

Supplementary material

Table S1 PCR primers used in this work

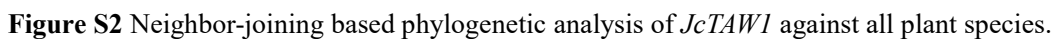
Primer	sequence(5'to3')	bases
Pt7Up-Fw	ACCGCGAAATTAATACGACTCAC	23
Tt7Dw-Rv	ACCGGATATAGTTCCTCCTTTTCAG	24
JcTAW1-Fw	GTACATCTCTTTATCCAAACATG	23
JcTAW1-Rv	CAACACTAGAAAACATAAACCCCT	23
JcTAW1-5Kn	GTTATGGTACCGACGCAACAATGGCTGCTGGCAATGGGAGTT	42
JcTAW1-3Sc	GCGGCGAGCTCACTACATGAGGAATAATC	48
JcTAW1-iFw	AgCATCgCCATCTCCTCAAC	20
JcTAW1-iRv	gCCTgTgCATCTCTCACTTC	20
Nt18S-iFw	gAAACggCTACCACATCCAAG	21
Nt18S-iRv	ggCAAATgCTTTCgCagTTg	20
35Spro-Fw	GACGTAAGGGATGACGCACAATC	23
NosTer-Rv	GACCGGCAACAGGATTCAATC	21

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1  ATGGCTGCTGGCAATGGGAGTTCTTCAAGAAATGATAATATATCCCCAGCATCGCCATCTCCTCAACCACCGCCAATAGCACCGCCCTCA
   M A A G N G S S S R N D N I S P A S P S P Q P P P I A P P S
91  CTTCCTGAGTCGTTACGAATCTCAAAAAAGACGTGACTGGAATACTTTCGGTCAATACCTAAGAAACCACCGGCCACCTTTAGCTCTG
   L P L S R Y E S Q K R R D W N T F G Q Y L R N H R P P L A L
181 TCACGGTGCAGCGGTGCTCATGTTCTTGAATTTTAAAGATATCTTGACCAATTTGGTAAGACTAAAGTGCATAACCAAACCTTGTCATTC
   S R C S G A H V L E F L R Y L D Q F G K T K V H N Q T C P F
271 TTTGGCCACCTCATCCACCTGCTCCTTGCCCTTGCCCACTTAAACAAGCTTGGGGTAGCCTTGACGCGCTCATCGGACGGCTGAGAGCA
   F G H P H P P A P C P C P L K Q A W G S L D A L I G R L R A
361 GCTTTTGAAGAGAATGGTGGCTTGCTGAGACTAATCCGTTTGGTGCACGCGCCGTCAGACTTTATCTTAGGGAAGTGAGAGATGCACAG
   A F E E N G G L P E T N P F G A R A V R L Y L R E V R D A Q
451 GCCAAAGCTAGAGGAATAGCTTATGAGAAGAAGAAGAAAGAAGCCACAACCTCAACAACAGTTACGATCTGAAAATGGTTACAATAAT
   A K A R G I A Y E K K K R K K P Q P Q Q Q L R S E N G Y N N
541 CAAAGTCTGCAAGCTGGTGGCGCGGTGGTGGATTTGTGGTTGAAAGAAATATGATAAACAGAGGTGTGGTTAATATGGGGAATTTGTCT
   Q S L Q A G G A G G G F V V E R N M I N R G V V N M G N L S
631 GTATTGAACTAA
   V L N *

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Figure S1 The nucleotide sequence of *JcTAW1* gene and its deduced protein sequence. The shadow represents a nuclear localization signal



