPQHITEEAKVE-----	465
OsPFK02	489	IPHRVTRSTRNKVKITDRMWARLSSTNQPS E LSQKDIDAAREADKLASKSPVNVNTKEHGENVKPANG	558
Bradi2g49280_1.p	488	IPHRVTRSTRNKVKITDRMWARLSSTNQPS E LTQKDIDAIREADRLANRPVPAGTSSELREHTEKHPAS	557
Sobic_003G290000_1.p	499	IPHRVTRSTRNKVRITDRMWARLSSTNQPS E LSQKDIDAAREADKAANAKNSAPALANGEK-----	561
Sobic_009G204600_1.p	497	IPFYRVTSTRNKVITDRMWARLSSTNQPS E LSQKDIDEASEADRLANRPPLPTGASSRVARSFQDQSS	566
Bradi2g19326_2.p	477	IPFYRVTSTRNKVITDRMWARLSSTNQPS E LSQKDIDEAREADRLANKPPLPTGASSRVARSFQDQSS	546
OsPFK05	491	IPFYRVTSTRNKVITDRMWARLSSTNQPS E LSQKDIDEAKENDRINTKPLPTGLSHHVANSFDQSS	560
AtPFK4	472	IPISQVTEVNTVKITDRMWARLSSTNQPS E LTGEGALQNVIDMETQEKFIDNMKISSI-----	530
Solyc03g093520_2.1	482	IPINRVTETTNTVNMIGRMWARLSSTNQPS E FVN-HOTLRERVDKNITIDAINNMKINST-----	539
Medtr1g090300_1	488	IPIA C TERNTVQLTGRMWARLSSTNQPS E FSVS--SDQQRVEKEMVEDTNKMNITSI-----	543
Sobic_006G114700_1.p	448	IPLEDVAVAKNPVDVN D HKNAWVRSV T NQPS E FLKSQA-----	484
Bradi5g12982_1.p	431	IPLEDVAVAKNPVDVN D HKNAWVRSV T DQPS E FLKPQDY-----	468
OsPFK03	230	IPLEDVAVAKNPVDVN D HKNAWVRSV T NQPS E FMKPKY-----	266
AtPFK2	407	IPLEEVAKTQNQVNTRDHKNAWVRSV T NQPS E ETTNVKG-----	444
Medtr4g134290_1	426	IPLEDVACAKNPVNTR D HNMWSWVRSV T NQPS E FLKS-----	460
Solyc04g015200_2.1	422	IPDEVAKAKNKVDTRDHKNAWVRSV T NQPS E FIRS-----	456
OsPFK09	427	IPMDEVAEAKNPVDTR D HKNAWVRSV T TNQPS E IRAGPTS-----	465
TbPFK	425	IPIKVATSVRRVLDLRGQLRQVREITV D DLGSDVRLARKLEIRRELEAINRNDRDLHEELAKL-----	487
Clustal Consensus	79	.*. : . * : :	83

