

Supplemental Table 5. Predicted targets of novel rubber tree miRNAs

miRNA_ID	Target Acc.#	Database [®]	Expectation*	Target Description
hbr-cand01	DV143305	Leafy spurge	3	similar to UniRef100_Q7QEF9 Cluster: AGAP000673-PA
	TC6408	Leafy spurge	3	similar to UniRef100_A7PULO Cluster
hbr-cand02	TC3505	Leafy spurge	1	similar to UniRef100_P46489 Cluster: Malate dehydrogenase [NADP], chloroplast precursor
	EC606162	rubber tree	2.5	Y33E01 YLX600 Hevea brasiliensis cDNA clone Y33E01 5', mRNA sequence
	TC12042	Cassava	3	similar to UniRef100_A7R311 Cluster
	TC1487	Leafy spurge	3	similar to UniRef100_A7QD66 Cluster
hbr-cand03	TC2597	Cassava	3	similar to UniRef100_Q5NE17 Cluster: Malate dehydrogenase
	BM259988	Cassava	2.5	homologue to UniRef100_A7PJV3 Cluster
	DB945786	Cassava	2.5	homologue to UniRef100_A7QQL7 Cluster
	DB941102	Cassava	2.5	homologue to UniRef100_A7QQL7 Cluster
	TC9050	Cassava	2.5	similar to UniRef100_A7PZQ8 Cluster
	DV450137	Cassava	3	
	TC1511	Leafy spurge	3	homologue to UniRef100_A7PW42 Cluster
	TC6326	Leafy spurge	2.5	similar to UniRef100_A7PC11 Cluster
hbr-cand04	DV155595	Leafy spurge	3	similar to UniRef100_A7P9Y9 Cluster
	DB936606	Cassava	2.5	
hbr-cand05	DB947720	Cassava	3	weakly similar to UniRef100_A7P423 Cluster
	CK643967	Cassava	3	similar to UniRef100_A2Q4Q8 Cluster: Zinc finger, RING-type
	DV137561	Leafy spurge	3	similar to UniRef100_A7PQV3 Cluster
	TC2090	Leafy spurge	2	similar to UniRef100_Q84VX9 Cluster
hbr-cand06	TC5522	Leafy spurge	2	similar to UniRef100_O80341 Cluster: Ethylene-responsive transcription factor 5
	DB929814	Cassava	2.5	similar to UniRef100_Q9LS65 Cluster: Gb AAD25622.1
	TC4909	Cassava	2.5	similar to UniRef100_A7R1E8 Cluster
	TC11928	Cassava	2.5	weakly similar to UniRef100_A7NX60 Cluster
	TC194	Leafy spurge	2.5	weakly similar to UniRef100_A7QD41 Cluster

