Plant Omics Journal POJ

POJ 8(3):264-269(2015) ISSN:1836-3644

Supplementary data

Construction and classification of a cDNA Library from *Miscanthus sinenesis* (Eulalia) treated with UV-B

Eun Soo Seong, Ji Hye Yoo, Jae Hoo Choi, Nam Jun Kim, Hee Young Kim, Kweon Heo, & Chang Yeon Yu[*]

Supplementary Table 1. EST clones and E-value matched to known functional genes.

Putative function	E-value[a]
(E)-beta-caryophyllene synthase	1.00E-120
26S proteasome AAA-ATPase subunit RPT6a	3.00E-24
26S proteasome ATPase subunit	1.00E-105
2-on-2 hemoglobin	1.00E-52
60S ribosomal protein L17	7.00E-75
Abscisic acid 8'-hydroxylase 1	5.00E-10
Acetyltransferase, GNAT family protein	6.00E-87
Acyl carrier protein 2, chloroplastic	2.00E-46
Adenosylhomocysteinase	4.00E-71
Alanine-glyoxylate aminotransferase 2, mitochondrial,	1.00E-101
Alcohol dehydrogenase 2	1.00E-129
Armadillo/beta-catenin repeat family protein	1.00E-99
ASF/SF2-like pre-mRNA splicing factor SRP32	3.00E-22
Asorbate peroxidase	1.00E-118
Aspartate aminotransferase	2.00E-25
ATP sulfurylase	1.00E-140
ATP synthase delta chain, chloroplastic	3.00E-78
ATP synthase gamma chain, mitochondrial	5.00E-74
ATP synthase subunit gamma, chloroplastic	4.00E-78
ATPase, AAA family protein	1.00E-123
Bifunctional aminoacyl-tRNA synthetase	1.00E-146
Bifunctional phosphopantetheine adenylyl transferase dephospho CoA kinase-like protein	8.00E-79
Bundle sheath cell specific protein 1	2.00E-35
BZIP transcription factor	9.00E-12
Calcineurin B-like protein 10	1.00E-84

Calmodulin-like protein	2.00E-59
CAX-interacting protein 4 (CAXIP4)-like	6.00E-17
Cellulose synthase-1	1.00E-104
Chlorophyll a/b-binding apoprotein CP26	1.00E-134
Chlorophyll a-b binding protein 1B-21, chloroplastic	2.00E-17
Chlorophyll a-b binding protein M9, chloroplastic	2.00E-71
Chloroplast ferredoxin 1 (Putative uncharacterized protein)	3.00E-32
Cyclin-T1-1	7.00E-31
Cytochrome P450 family protein	1.00E-23
Cytochrome P450-like	2.00E-91
DNA-directed RNA polymerase	5.00E-94
DnaJ-related protein ZMDJ1	1.00E-136
DnaK-type molecular chaperone hsp70-rice	1.00E-127
DREB 2A (Transcription factor DREB2A)	0.073
Elongation factor 1-alpha	1.00E-150
Enolase	1.00E-117
Ethylene-responsive factor-like transcription factor ERFL1a	3.00E-50
Eukaryotic translation initiation factor 5A	6.00E-86
Ferredoxin--NADP reductase	1.00E-112
Ferritin-1, chloroplastic	7.00E-99
Filamentation temperature-sensitive H 2A	7.00E-51
Glutathione S-transferase 4	1.00E-104
Glutathione S-transferase GST 17	1.00E-105
Glutathione S-transferase GST 22	5.00E-82
Glutathione S-transferase GST 30	3.00E-67
Glutathione S-transferase GST 42	4.00E-21
Glutathione transferase	3.00E-78
Glutathione transferase	1.00E-71
Glyceraldehyde-3-phosphate dehydrogenase A, chloroplastic	1.00E-146
Glycine-rich RNA-binding protein	3.00E-40
GrpE2	1.00E-111
H0103C06.6 protein	1.00E-128
Haloacid dehalogenase-like hydrolase family protein	1.00E-104
Heat shock cognate 70 kDa protein	1.00E-155
Heat shock protein 26	5.00E-92
Histidine-containing phosphotransfer protein	7.00E-54
Histone H3	3.00E-69
Hydrolase, carbon-nitrogen family protein	1.00E-102
Hydroperoxide lyase	2.00E-86

Hydroxyproline-rich glycoprotein family protein	5.00E-60
Indole-3-glycerol phosphate lyase	3.00E-10
Isochorismatase hydrolase-like	2.00E-72
Leucine Rich Repeat family protein	3.00E-37
Leucine Rich Repeat family protein	2.00E-35
LHCII type III chlorophyll a/b binding protein	1.00E-86
Lipase class 3 protein-like	9.00E-21
Lipoxygenase 1	2.00E-05
Lipoxygenase	7.00E-89
Maf-like protein	2.00E-52
Malate dehydrogenase	1.00E-121
Metallothionein	2.00E-12
Metallothionein-like protein	1.00E-11
Methionine synthase protein	1.00E-168
Methylenetetrahydrofolate reductase 1	1.00E-114
Mitochondrial aldehyde dehydrogenase	1.00E-111
Mitochondrial uncoupling protein 4	4.00E-66
Mitogen activated protein kinase 6	1.00E-12
Monosaccharide transport protein 1	2.00E-65
Multidrug resistance associated protein MRP2	6.00E-80
Multidrug resistance-associated protein MRP1	1.00E-109
NADP-specific isocitrate dehydrogenase	1.00E-126
NBS-LRR resistance-like protein	6.00E-50
NBS-LRR type R protein, Nbs2-Pi2	4.00E-05
NOD26-like major intrinsic protein	1.00E-125
Non-specific lipid-transfer protein 1	3.00E-40
Non-specific lipid-transfer protein	4.00E-36
OSJNBa0085I10.10 protein	3.00E-39
Peptidyl-prolyl cis-trans isomerase	9.00E-40
Phosphoenolpyruvate carboxylase 2	2.00E-31
Pre-mRNA splicing factor ATP-dependent RNA helicase	1.00E-101
Proteasome subunit beta type	4.00E-53
PSI type III chlorophyll a/b-binding protein	4.00E-19
Putative 1-deoxy-D-xylulose 5-phosphate reductoisomerase	3.00E-76
Putative 3-beta hydroxysteroid dehydrogenase/isomerase (NAD dependent epimerase/dehydratase family protein)	3.00E-57
Putative 3-hydroxyisobutyryl-coenzyme A hydrolase	1.00E-125
Putative 5-alpha-taxadienol-10-beta-hydroxylase	1.00E-86
Putative 5-formyltetrahydrofolate cycloligase	3.00E-82
Putative 60S ribosomal protein L37	1.00E-42