Solyc04g014270.2.1	533	-----	533
Solycl1g010450.1.1	532	-----	532
AtPfk5	537	-----	537
Medtr5g032570.1	533	-----	533
Medtr8g069040.1	529	-----	529
OsPfk07	535	-----	535
Bradi3g37020.1.p	530	-----	530
Sobic.007G139500.1.p	527	-----	527
Sobic.002G201700.1.p	529	-----	529
Bradi4g30260.1.p	531	-----	531
OsPfk08	527	-----	527
OsPfk10	524	-----	524
Sobic.001G253300.1.p	524	-----	524
Bradi3g25910.2.p	526	-----	526
Cre06.g262900.t1.2	529	-----	529
Vocar20003037m	523	-----	523
Cre12.g553250.t1.2	512	-----	512
Vocar20006307m	513	-----	513
Medtr6g090130.1	488	CLAPLA VPLRTGGISGV	505
Medtr8g102190.1	475	-----	475
AtPfk3	489	K-----	489
AtPfk7	485	K-----	485
Sobic.010G041400.1.p	539	-----	539
Bradi1g49300.2.p	548	NGVK-----	551
OsPfk06	556	AVK-----	558
AtPfk1	473	-----	473
Solytc08g066100.2.1	492	LLPCLSCGQ-----	500
Solycl2g095880.1.1	485	-----	485
Medtr3g110395.1	492	PTQLMEGDKSKDNQKSRNLADSDSCKK	519
AtPfk6	462	-----	462
Solytc04g072580.1.1	480	INEANKNKEPPTELSDFGETN-----	499
Solytc07g045160.2.1	489	TF-----	490
OsPfk01	525	NGTAAPV-----	531
Sobic.003G034700.1.p	527	NGTV-----	530
Bradi2g05720.1.p	536	NGFAAPL-----	542
OsPfk04	529	ANAGDRAALCNGAA-----	542
Bradi2g33290.1.p	523	MCNGHGHF-----	530
Sobic.001G052500.1.p	528	DVQRANGNGHL-----	538
Sobic.009G071800.1.p	526	NGNGHLCSGAA-----	536
Medtr2g100710.1	465	-----	465
OsPfk02	559	EK-----	560
Bradi2g49280.1.p	558	ESANGEK-----	564
Sobic.003G290000.1.p	561	-----	561
Sobic.009G204600.1.p	567	CSSNGEI-----	573
Bradi2g19326.2.p	547	SSSNGBI-----	553
OsPfk05	561	SSNSSQI-----	567
AtPfk4	530	-----	530
Solytc03g093520.2.1	539	-----	539
Medtr1g090300.1	543	-----	543
Sobic.006G114700.1.p	484	-----	484
Bradi5g12982.1.p	468	-----	468
OsPfk03	266	-----	266
AtPfk2	444	-----	444
Medtr4g134290.1	460	-----	460
Solytc04g015200.2.1	456	-----	456
OsPfk09	465	-----	465
TbPfk	487	-----	487
Clustal Consensus	83		83

Supplementary Figure S4 (next page): Significance of the remaining conserved Cys for redox regulation. Cys to serine single and double mutations were introduced into *A. thaliana* AtPfk5 (**A**) and AtPfk3 (**B;C**). The variants were transiently overexpressed in tobacco leaves. PFKs from the tobacco leaf samples were extracted with buffer containing 5 mM β -mercaptoethanol (β -ME). After initial activity determination, samples were oxidized with 2.5 mM sodium tetrathionate (TT) for 20 min, and afterwards re-reduced with 5 mM dithiotreitol (DTT). Upper case letters indicate significant differences for each isoform to buffer and GFP control, lower case letters indicate significant differences among treatments for each isoform at $p < 0.05$ (ANOVA, Post-hoc Tukey test, $n=3-6$). The results are means \pm SD. (**D-F**) Details of the protein alignment of conserved Cys in PFKs from *A. thaliana* and *O. sativa*. The mutated Cys are marked with an arrow.



D

OsPfk01	YMIRAVRSNASDNVYCTLLA	430
OsPfk04	YMIRAVPSNASDNVYCSLLA	437
AtPfk6	YMIRAIIPANASDNVYSTLLA	393
AtPfk3	YMIRAVPSNASDNVYCTLLA	394
AtPfk7	YMIRAVPSNASDNVYCTLLA	393
OsPfk06	YMIRAIIPSNASDNVYCTLLA	460
AtPfk1	YMIRAVPSNASDNVCCTLLA	395
OsPfk02	YMIRRAIIPSNASDNVYCTLLA	464
OsPfk05	YMIRRAIIPSNASDNVYCTLLA	466
AtPfk4	YMIRRAIIPSNASDNVYCTLLA	446
AtPfk2	YMIRAVPANATDNLYCTLLA	381
OsPfk03	YMIRAVPANATDNLYCTLLA	204
OsPfk09	YMIRAVPANAGDNLYCTLLA	401
OsPfk07	YMVRACRANASDAILLCTVLG	477
OsPfk08	YMVRACRANASDAILLCTVLG	469
OsPfk10	YMVRAVRANASDAILLCTVLG	466
AtPfk5	YMIRAVRANASDGILCTVLG	479