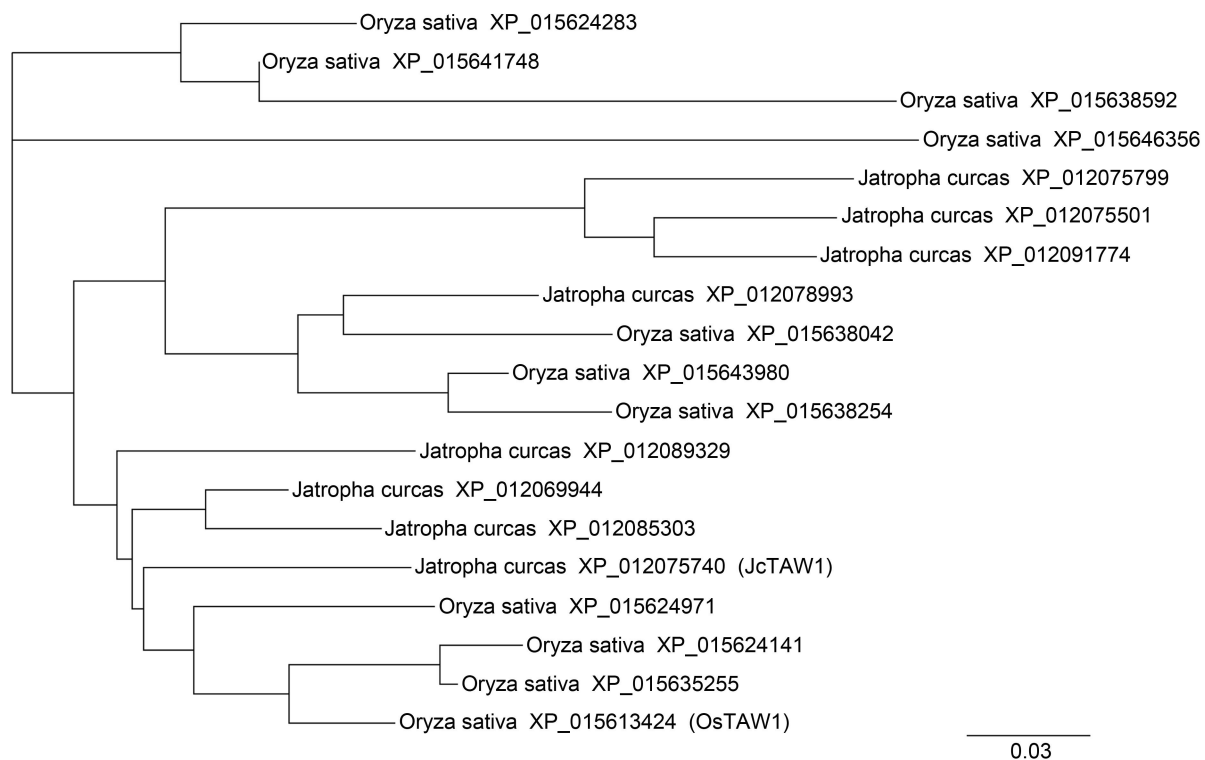


Figure S3 Neighbor-joining based phylogenetic analysis of OsTAW1 against its orthologs of *Jatropha curcas*.

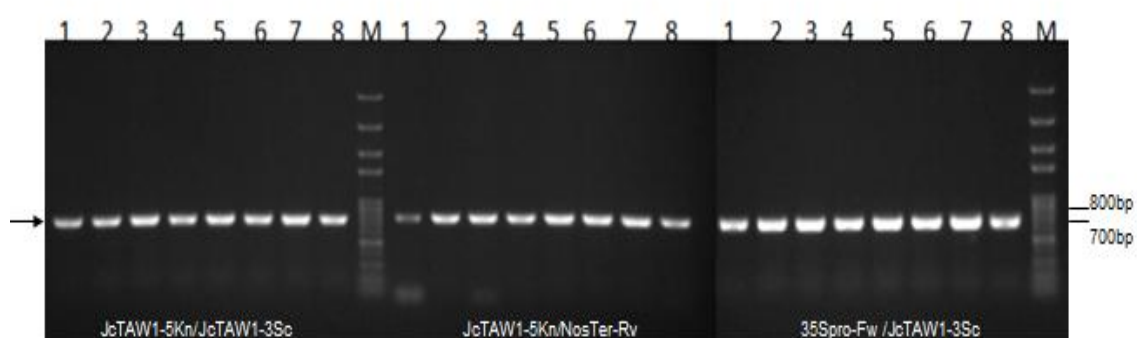


Figure S4 Identification of the JcTAW1 positive lines.

