

Table 2 Selected set of specific sequences and their putative functions

Functional class	Unigene ID	Putative annotation	
Energy/metabolism	gppca0_0006_B01.ab1	Aconitase A	
	gppca0_0007_F11.ab1	UDP-glucose: flavonoid 3-O-glucosyltransferase	
	gppca.CleanEST.seq.Contig5	Flavonoid 3'5' hydroxylase	
	gppca0_0010_A06.ab1	Chalcone synthase	
	gppca0_0001_B08.ab1	Alcohol dehydrogenase 2	
	gppca.CleanEST.seq.Contig92	Cytochrome P450 like_TBP	
	gppca.CleanEST.seq.Contig32	Dtdp-glucose 4-6-dehydratase	
	gppca.CleanEST.seq.Contig121	Ripening-related protein-like	
	gppca0_0008_C09.ab1	Lactate dehydrogenase	
	gppca0_0006_E03.ab1	Isocitrate dehydrogenase	
	gppca0_0003_F03.ab1	Acetyltransferase	
	gppca0_0003_E04.ab1	Pyruvate kinase	
	gppca0_0006_C11.ab1	Predicted O-methyltransferase	
	gppca.CleanEST.seq.Contig89	Glycosyltransferase	
	gppca0_0013_B09.ab1	Acyl dehydratase	
	gppca0_0010_E06.ab1	ATP binding	
	gppca0_0010_A09.ab1	Aminopeptidase N	
	gppca.CleanEST.seq.Contig30	Isopenicillin N synthase	
	gppca0_0010_G07.ab1	Phosphopantothencysteine decarboxylase	
	gppca0_0006_F06.ab1	Glucose-6-phosphate isomerase	
	gppca0_0006_B08.ab1	Pectin methylesterase isoform alpha	
	gppca0_0001_A09.ab1	Vacuolar ATP synthase proteolipid subunit 1, 2, 3	
	gppca0_0011_E05.ab1	phosphomannomutase	
	gppca0_0005_D01.ab1	Probable pyridoxal biosynthesis protein PDX1	
	gppca.CleanEST.seq.Contig65	Ribulose-1,5-bisphosphate carboxylase	
	gppca0_0012_G09.ab1	Formate hydrogenlyase subunit 6	
	gppca0_0002_F12.ab1	S-adenosylhomocysteine hydrolase	
	gppca0_0003_B02.ab1	Acyl-coenzyme A synthetases	
	gppca0_0013_D08.ab1	NADPH:quinone reductase and related Zn-dependent oxidoreductases	
	gppca0_0011_G06.ab1	Glyceraldehyde-3-phosphate dehydrogenase	
	gppca0_0012_E01.ab1	Fatty acid desaturase	
	gppca0_0005_F02.ab1	3-hydroxyisobutyrate dehydrogenase	
	gppca0_0012_D07.ab1	Enolase	
	gppca.CleanEST.seq.Contig53	6-phosphogluconate dehydrogenase	
	gppca0_0012_D11.ab1	Beta-glucosidase	
	gppca0_0010_E07.ab1	Myo-inositol-1-phosphate synthase	
	gppca0_0010_C08.ab1	5,10-methylene-tetrahydrofolate dehydrogenase	
	gppca0_0008_D10.ab1	Aromatic aminotransferase	
	gppca0_0002_A08.ab1	NAD synthase	
	gppca.CleanEST.seq.Contig103	Heme binding	
	gppca.CleanEST.seq.Contig95	Catalase	
	Protein synthesis	gppca0_0008_A10.ab1	Ribosomal protein L14
		gppca0_0003_F04.ab1	Ribosomal protein L20A (L18A)
gppca0_0006_G04.ab1		Translation elongation factor Ts	
gppca0_0010_H11.ab1		ribosomal protein L2	
gppca.CleanEST.seq.Contig111		Ribosomal protein L15	
gppca0_0002_E08.ab1		Ribosomal protein S9	
gppca.CleanEST.seq.Contig83		Ribosomal protein S3AE	
gppca0_0003_C06.ab1		Translation elongation factor P	
gppca.CleanEST.seq.Contig97		Ribosomal protein S27E	
gppca.CleanEST.seq.Contig1		Ribosomal protein S19E (S16A)	

Functional class	Unigene ID	Putative annotation
Protein synthesis	gppca.CleanEST.seq.Contig48	Ribosomal protein S24E
	gppca.CleanEST.seq.Contig115	Ribosomal protein L6P/L9E
	gppca0_0004_B05.ab1	Ribosomal protein S4E
	gppca0_0004_C02.ab1	Ribosomal protein L24E
	gppca.CleanEST.seq.Contig31	Ribosomal protein S12
	gppca0_0005_F03.ab1	Ribosomal protein S8
	gppca0_0008_C01.ab1	Ribosomal protein S10
Signal transduction	gppca.CleanEST.seq.Contig37	Ca ²⁺ -binding protein
	gppca0_0009_G06.ab1	GTPase SAR1 and related small G proteins
	gppca0_0006_A07.ab1	Signal peptidase complex
	gppca0_0005_A03.ab1	Serine/threonine protein kinase
	gppca0_0013_A02.ab1	G-protein coupled receptor protein
Cell disease/denfence	gppca0_0012_D05.ab1	DnaJ-like protein
	gppca0_0009_A09.ab1	Polygalacturonase-inhibiting protein
	gppca0_0012_F07.ab1	Pathogenesis-related protein 1
	gppca.CleanEST.seq.Contig64	Stress-related protein
	gppca.CleanEST.seq.Contig125	Abscisic stress ripening protein
	gppca.CleanEST.seq.Contig3	Heat shock protein 90
	gppca.CleanEST.seq.Contig105	Pathogenesis-related protein 10
	gppca.CleanEST.seq.Contig120	Glutathione S-transferase
	gppca0_0006_C12.ab1	Expansin
	gppca.CleanEST.seq.Contig66	Non-specific lipid transfer protein
Transport	gppca0_0005_D11.ab1	Proton-transporting ATP synthase complex, coupling factor F(o)
	gppca0_0005_H09.ab1	Proton-transporting ATP synthase complex, catalytic core F(1)
	gppca0_0003_B07.ab1	Di- and tricarboxylate transporters
	gppca0_0012_D09.ab1	Permeases of the drug/metabolite transporter (DMT) superfamily
	gppca0_0012_D04.ab1	Elongation factor Tu, chloroplastic
Photosynthesis	gppca0_0007_C04.ab1	PSII 44kDa protein
	gppca0_0004_C08.ab1	Photosystem II protein K
	gppca0_0013_C02.ab1	Chloroplast /photosystem II
Transcription	gppca0_0002_H07.ab1	Myb-related transcription factor
	gppca0_0003_F10.ab1	Splicing factor 3a, subunit 3
Protein regulation	gppca0_0003_A01.ab1	Polyubiquitin UBQ14
	gppca0_0005_H06.ab1	Ubiquitin-protein ligase
	gppca0_0006_C01.ab1	SCF ubiquitin ligase, SKP1 component
Cell structure	gppca0_0008_E12.ab1	Cell cycle control protein, G10 family/nucleus
	gppca.CleanEST.seq.Contig107	Cytoplasm
	gppca0_0012_F12.ab1	Membrane
	gppca0_0008_A12.ab1	Endoplasmic reticulum
	gppca0_0007_D11.ab1	Mitochondrion
	gppca.CleanEST.seq.Contig67	Cell wall