↑

E

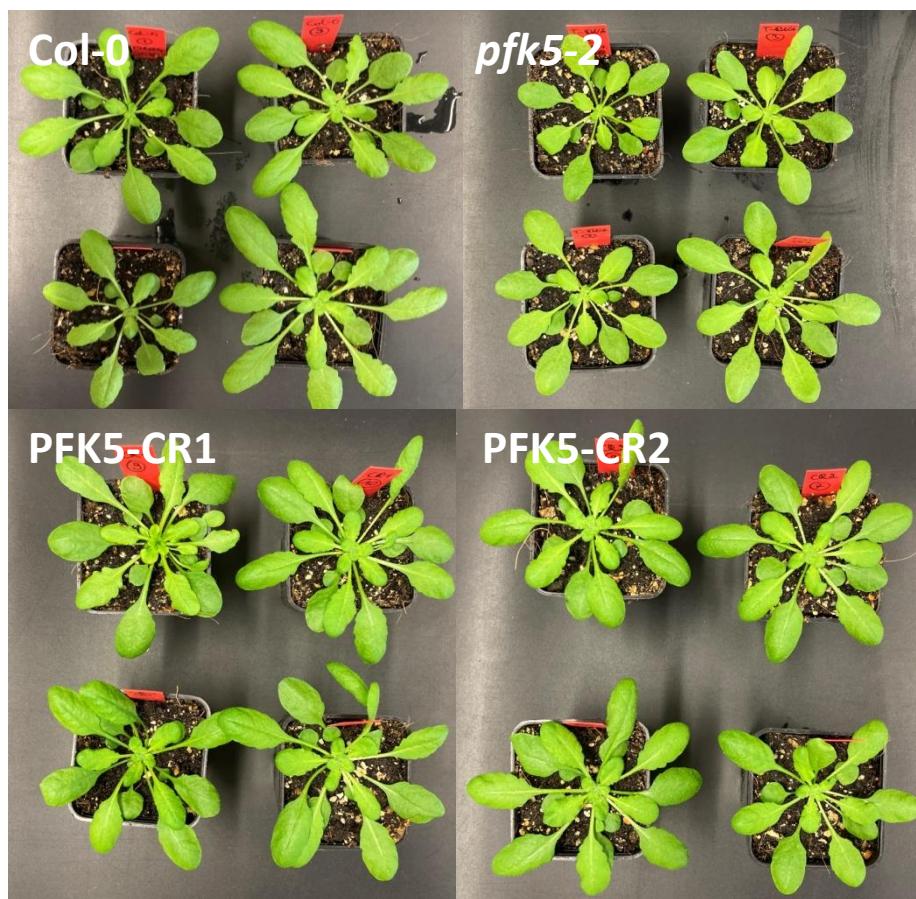
OsPfk01	VNAAIIVTCGGLCPG	140
OsPfk04	VSAAIIVTCGGLCPG	147
AtPfk6	VRACIIVTCGGLCPG	106
AtPfk3	VHACIIVTCGGLCPG	105
AtPfk7	VHACIIVTCGGLCPG	105
OsPfk06	VHACIIVTCGGLCPG	172
AtPfk1	VLACIIVTCGGLCPG	106
OsPfk02	VKACIIVTCGGLCPG	175
OsPfk05	VKACIIVTCGGLCPG	177
AtPfk4	VKACIIVTCGGLCPG	156
AtPfk2	VKAIIIVTCGGLCPG	90
OsPfk03	-----	1
OsPfk09	VRAAIIFTTCGGLCPG	103
OsPfk07	VKAAIIVTCGGLCPG	185
OsPfk08	VKAAIIVTCGGLCPG	183
OsPfk10	VKAGIIVTCGGLCPG	180
AtPfk5	VKAIIITTCGGLCPG	193