	TC10089	Leafy spurge	2.5	weakly similar to UniRef100_A7QF30 Cluster
	TC2628	Leafy spurge	2.5	
	TC207	Leafy spurge	2.5	similar to UniRef100_Q8LBH4 Cluster: Ids4-like protein
	DB947420	Cassava	3	similar to UniRef100_A7NTP8 Cluster
	FF536189	Cassava	3	similar to UniRef100_A7QW82 Cluster
	TC4755	Cassava	3	homologue to UniRef100_A9PL14 Cluster: Alpha-tubulin
	TC779	Cassava	3	similar to UniRef100_A7PH89 Cluster
	DV152884	Leafy spurge	3	
	DV150096	Leafy spurge	3	similar to UniRef100_A7QHL7 Cluster
	TC10535	Leafy spurge	3	similar to UniRef100_A7QS76 Cluster
	DV135330	Leafy spurge	3	
hbr-cand07	CK645365	Cassava	2.5	similar to UniRef100_Q10DK1 Cluster: Protein kinase domain containing protein
	DV457564	Cassava	2.5	weakly similar to UniRef100_A7PNG6 Cluster
	TC2604	Cassava	3	homologue to UniRef100_A2Q4X4 Cluster: Epsin, N-terminal
	TC10541	Leafy spurge	3	
hbr-cand08	TC7718	Cassava	2	similar to UniRef100_Q94A20 Cluster: Protein FBL4
	DB952123	Cassava	2	similar to UniRef100_Q680F9 Cluster: MRNA, complete cds, clone: RAFL22-56-M10
	TC7516	Cassava	2	weakly similar to UniRef100_A0EG84 Cluster
	TC9663	Cassava	2.5	homologue to UniRef100_A1EC31 Cluster: CLAVATA3/ESR-related protein
	TC3841	Cassava	2.5	weakly similar to UniRef100_Q1MS46 Cluster: Maltose O-acetyltransferase
	DV449658	Cassava	2.5	similar to UniRef100_A7Q2N1 Cluster
	DV126292	Leafy spurge	2.5	
	TC6617	Leafy spurge	2.5	
	DV151844	Leafy spurge	2.5	similar to UniRef100_A0CX29 Cluster
	EC604249	rubber tree	2.5	A44 YLX600 Hevea brasiliensis cDNA clone A44 5', mRNA sequence
	TC7658	Cassava	3	similar to UniRef100_Q94BX3 Cluster: AT4g25670/L73G19_50
	FF534706	Cassava	3	similar to UniRef100_A7NTI6 Cluster

	DB932290	Cassava	3	UniRef100_A7R1W0 Cluster
	TC7274	Cassava	3	
	TC9647	Cassava	3	similar to UniRef100_A9TSJ9 Cluster: Predicted protein
	TC3566	Cassava	3	similar to UniRef100_A7QMH9 Cluster
	DV447643	Cassava	3	weakly similar to UniRef100_Q9H4G1 Cluster: Cystatin-9-like precursor
	CK640990	Cassava	3	UniRef100_Q5LRD3 Cluster: Diaminopropionate ammonia-lyase
	TC214	Cassava	3	similar to UniRef100_Q6L4B1 Cluster: EF hand family protein
	DV448335	Cassava	3	similar to UniRef100_Q6L4B1 Cluster: EF hand family protein
	TC3544	Cassava	3	similar to UniRef100_Q7RJ87 Cluster: Malate dehydrogenase
	DV151070	Leafy spurge	3	
	DV122719	Leafy spurge	3	similar to UniRef100_UPI000036F3DC Cluster: PREDICTED: sarcospan
	DV150240	Leafy spurge	3	similar to UniRef100_A7PYE0 Cluster
	DV124243	Leafy spurge	3	homologue to UniRef100_A7QT33 Cluster
	TC1956	Leafy spurge	3	similar to UniRef100_A9V7C9 Cluster: Predicted protein
	TC5303	Leafy spurge	3	similar to UniRef100_A7QBT8 Cluster
	DV149391	Leafy spurge	3	weakly similar to UniRef100_Q9FJ12 Cluster
	DV155430	Leafy spurge	3	weakly similar to UniRef100_Q9FJ12 Cluster
	TC10681	Leafy spurge	3	
	TC9110	Leafy spurge	3	similar to UniRef100_Q0E424 Cluster: Os02g0140100 protein
	TC7558	Leafy spurge	3	similar to UniRef100_A7Q218 Cluster
	TC5692	Leafy spurge	3	similar to UniRef100_P52413 Cluster: Acyl carrier protein 3, chloroplast precursor
	EC609505	rubber tree	3	LatexY13D05 YLX600 Hevea brasiliensis cDNA clone LatexY13D05 5', mRNA sequence
hbr-cand09	DB944810	Cassava	3	similar to UniRef100_A7PY52 Cluster
hbr-cand10	TC11386	Cassava	2	weakly similar to UniRef100_A7PF66 Cluster
	TC9174	Cassava	2.5	similar to UniRef100_Q39079 Cluster: Chaperone protein dnaJ 13
	DV448197	Cassava	3	weakly similar to UniRef100_Q1IRM0 Cluster: Pyrroline-5-carboxylate reductase
	DV128909	Leafy spurge	3	similar to UniRef100_A7NYW5 Cluster

