

**Supplementary Table S1.** Sequences of oligonucleotide primers used for RT-PCR analysis.

Gene name	Gene ID	Forward or reverse primer (5' - 3') (F or R)
AtMPK1	AT1G10210	5'-ATAGGATCGATGCGTTGAGG-3' 5'-TCGGTACCAACGAGTCACAA-3'
AtMPK2	AT1G59580	5'-TCTGGTCAGTCGGTTGCATA-3' 5'-TCATCTCTGCTCCCAAATCC-3'
AtMPK3	AT3G45640	5'-ATGAACACCGGCGGTGGC-3' 5'-ATGAACACCGGCGGTGGC-3'
AtMPK4	AT4G01370	5'-CTGCTGCACTTCTAACCG-3' 5'-GGAGCTCGATACCAACGTGT-3'
AtMPK5	AT4G11330	5'-GACTTTGGTTTGGCAAGGAC-3' 5'-GACGGATCCTCAAAATGGAA-3'
AtMPK6	AT2G43790	5'-TCTCCTCCTGAACGCAAAT-3' 5'-GATGGATTGGCGAGGATAAG-3'
AtSnRK2.2	AT3G50500	5'-CCGATTATGCCGATTGATTT-3' 5'-TATCGGTCATGAGACGAGCA-3'
AtSnRK2.3	AT5G66880	5'-GCAATGCAGGACGGTTTAGT-3' 5'-GAGCAGGACTTCCATCCAAC-3'
AtSnRK2.6	AT4G33950	5'-AACTTTTCGAGCGAATCTGC-3' 5'-GCCGGGCTACCATCTAATAAC-3'
AtACT2	AT3G18780	5'-GCCGGACTTACCGTTGTATGTACCGTCC-3' 5'-ACAATGGAAGTGAATGGTGAAGGCTGG-3'

Supplementary Table S2.. List of phosphorylated proteins identified by MALDI-TOF MS.

PROTEIN	PI	MR, DA	PEPTIDE MR, DA	PEPTIDE AMINO ACID SEQUENCE
ANNEXIN (ANNAT2) (SPOT 2)	5.76	36243	928.5612; 965.5169 982.4814; 1096.5354 1117.5187; 158.7420 1165.5585; 181.5619 1427.7725 1656.8458	K.HFEKVLRL; R.IKEEYQR.R; K.ELSSDFER.A; K.AFGSWGVTNEK.L; K.SYSDDDFIR.I; K.LLLPLVSTFR.Y; K.MGTDEWGLTR.V; K.MGTDEWGLTR.V; R.AVMLWTLDPER.D; K.SIEEDVAQHTSGDLR.K
NADP-DEPENDENT OXIDOREDUCTASE (SPOT 1)	5.8	38133	1223.5746; 238.7157; 1270.7541; 417.7319; 1600.8006 2234.1640 2527.1566 2861.3954	K.FGFDDAFNYK.E; K.APEALVGLFHGK.N; K.FLEFVLPHIR.E; R.IQGFVVSDFYDK.Y K.MLDAVLVNMNMHGR.I; K.EGETVYVSAASGAVGQLVGLAK.M; K.DYVSGFPTESDFDFTTTTVELR.V; R.MGKPD PSTAALAQAYTPGQPIQGYGVSRI
ALDO/KETO REDUCTASE (SPOT 3)	5.92	37900	810.3996; 835.3664; 971.5091; 1100.5677; 213.6559; 1229.7031; 1367.7360; 374.6794; 1444.8326; 1679.8475	R.GFFASGPK.L; R.GDPEYVR.A; K.FGISYAEGK.R; R.YSNMIPTFK.N; K.NAETPPLSAWK.A; R.VPIEITMGELK.K; K.YIGLSEASASTIR.R; R.DVEEIIPTCR.E; R.ELGIGIVAYSPLGR.G; R.GDPEYVRAACEASLK.R
PYRABACTIN RESISTANCE-LIKE 8 (PYL8) (SPOT 4)	6.07	21397	873.4504; 1187.6611 1360.7544; 2266.1177; 2349.1974	R.ALGQISER.L; K.VQTSSGEKPVRE.E; K.MELIDAAFLLK.G; K.NVIIWGNHSSSQYPDVNHAK.V; R.ELVKDDAWLDGEFISTVQQR.G
GLYCERALDEHYDE-3-PHOPHATE-DEHYDROGENASE (SPOT 5)	6.67	36913	910.4607; 1677.0152; 1734.8526; 1761.8269; 2033.0968; 2172.0374; 2923.4282	K.AATYDEIK.K; K.TLLFGEKPVTVFGIR.N K.DAPMFVVGVNEHEYK.S; K.LVSWYDNEWGYSSR.V; R.FGIVEGLMTTVHSITATQK.T; K.GILGYTEDDVVSTDFVGDNR.S; R.NPEDIPWGEAGADFVVESTGVFTDKDK.A
TRANSLATION INITIATION FACTOR 4A (EF4A), (SPOT 10)	5.47	46674	876.4314; 976.5455; 1004.5385; 104.6503; 1114.6505; 135.5559; 1173.6530; 1348.6169; 1401.7292; 1555.7149; 1589.8197; 1784.7525; 1827.9360	K.VDWLTDK.M; K.GVAINFVTR.D; R.KVDWLTDK.M; R.KGVAINFVTR.D; R.VLITDDLAR.G; R.TWPICCEGR.K; K.RDELTLEGIK.Q; M.AGSAPEGTQFDAR.Q; K.GLDVIQQAQSGTGK.T; K.MFVLDEADEMLSR.G; K.DQIYDIFQLPPK.I; R.DHTVSATHGDMQDQNR.D; R.GIYAYGFEKPSAIQQR.G
BIFUNCTIONAL ENOLASE (SPOT 9)	5.54	47689	765.3841; 806.4558; 1101.5309; 229.6311; 2005.0843; 2324.0910	R.QIFDSR.G; K.YNQLLR.I; K.AGWGVMTSHR.S; K.KAGWGMVMTSHR.S; K.VTAAVPSGASTGIYEALER.D; K.YGQDATNVGDEGGFAPNIQENK.E
MITOGEN-ACTIVATED PROTEIN KINASE11 (MPK11)	5.54	47689	765.3837; 806.4539; 900.4698; 1101.5264; 1117.5288; 212.6180;	R.QIFDSR.G; K.YNQLLR.I; K.TYDLNFK.E; K.AGWGVMTSHR.S; K.AGWGVMTSHR.S; K.MGVEVYHHLK.S;