↑

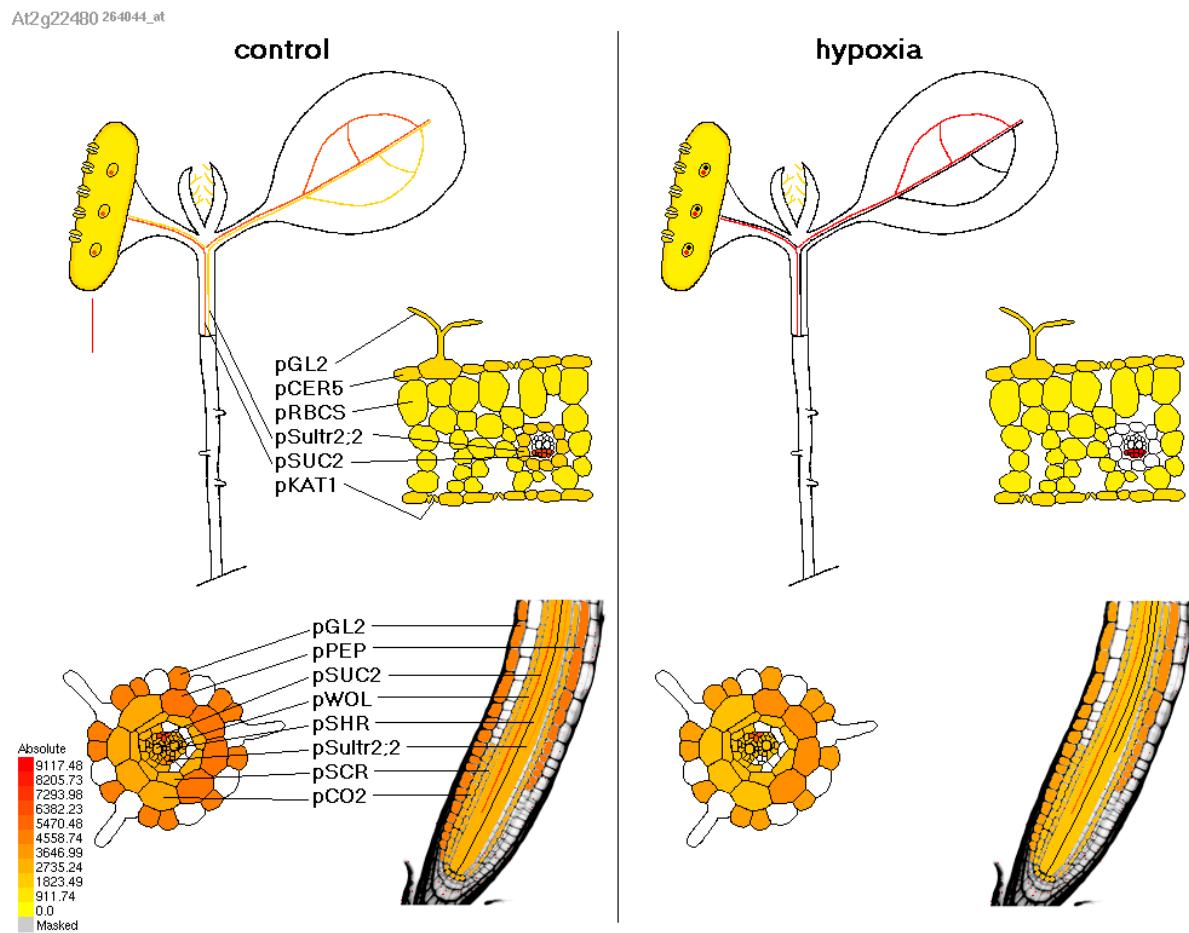
F

OsPfk01	DCCLIPESPSPFYTEGKGGLLE	336
OsPfk04	DLCLIPESPSPFYTEGKGGLLE	343
AtPfk6	DCCLIPESPSPFYTEGKGGLYE	302
AtPfk3	DCCLIPESPSPFYTEGEGGLFE	301
AtPfk7	DCCLIPESPSPFYTEGEGGLFE	301
OsPfk06	DCCLIPESPSPFYTEGEGGLFR	368
AtPfk1	DCCLIPESPSPFYIEGEGGLFE	302
OsPfk02	DCCLIPESPSPFYIEGEGGLFE	371
OsPfk05	DCCLIPESPSPFYMDGEGGLLQ	373
AtPfk4	DCCLIPESPSPFYIEGKGGLFE	352
AtPfk2	DCCLIPESPEMDFYIEGKGGLFE	286
OsPfk03	DCCLIPESPEVDFYIEGKGGLFE	109
OsPfk09	DCCLIPESPEDEFYLRGAGGLFD	301
OsPfk07	DVCLIPESPVPEFTLDGEYGVLR	382
OsPfk08	DVCLIPESVSEFTLDGEHGVMR	380
OsPfk10	DICLIPESPVPEFTLDGPNGVLQ	377
AtPfk5	DICLIPESPVPEFTLDGPNGVLK	390