	TC5750	Leafy spurge	3	homologue to UniRef100_A7NYW5 Cluster
	DV141339	Leafy spurge	3	similar to UniRef100_Q66Q67 Cluster: Homeodomain protein HOX3
	EC606284	rubber tree	3	A364 YLX600 Hevea brasiliensis cDNA clone A364 5', mRNA sequence
	EC600724	rubber tree	3	Y89D10 YLX600 Hevea brasiliensis cDNA clone Y89D10 5', mRNA sequence
	EC606931	rubber tree	3	Y10H05 YLX600 Hevea brasiliensis cDNA clone Y10H05 5', mRNA sequence
	EC609097	rubber tree	3	Y20E01 YLX600 Hevea brasiliensis cDNA clone Y20E01 5', mRNA sequence
	EC606501	rubber tree	3	Y61C06 YLX600 Hevea brasiliensis cDNA clone Y61C06 5', mRNA sequence
	EC604245	rubber tree	3	Y63G02 YLX600 Hevea brasiliensis cDNA clone Y63G02 5', mRNA sequence
	EC605511	rubber tree	3	Y36C01 YLX600 Hevea brasiliensis cDNA clone Y36C01 5', mRNA sequence
hbr-cand11	DB938820	Cassava	2	weakly similar to UniRef100_A7QLW0 Cluster
	TC5377	Cassava	3	homologue to UniRef100_Q94DM8 Cluster: Probable ubiquitin-fold modifier 1 precursor
	DV154369	Leafy spurge	3	similar to UniRef100_A7PI18 Cluster
hbr-cand12	DV137624	Leafy spurge	2.5	weakly similar to UniRef100_A7NW61 Cluster
	TC9374	Leafy spurge	3	similar to UniRef100_A7QJB6 Cluster
hbr-cand13	TC10348	Cassava	2.5	weakly similar to UniRef100_A7QUC4 Cluster
	DV449231	Cassava	2.5	
	DV131332	Leafy spurge	3	weakly similar to UniRef100_A2R1R2 Cluster
	DV144220	Leafy spurge	3	UniRef100_A6ZZ69 Cluster: Down-regulator of invasive growth
	TC1168	Leafy spurge	3	similar to UniRef100_Q38M74 Cluster: Brittle 1 protein-like
hbr-cand14	DB950399	Cassava	3	homologue to UniRef100_A7PV61 Cluster
hbr-cand15	DB929249	Cassava	3	
	TC2014	Cassava	3	similar to UniRef100_A7QNF6 Cluster
	TC9999	Leafy spurge	3	similar to UniRef100_A7QMV3 Cluster
hbr-cand16	TC8347	Leafy spurge	1.5	similar to UniRef100_A7PHI8 Cluster
	DB952942	Cassava	2.5	homologue to UniRef100_Q3EC78 Cluster
	TC11068	Cassava	2.5	homologue to UniRef100_Q9ZTV4 Cluster: COP1
	TC2387	Cassava	3	similar to UniRef100_A7R237 Cluster

