**TABLE S3 |** Pearson correlated expression analysis of *GmUBC9*. The annotation of correlated genes (an important part of it) (**support** **FIGURE S4**). Protein sequence and functional comments came from Phytozome site (https://phytozome.jgi.doe.gov/pz/portal.html#). Subcellular localization prediction was performed at sites PSORT II Prediction (https://psort.hgc.jp/form2.html) and Predict Protein (https://www.predictprotein.org/home).

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Number | Gene ID | The protein sequence | Results of the k-NN Prediction by PSORT II Prediction | Results of the prediction by Predict Protein | Annotation |
| 1 | Glyma.01G154400.1 | >MPQNCIAPKPEFCNSHNSVEGPPEMTEPHNSTVLSYPMQANEQQQQPFPKLIMYPITLKFEELVYKVKLEQKGGCWGSTWTCKEKTILNGITGVVCPGEILAMLGPSGSGKTTLLTALGGRLNGKLSGKITYNGQPFSGAMKRRTGFVAQDDVLYPHLTVTETLVFTALLRLPNTLKRDEKVQHVERVITELGLTRCRSSMIGGPLFRGISGGEKKRVSIGQEMLINPSLLLLDEPTSGLDSTTAQRILNTIKRLASGGRTVVTTIHQPSSRLYYMFDKVVLLSEGCPIYYGPASTALDYFSSVGFSTCVTVNPADLLLDLANGIAPDSKHATEQSEGLEQERKQVRESLISAYEKNIATRLKAEVCSLEANNYNITKDACARNSIKPDQWCTSWWHQFKVLLQRGVRERRYEAFNRLRIFQVVSVAFLGGLLWWHTPESHIDDRVALLFFFSVFWGFYPLYNAVFTFPQERRMLIKERSSGMYRLSSYFLARTIGDLPLELALPTAFVFIIYWMGGLKPDPMTFILSLLVVLYSVVVSQSLGLAFGAILMEVKQATTLASVTTLVFLIAGGYYIQQIPPFIVWLKYLSYSYYCYKLLLGVQYNENDYYECSKEELCKVADFPPIKSMGLNHLWVDVCIMAMMLVGYRLVAYLALHRVR | *k* = 9/2352.2 %: plasma membrane26.1 %: endoplasmic reticulum8.7 %: nuclear8.7 %: mitochondrial4.3 %: vesicles of secretory system>> prediction for QUERY is pla (k=23) | Predicted localization for the Eukarya domain: Plasma Membrane (GO term ID: [GO:0005886](http://amigo.geneontology.org/cgi-bin/amigo/term_details?term=GO:0005886)) Prediction confidence 18C:\Users\f\Desktop\plasmaMembrane.PNG | (1 of 5) PTHR19241:SF213 - ABC TRANSPORTER G FAMILY MEMBER 14 |
| 2 | Glyma.07G119100.1 | >MAEEESPSVMPKVITFLSSLLERVAESNDHNQQHQKISVFHGLTRPNISIHSYLERIFKYANCSPSCFVVAYVYLDRFTQRQPSLPINTFNVHRLLITSVMVAAKFMDDMYYNNAYYAKVGGITKIEMNFLELDFLFGLGFHLNVTPGTFQAYCVNLQREMLLIQQPLNFADSTLNLGKSLKAHLCFNEDESSHQKQQQLAV | k = 9/2360.9 %: cytoplasmic13.0 %: nuclear4.3 %: Golgi4.3 %: cytoskeletal4.3 %: vacuolar4.3 %: endoplasmic reticulum4.3 %: vesicles of secretory system4.3 %: mitochondrial>> prediction for QUERY is cyt (k=23) | Predicted localization for the Eukarya domain: Cytoplasm (GO term ID: GO:0005737) Prediction confidence 25C:\Users\f\Desktop\cytoplasm.PNG | (1 of 6) PTHR15615:SF28 - CYCLIN-U4-1 |
| 3 | Glyma.09G250300.1 | >MAFVTTAEVCDANPQLILSGELRALQPVFQIYGRRQVFSGPIVTLKVFEDNVLVREFLEEKGNGRVLVVDGGASLRCAILGGNPVVQAQNNGWAGIVVNGCIRDVDEINGCDIGVRALASHPMKANKKGMGEKHVPVNIAGTRISDGDWLYADTDGILISRTELSV | k = 9/2360.9 %: cytoplasmic17.4 %: nuclear13.0 %: mitochondrial4.3 %: vesicles of secretory system4.3 %: vacuolar>> prediction for QUERY is cyt (k=23) | Predicted localization for the Eukarya domain: Cytoplasm (GO term ID: GO:0005737) Prediction confidence 24C:\Users\f\Desktop\cytoplasm.PNG | (1 of 4) 4.1.1.3 - Oxaloacetate decarboxylase / Oxaloacetate carboxy-lyase |
| 4 | Glyma.13G306700.1 | >MATGGDGDTSKQELFQLIKRFGAYVTFKISNLFPLSLHNLDLRSIGAVAGLAVAIVFTWRLLRSPSGSQRRQQKRQGPSSSNPGVGTNSNSNASVVPSDACSPSDDSRAQNVVDEFFQPVKPTLGQIVRQKLSEGRKVTCRLLGVILEESSPEELQKQATVRSSVLEVLLEVTKFCDLYLMERVLDDESEKRVLVALEEAGVFTSGGLVKDKVLFCSTENGRSSFVRQLEPDWHIDSNPEIVTQLARFIKYQLHVSPYKTERTAANVFSAPSLEQFFGSI | k = 9/2339.1 %: cytoplasmic21.7 %: nuclear17.4 %: mitochondrial8.7 %: endoplasmic reticulum4.3 %: Golgi4.3 %: peroxisomal4.3 %: vesicles of secretory system>> prediction for QUERY is cyt (k=23) | Predicted localization for the Eukarya domain: Nucleus (GO term ID: GO:0005634) Prediction confidence 27C:\Users\f\Desktop\nucleus.PNG | (1 of 2) PTHR34126:SF1 - PEROXISOME BIOGENESIS PROTEIN 22 |
| 5 | Glyma.20G054900.1 | >MPHKAKHSKKRGSHGISNLVAHASSQAQSYAPTLSHIPSSIPTTLDPLSRSLLPQNVFSSILNLICQAAYQGYSMLEELPQHSSKLAQPFAPTITDIRPSIPIAQDLVSQSNIPSCSMLRKSKRSKKRVSHAISNLMPHASSQGHSKPMELPLQPSELAQPCAPPVVLVPSSISVTQDPVLPSDPSSIPVNQDPVLPSDPSSIPVNQDLVSPSDSSSIPANQDPSSIAVNQDPVSPSDSSSIPVNQDPVSPSDPSSSPILKI | k = 9/2352.2 %: mitochondrial39.1 %: nuclear8.7 %: cytoskeletal>> prediction for QUERY is mit (k=23) | Predicted localization for the Eukarya domain: Plasma Membrane (GO term ID: GO:0005886) Prediction confidence 8C:\Users\f\Desktop\plasmaMembrane2.PNG | (1 of 2) PTHR33144:SF3 - PLANT TRANSPOSASE (PTTA/EN/SPM FAMILY) |