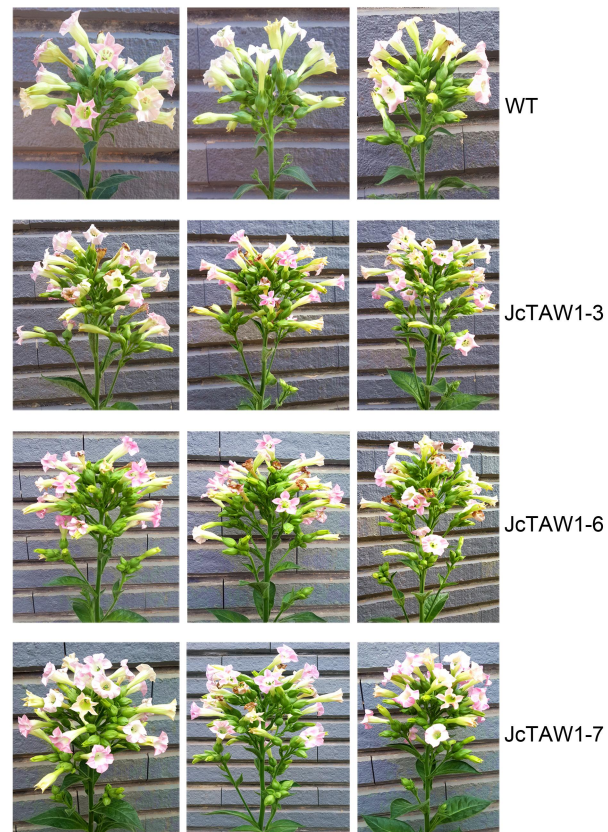


Figure S5 The *JcTAW1* transgenic tobacco plants exhibiting an increased flowering phenotype.

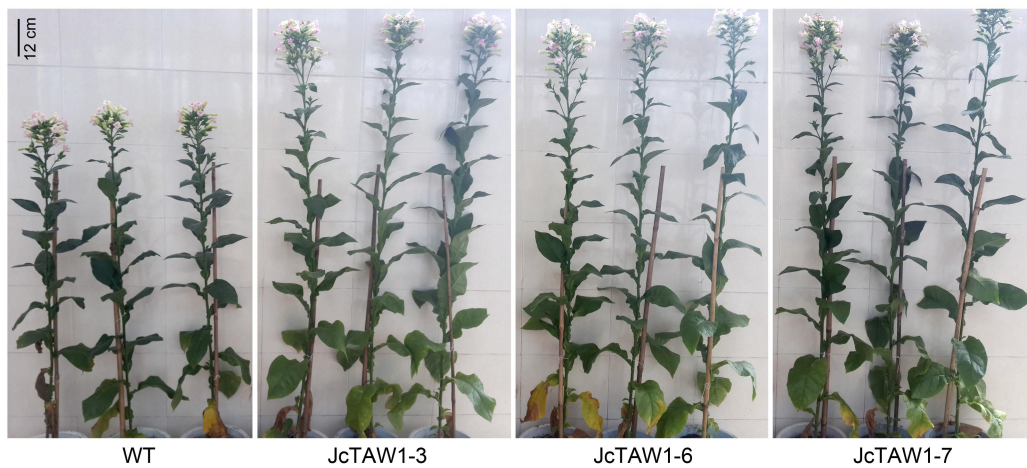


Figure S6 The stem length of the *JcTAW1* transgenic tobacco plants were significantly higher then the WT plants