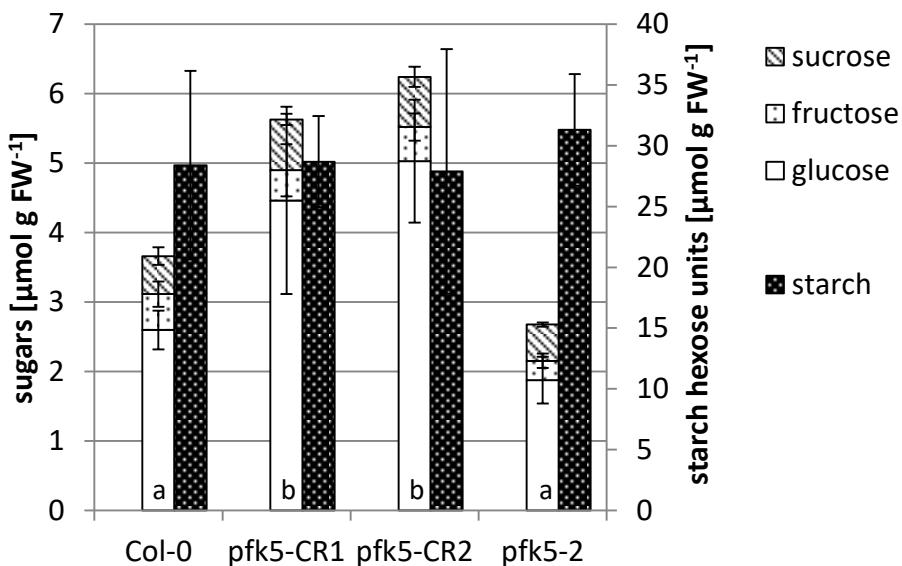
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Supplementary Figure S5: Representative pictures of five-week-old *pfk5-CR1*, *pfk5-CR2*, *pfk5-2* and wildtype Col-0 plants grown on soil (representative pictures from the experiment in Figure 9C). One pot has the width of 5.3 cm.



Supplementary Figure S6: Expression atlas of *AtPFK5* from the eFP browser (<http://bar.utoronto.ca/>, Winter et al. 2007, Mustroph et al. 2009).



Supplementary Figure S7: Sugar content in leaves of five-week-old *pfk5-CR1*, *pfk5-CR2*, *pfk5-2* and wildtype Col-0 plants grown on soil, harvested at the end of the day. Data are means \pm SD of n=4. Letters indicate significant differences at $p < 0.05$ for glucose content (ANOVA, Post-hoc Tukey test). Fructose, sucrose and starch contents were not significantly different between genotypes.

Supplementary Table S1 (separate Excel file): Primer sequences (a) and Protein IDs (b) used in this study

Supplementary References:

- Huerta-Cepas J, Serra F, Bork P (2016) ETE 3: Reconstruction, Analysis, and Visualization of Phylogenomic Data. Mol Biol Evol 33: 1635-1638.
- Mustroph A, Zanetti ME, Jang CJ, Holtan HE, Repetti PP, Galbraith DW, et al. (2009) Profiling translatomes of discrete cell populations resolves altered cellular priorities during hypoxia in Arabidopsis. Proc Natl Acad Sci USA 106: 18843-18848.
- Winter D, Vinegar B, Nahal H, Ammar R, Wilson GV, Provart NJ (2007) An "Electronic Fluorescent Pictograph" browser for exploring and analyzing large-scale biological data sets. PLoS One 2: e718.