(SPOT 11)			1549.8799; 1573.8236; 1852.9397; 1896.9037; 2005.0633; 3000.4809	K.AVGNVNNIIGPALIGK.D; K.VNQIGSVTESIEAVK.M; K.LAMQEFMILPVGAASFKE.E; R.IEEELGSEAIYAGVNF.R.K; K.VTAAVPSGASTGIYEALER.D; K.SFVAEYPIVSIEDPFDQDDWEHYAK.M
SCARECROW-LIKE 9 (SCL9) (SPOT 12)	5.66	53344	906.4796; 994.5125; 998.6149; 1025.5364; 1026.4678; 071.6515; 1129.5799; 137.5915; 1475.7779; 1771.8082; 2361.1747	R.WVFPETK.A; R.DSAAVFAWK.G; K.AGIIVLAEGR.L; R.HSLPDGLMR.A; K.DMSQADFGR.L; R.ITIKPQTDR.W; K.DIIMVDHMR.K; R.TEFGPSQPFK.G; R.LVGVSEETTTGVKR.L; K.GETLQEYWWCTER.A; K.DQSDYVSIPIEGPYKPPHYR.Y
KIP-RELATED PROTEIN 4 (KRP4) (SPOT 6)	9.61	31699	738.3476; 815.3790; 1205.6408; 1373.6453; 1418.7262; 1438.7450	R.FEWK.V; R.GADGGPWR.R; K.VGTLGLDMMLR.T; R.SHIWTDTKDR.T; K.EAGFLNAVDEVVR.T; K.FGFEVNTLRPMK.Y
ENOLASE (SPOT 7)	5.79	51477	765.3763; 1101.5415; 1174.6890; 1859.8669; 1896.9358; 2005.0788; 2252.1494; 2324.0840; 2452.1979	R.QIFDSR.G; K.AGWGVMTSHR.S; K.AGAVVSGIPLYK.H; K.VVIGMDVAASEFYSEDK.T; R.IEEELGSEAIYAGVNF.R.K; K.VTAAVPSGASTGIYEALER.D; R.SGETEDTFIADLAVGLSTGQIK.T; K.YGQDATNVGDEGGFAPNIQENK.E; K.KYGQDATNVGDEGGFAPNIQENK.E
ATP SYNTHASE B- SUBUNIT (SPOT 8)	6.18	59713	1173.6724; 262.6395; 1393.8010; 1425.7446; 1699.9394 2061.0296 2186.1362 2539.2323	K.VVDLLAPYQR.G; R.TIAMDGTEGLVR.G; K.VLNTGAPITVPVGR.A; R.VGLTGLTVAEYFR.D; R.LVLEVSHHLGQNVVR.T; R.QISELGIYPAVDPLDSTSR.M; R.IPSAVGYQPTLASDLGALQER.I; R.FEDQEGLPPIMTSLEVQDHPTR.L