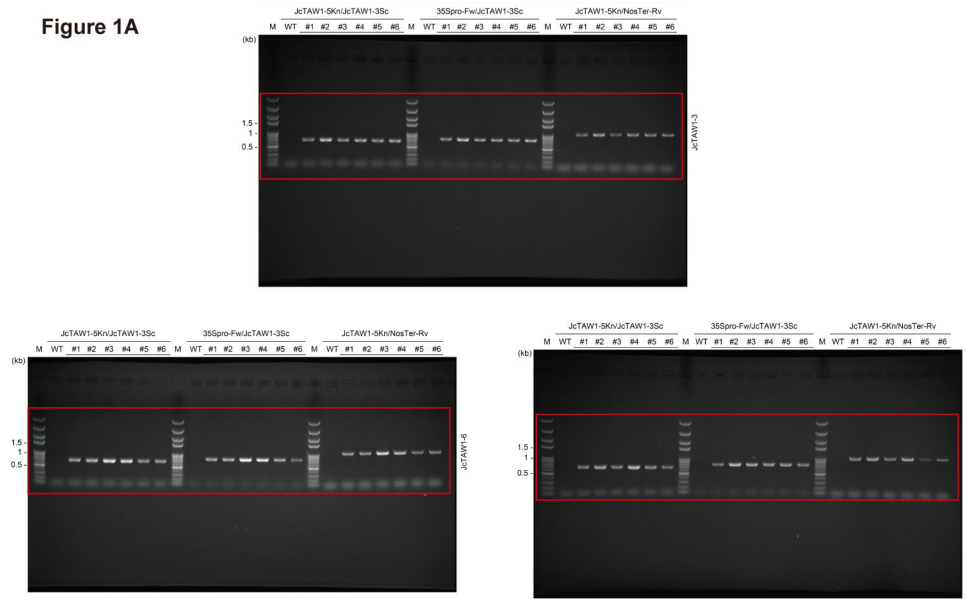
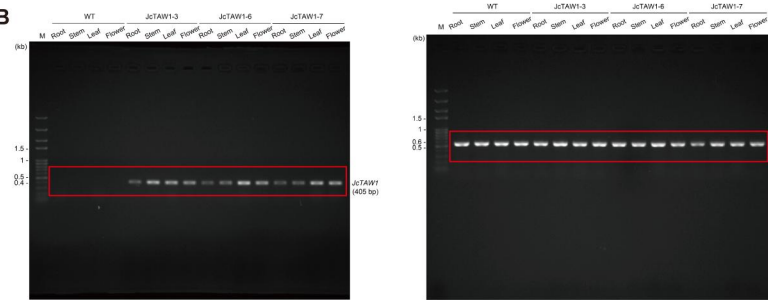
Figure 1A**Figure 1B**

Figure S7 Uncropped original gel electrophoresis data. The uncropped scans of gels in Figure 1 are shown above, with a black outline to show the excerpted portion.

Table S2 GO enrichment analysis of enriched biological processes in interesting modules.

ID	Description	pvalue	GeneRatio
GO:0005975	carbohydrate metabolic process	8.00E-11	41/143
GO:0055114	oxidation-reduction process	6.24E-10	33/143
GO:0042592	homeostatic process	1.92E-08	32/143
GO:0006811	ion transport	2.31E-08	30/143
GO:0042221	response to chemical	3.59E-08	34/143
GO:0044262	cellular carbohydrate metabolic process	9.37E-08	25/143
GO:0006091	generation of precursor metabolites and energy	2.95E-07	26/143
GO:0016310	phosphorylation	4.35E-07	31/143
GO:0071554	cell wall organization or biogenesis	4.64E-07	17/143
GO:0007154	cell communication	1.37E-06	32/143
GO:0006979	response to oxidative stress	1.39E-06	14/143
GO:0015980	energy derivation by oxidation of organic compounds	2.15E-06	18/143
GO:0006952	defense response	2.81E-06	17/143
GO:0034599	cellular response to oxidative stress	3.14E-06	10/143
GO:0062197	cellular response to chemical stress	3.14E-06	10/143
GO:0055085	transmembrane transport	4.68E-06	24/143

GO:0071555	cell wall organization	5.45E-06	13/143
GO:0045229	external encapsulating structure organization	6.98E-06	13/143
GO:0034220	ion transmembrane transport	7.40E-06	18/143
GO:0042546	cell wall biogenesis	7.57E-06	11/143
GO:0016051	carbohydrate biosynthetic process	8.04E-06	18/143
GO:0005976	polysaccharide metabolic process	8.64E-06	16/143
GO:0006073	cellular glucan metabolic process	8.88E-06	13/143
GO:0007165	signal transduction	9.52E-06	28/143
GO:0044042	glucan metabolic process	9.99E-06	13/143
GO:0015979	photosynthesis	1.29E-05	14/143
GO:0032787	monocarboxylic acid metabolic process	1.36E-05	26/143
GO:0023052	signaling	1.44E-05	28/143
GO:0009832	plant-type cell wall biogenesis	1.45E-05	9/143
GO:0009891	positive regulation of biosynthetic process	1.69E-05	24/143
GO:0010557	positive regulation of macromolecule biosynthetic process	1.69E-05	24/143
GO:0031328	positive regulation of cellular biosynthetic process	1.69E-05	24/143
GO:0045454	cell redox homeostasis	1.74E-05	9/143
GO:0044264	cellular polysaccharide metabolic process	1.75E-05	14/143
GO:0006468	protein phosphorylation	1.82E-05	19/143
GO:0032502	developmental process	1.86E-05	28/143
GO:0044419	interspecies interaction between organisms	2.18E-05	13/143
GO:0045934	negative regulation of nucleobase-containing compound metabolic process	2.22E-05	18/143
GO:0006812	cation transport	2.29E-05	17/143
GO:0051172	negative regulation of nitrogen compound metabolic process	2.40E-05	22/143
GO:0045333	cellular respiration	2.59E-05	15/143
GO:0071669	plant-type cell wall organization or biogenesis	3.42E-05	9/143
GO:0000278	mitotic cell cycle	3.44E-05	25/143
GO:0034637	cellular carbohydrate biosynthetic process	3.65E-05	13/143
GO:0015977	carbon fixation	3.77E-05	6/143
GO:1901615	organic hydroxy compound metabolic process	3.85E-05	22/143
GO:0010558	negative regulation of macromolecule biosynthetic process	3.88E-05	19/143
GO:2000113	negative regulation of cellular macromolecule biosynthetic process	3.88E-05	19/143
GO:1901617	organic hydroxy compound biosynthetic process	3.91E-05	17/143
GO:0007049	cell cycle	3.93E-05	32/143