Putative 60S ribosomal protein L38	3.00E-30
Putative acetylornithine aminotransferase	5.00E-65
Putative aconitate hydratase, cytoplasmic	1.00E-101
Putative alcohol dehydrogenase 1	1.00E-121
Putative alpha-soluble NSF attachment protein	1.00E-15
Putative beta-1,3-glucanase	1.00E-76
Putative C4 phosphoenolpyruvate carboxylase	9.00E-91
Putative C4 phosphoenolpyruvate carboxylase	1.00E-123
Putative clathrin coat assembly protein AP17	3.00E-60
Putative collagen (PHD-finger family protein)	1.00E-63
Putative cytochrome P450	1.00E-112
Putative DegP2 protease	1.00E-165
Putative dehydratase/deaminase	3.00E-85
Putative disease resistance protein I2	3.00E-43
Putative ER6 protein	1.00E-53
Putative esterase	1.00E-110
Putative exoribonuclease (3' exoribonuclease family, domain 1 containing protein)	1.00E-120
Putative gag-pol polyprotein	5.00E-95
Putative glucosyl transferase	3.00E-24
Putative iron inhibited ABC transporter 2	1.00E-121
Putative ketol-acid reductoisomerase	1.00E-122
Putative leucine zipper protein	2.00E-08
Putative leucine-rich repeat protein (BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1)	1.00E-101
Putative LMW heat shock protein	1.00E-17
Putative MAP3K delta-1 protein kinase	5.00E-47
Putative mitochondrial energy transfer protein	8.00E-63
Putative Mob1-like protein (Mps one binder kinase activator-like 1A)	1.00E-115
Putative NADPH-dependent retinol dehydrogenase/reductase	1.00E-99
Putative N-ethylmaleimide sensitive fusion protein	1.00E-143
Putative nuclear protein p30	1.00E-59
Putative nucleic acid binding protein	3.00E-76
Putative Oxygen-evolving enhancer protein 3-2, chloroplast	1.00E-58
Putative phosphate transport protein, mitochondrial	9.00E-62
Putative phosphoenolpyruvate carboxylase	1.00E-55
Putative phosphoglucomutase	1.00E-132
Putative phospholipase D-like protein	1.00E-60
Putative photosystem I antenna protein	1.00E-120
Putative Phytosulfokine receptor	5.00E-68
Putative PrMC3	4.00E-96

Putative receptor-like protein kinase(Protein kinase domain containing protein)	3.00E-28
Putative RGH1A	7.00E-69
Putative ribosomal protein S15(40S ribosomal protein S15)	2.00E-40
Putative RING finger 1	6.00E-92
Putative ripening regulated protein DDTFR18	2.00E-19
Putative RRM-containing protein	5.00E-49
Putative Ser/Thr kinase	6.00E-81
Putative SET-domain transcriptional regulator	1.00E-110
Putative trehalose-phosphatase	3.00E-46
Putative tRNA-glutamine synthetase	5.00E-97
Putative UDP-glucose dehydrogenase (UDP-glucose 6-dehydrogenase)	4.00E-53
Putative UOS1	1.00E-110
Rab7 OS=Pennisetum americanum	1.00E-110
Receptor-like protein kinase ARK1	1.00E-98
Rhamnose biosynthetic enzyme 1	1.00E-66
Ribosomal protein L35A	6.00E-58
Ribosomal protein S21-like protein	2.00E-16
Ribosomal protein s6 RPS6-2	1.00E-101
RING zinc finger protein-like	1.00E-36
RING zinc finger protein-like	1.00E-16
RNA-binding protein	0.001
Sedoheptulose-1,7-bisphosphatase	1.00E-108
Serine/threonine protein kinase	1.00E-133
Serine/threonine-protein phosphatase PP1	1.00E-116
SIR2-like histone deacetylase	3.00E-92
Small GTP binding protein Rab2A	1.00E-105
Terpene synthase 2	4.00E-93
Transcription elongation factor	9.00E-42
Tropinone reductase 1	3.00E-86
U1 snRNP	4.00E-90
UDP-glucose 6-dehydrogenase	1.00E-127
UDP-glucose-4-epimerase	1.00E-124
Vacuolar H+-ATPase c subunit	1.00E-57
V-ATPase subunit c	4.00E-58
VIP3 protein	3.00E-60
YDG/SRA domain containing protein	1.00E-130
Zinc finger protein-like	1.00E-125

[a] E-value of the most significant BLASTX match.