

Table S1. Outlier loci obtained for *Platonia insignis* samples.

ID	Sequences	Blastx	% identity	% cover	Uniprot	Function	Interpro
CLocus _385	TGCAGCTCCAATTGCAGACAT TCCTTTGGCTTTCAAGGCAGA AATAACCTGTTTGGCATCTTC ATATCCTTTGTCCTACCAAGG AATCAAAT	Endo-1,3;1,4-beta-D- glucanase-like	80%	81%	Q6ZJQ2 (rice)	Hydrolase activity (group of enzymes that catalyze the breaking of covalent bonds in reaction with water)	none predicted
CLocus _3725	TGCAGGTGCTGTAGGAGGTG TTGCAGCTTCTCTTATTCGTG TTCCTACAGAGGTTTATTTGC CTTTTCTAGCTAGAAGTATGA GCTTTGATT	S-adenosylmethionine carrier 1, chloroplastic/mitochon drial	94.44%	58%	A3BIT2_ORYSJ (rice)	Integral component of the membrane, transmembrane transport	none predicted
CLocus _4575	TGCAGTAGTGACTTCTAGCAT CCATGTAGCTGGGTTGTATCC ATCTTTGATTTTAGGGACTCC TTGAATTCCCTTCAAAAGAGA AAGATGCC	Pleiotropic drug resistance protein 1- like isoform X1	72.41%	94%	A0A6P5ZSC7_DURZ I (durian)	Integral component of the membrane, transport activity, ATP binding	none predicted
CLocus _6950	TGCAGGTAACATCAGTAAAT GACATGTACAACTTTTACAA GAGTACAATGCTAGCTTGCA GCTGTACAATAGTAACTTCA ACAAGACCTC	kinesin-like protein KIN-14N isoform X3	83.33%	97%	A0A8B8NG63_9MY RT (<i>Rhodamnia argentea</i>)	ATP binding, binding/movement/ microtubule motor activity, cytoskeletal motor activity	none predicted
CLocus _7172	TGCAGCTGTGAAACTAGGAT CTCTAGCCAAGGAAGAAGCC ATTTGTTGGATGAATATCTGT TCAGTTGAGGATGATTTGCTT TCAAGCAGCA	Probable WRKY transcription factor 60	53.57%	91%	A0A8B8NNR4_9MY RT (<i>Rhodamnia argentea</i>)	DNA binding, transcription factor activity	none predicted
CLocus _9256	TGCAGTTGGGCTACAAGGAT CAATATGTGTGTTACGATGT GCTTCGAGTCAAAAAGATGG TATTAGTCCCGCCATTGGAGC AAGAACTTCG	Probable apyrase 7	53.33%	97%	Q6Z4P2 · APY2_ORYSJ (rice)	Catalyzes hydrolysis of phosphoanhydride bonds of nucleoside tri- and diphosphates, nucleotide binding, hydrolase activity, integral component of membrane	none predicted
CLocus _12465	TGCAGCTAAATGGCCCATCTG ACCACATAGAAAGCATTTAT CTTGCTGTCCAGGAGTGAAA ACAACCTGAATGATAACATC AAAGGGCAGAT	5'-3' exoribonuclease 3-like isoform X1	78.57%	91%	A0A1S4BJW1_TOB AC - protein RRP6- like 3 isoform X1 (<i>Nicotiana tabacum</i> (Common tobacco))	Nucleotide and RNA binding, exoribonuclease activity, integral membrane component, nuclear exosome, histone mRNA catabolic process, nuclear polyadenylation	none predicted

CLocus _16070	TGCAGGTCCAGTGATGTCATA ACTTCCAAGCCCTATCAAGTA ATTGGAAGCAGAGAGAACCA TTCCACCATTTGAAAAGAAAC AGTAGCAAAT	Neutral ceramidase 1- like	73.33%	97%	A0A7J0EBD9_9ERIC (kiwi)	Ceramidase activity (enzyme that cleaves fatty acids from ceramide, producing sphingosine which in turn is phosphorylated by a sphingosine kinase to form sphingosine-1-phosphate), kinase, phosphorylation, hydrolase, transferase	none predicted
CLocus _18131	TGCAGGTACTCTCCCTTCAGA CCTAAGGAACCTTACTCAACT AGAGAGGTTAGAGCTCCAAT GGAACAATATCTCTGGCCCTT TGCCTAGTT	Receptor protein kinase TMK1-like isoform X1	93.10%	94%	A0A6P5T5E6 · A0A6P5T5E6_PRUA V - (Cherry) (<i>Cerasus avium</i>)	Integral component of membrane, ATP binding, kinase activity, protein phosphorylation	none predicted
CLocus _18216	TGCAGTTCACAAGGAACTAA AGTAACGTTACCTCGAGACCT GAAAGAGCATTCCAAGAAGA CAAAGGTTCAACGGCAGAAT CATCGATGAGA	Protein phosphatase 1 regulatory subunit pprA	75.00%	65%	A0A654FLL7 · A0A654FLL7_ARAT H - <i>Arabidopsis</i>	Not found	none predicted
CLocus _18499	TGCAGGTTTCCAAGCTTTATG AGGTTGTGCCTCCAGTTCTTC ATGAGCTGGGCAAGGCATGT GCATTTTCTTACTGGAGCGTA AGGTATGCC	Low Quality Protein: citrate synthase, mitochondrial-like	88.24%	55%	P20115 · CISY4_ARATH	Citrate synthase is found in almost all cells capable of oxidative metabolism. A	none predicted