Table S3 GO enrichment analysis of enriched cellular component in interesting modules.

ID	Description	pvalue	GeneRatio
GO:0005886	plasma membrane	1.24E-14	51/143
GO:0005576	extracellular region	3.53E-11	28/143
GO:0031984	organelle subcompartment	3.62E-11	34/143
GO:0031967	organelle envelope	1.02E-07	37/143
GO:0031975	envelope	1.02E-07	37/143
GO:0009534	chloroplast thylakoid	1.31E-07	22/143
GO:0031976	plastid thylakoid	1.31E-07	22/143

GO:0009579	thylakoid	1.42E-07	23/143
GO:0005794	Golgi apparatus	1.54E-07	30/143
GO:0048046	apoplast	1.66E-06	10/143
GO:0009535	chloroplast thylakoid membrane	2.63E-06	18/143
GO:0055035	plastid thylakoid membrane	2.63E-06	18/143
GO:0042651	thylakoid membrane	3.19E-06	18/143
GO:0034357	photosynthetic membrane	3.87E-06	18/143
GO:0005783	endoplasmic reticulum	7.33E-06	27/143
GO:0005615	extracellular space	8.35E-06	10/143
GO:0005740	mitochondrial envelope	8.82E-06	23/143
GO:0009526	plastid envelope	1.35E-05	18/143
GO:0019866	organelle inner membrane	1.56E-05	20/143
GO:0031966	mitochondrial membrane	1.59E-05	22/143
GO:0005743	mitochondrial inner membrane	1.80E-05	19/143
GO:0098791	Golgi apparatus subcompartment	2.02E-05	14/143
GO:0005802	trans-Golgi network	2.52E-05	12/143
GO:0098796	membrane protein complex	3.58E-05	31/143
GO:0009941	chloroplast envelope	5.66E-05	16/143
GO:0005789	endoplasmic reticulum membrane	0.000105354	25/143
GO:0042175	nuclear outer membrane-endoplasmic reticulum membrane network	0.000105354	25/143
GO:0005773	vacuole	0.000147194	20/143
GO:0031301	integral component of organelle membrane	0.000151097	19/143
GO:0031300	intrinsic component of organelle membrane	0.000170584	19/143
GO:0042170	plastid membrane	0.000232258	12/143
GO:0031226	intrinsic component of plasma membrane	0.000314837	11/143
GO:0005938	cell cortex	0.000344184	9/143
GO:0090575	RNA polymerase II transcription regulator complex	0.000619586	10/143
GO:0005759	mitochondrial matrix	0.000636657	14/143
GO:0019867	outer membrane	0.000671743	9/143
GO:0031968	organelle outer membrane	0.000671743	9/143
GO:0030880	RNA polymerase complex	0.000680568	14/143
GO:0009521	photosystem	0.000782837	7/143
GO:0031969	chloroplast membrane	0.001065272	10/143
GO:0005618	cell wall	0.001068465	8/143
GO:0030312	external encapsulating structure	0.001068465	8/143
GO:0009506	plasmodesma	0.001325373	8/143
GO:0055044	sympplast	0.001325373	8/143
GO:0016591	RNA polymerase II, holoenzyme	0.001327747	11/143
GO:0061695	transferase complex, transferring phosphorus-containing groups	0.001462067	19/143
GO:0070469	respirasome	0.001629242	8/143
GO:1990204	oxidoreductase complex	0.001656129	11/143
GO:0031225	anchored component of membrane	0.001707864	5/143
GO:0005654	nucleoplasm	0.001838463	23/143

Table S4 GO enrichment analysis of enriched molecular function in interesting modules.

ID	Description	pvalue	GeneRatio
GO:0098772	molecular function regulator	3.72E-08	40/148
GO:0015318	inorganic molecular entity transmembrane transporter activity	6.54E-08	29/148
GO:0015075	ion transmembrane transporter activity	1.90E-07	29/148
GO:0008324	cation transmembrane transporter activity	5.74E-07	23/148
GO:0004497	monooxygenase activity	8.46E-07	14/148
GO:0030234	enzyme regulator activity	1.07E-06	27/148
GO:0016209	antioxidant activity	1.07E-06	12/148
GO:0016651	oxidoreductase activity, acting on NAD(P)H	1.36E-06	13/148
GO:0005215	transporter activity	1.98E-06	34/148
GO:0022857	transmembrane transporter activity	2.12E-06	32/148
GO:0050660	flavin adenine dinucleotide binding	5.67E-06	15/148
GO:0046527	glucosyltransferase activity	6.38E-06	11/148
GO:0004362	glutathione-disulfide reductase activity	1.00E-05	5/148
GO:0009055	electron transfer activity	1.00E-05	14/148
GO:0015078	proton transmembrane transporter activity	1.08E-05	15/148
GO:0022890	inorganic cation transmembrane transporter activity	1.19E-05	20/148
GO:0019207	kinase regulator activity	1.46E-05	12/148
GO:0005509	calcium ion binding	1.47E-05	16/148
GO:0015077	monovalent inorganic cation transmembrane transporter activity	1.77E-05	16/148
GO:0008309	double-stranded DNA exodeoxyribonuclease activity	2.98E-05	5/148
GO:0008311	double-stranded DNA 3'-5' exodeoxyribonuclease activity	2.98E-05	5/148
GO:0015037	peptide disulfide oxidoreductase activity	4.71E-05	5/148
GO:0015038	glutathione disulfide oxidoreductase activity	4.71E-05	5/148
GO:0016709	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen	5.64E-05	9/148
GO:0004674	protein serine/threonine kinase activity	6.36E-05	16/148
GO:0046983	protein dimerization activity	6.47E-05	15/148
GO:0000981	DNA-binding transcription factor activity, RNA polymerase II-specific	8.25E-05	7/148
GO:0004672	protein kinase activity	9.16E-05	18/148
GO:0016798	hydrolase activity, acting on glycosyl bonds	0.000124544	17/148
GO:0022804	active transmembrane transporter activity	0.000136336	18/148
GO:0016829	lyase activity	0.000161072	26/148
GO:0005506	iron ion binding	0.000190843	14/148
GO:0035251	UDP-glucosyltransferase activity	0.000261305	8/148
GO:0004528	phosphodiesterase I activity	0.00027264	5/148
GO:0016758	transferase activity, transferring hexosyl groups	0.000290338	16/148
GO:0051536	iron-sulfur cluster binding	0.000321934	18/148
GO:0051540	metal cluster binding	0.000321934	18/148
GO:0046906	tetrapyrrole binding	0.000325616	14/148
GO:0003700	DNA-binding transcription factor activity	0.000367197	11/148

GO:0015036	disulfide oxidoreductase activity	0.000424432	7/148
GO:0004519	endonuclease activity	0.00044514	17/148
GO:0008081	phosphoric diester hydrolase activity	0.000450532	8/148
GO:0016668	oxidoreductase activity, acting on a sulfur group of donors, NAD(P) as acceptor	0.000466512	5/148
GO:0022853	active ion transmembrane transporter activity	0.00052553	12/148
GO:0004611	phosphoenolpyruvate carboxykinase activity	0.000543393	4/148
GO:0016984	ribulose-bisphosphate carboxylase activity	0.000543393	4/148
GO:0016538	cyclin-dependent protein serine/threonine kinase regulator activity	0.000550314	6/148
GO:0019887	protein kinase regulator activity	0.000586295	9/148
GO:0016830	carbon-carbon lyase activity	0.000612812	14/148
GO:0004386	helicase activity	0.000662063	15/148