	DV448422	Cassava	3	similar to UniRef100_Q84VZ3 Cluster
	GR421465	Cassava	3	homologue to UniRef100_Q8H1N8 Cluster: At1g20880/F9H16_14
hbr-cand17	DV154630	Leafy spurge	2	similar to UniRef100_A7Q4M5 Cluster
	TC2669	Leafy spurge	2	
	TC5419	Cassava	2.5	homologue to UniRef100_A7Q9V9 Cluster
	DB935017	Cassava	2.5	homologue to UniRef100_A5AJ03 Cluster: Phosphoribosylformylglycinamide cyclo-ligase
	BM259772	Cassava	2.5	weakly similar to UniRef100_A7PXL8 Cluster
	DV136631	Leafy spurge	2.5	similar to UniRef100_A7Q421 Cluster
	DV157275	Leafy spurge	2.5	similar to UniRef100_A7Q421 Cluster
	DV136981	Leafy spurge	2.5	similar to UniRef100_A7PZJ0 Cluster
	DV444142	Cassava	3	similar to UniRef100_A7P3C7 Cluster
	TC5281	Cassava	3	homologue to UniRef100_A7NZ90 Cluster
	TC3085	Cassava	3	similar to UniRef100_Q84UH4 Cluster: Dehydroascorbate reductase
	TC247	Cassava	3	similar to UniRef100_Q84UH4 Cluster: Dehydroascorbate reductase
	DV142222	Leafy spurge	3	
	TC551	Leafy spurge	3	weakly similar to UniRef100_A7QPC2 Cluster
	DV138595	Leafy spurge	3	similar to UniRef100_A7PL18 Cluster
	DV143108	Leafy spurge	3	similar to UniRef100_Q0IY26 Cluster: Os10g0377300 protein
	TC2262	Leafy spurge	3	similar to UniRef100_A7PZJ0 Cluster
	EC608350	rubber tree	3	Y41G09 YLX600 Hevea brasiliensis cDNA clone Y41G09 5', mRNA sequence
hbr-cand19	TC9479	Cassava	2.5	similar to UniRef100_A7P1K0 Cluster
	DB945615	Cassava	3	
	DB932347	Cassava	3	similar to UniRef100_A4TKN1 Cluster: Membrane protein
	TC2094	Cassava	3	homologue to UniRef100_A7P6F6 Cluster
	TC10890	Cassava	3	similar to UniRef100_Q94KD3 Cluster: At1g71270/F3I17_8
	TC618	Cassava	3	similar to UniRef100_Q41249 Cluster: Protochlorophyllide reductase, chloroplast precursor
	TC6513	Cassava	3	homologue to UniRef100_Q9LKH8 Cluster: NADPH-protochlorophyllide oxidoreductase

	TC4219	Cassava	3	homologue to UniRef100_Q9LKH8 Cluster: NADPH-protochlorophyllide oxidoreductase
	DB920759	Cassava	3	similar to UniRef100_A7P1K0 Cluster
	DV132789	Leafy spurge	3	homologue to UniRef100_Q9LKJ2 Cluster: Phosphoglycerate kinase
	DV137857	Leafy spurge	3	homologue to UniRef100_A7BVP1 Cluster: Indole-3-glycerol-phosphate synthase
	TC8254	Leafy spurge	3	similar to UniRef100_Q41249 Cluster: Protochlorophyllide reductase, chloroplast precursor
	TC1518	Leafy spurge	3	weakly similar to UniRef100_A7NX60 Cluster
hbr-cand20	DV141266	Leafy spurge	2.5	similar to UniRef100_UPI00006D02CD Cluster: ATPase histidine kinase- DNA gyrase B- and HSP90-like domain containing protein
	TC2517	Leafy spurge	2.5	similar to UniRef100_Q84L32-2 Cluster: Isoform 2 of Q84L32
	TC5265	Cassava	3	similar to UniRef100_A7P102 Cluster
	EC604730	rubber tree	3	Y77F08 YLX600 Hevea brasiliensis cDNA clone Y77F08 5', mRNA sequence
hbr-cand18	DV448675	Cassava	3.5	similar to UniRef100_A7Q8K6 Cluster
	DV444891	Cassava	3.5	UniRef100_A0C6T1 Cluster
	DB938590	Cassava	3.5	similar to UniRef100_A7QHW8 Cluster
	TC9189	Leafy spurge	3.5	similar to UniRef100_Q4JLU9 Cluster: Homeodomain protein Msx
	DV137655	Leafy spurge	3.5	similar to UniRef100_Q9LSH1 Cluster: Dihydroxyacetone/glycerone kinase-like protein
	TC3439	Leafy spurge	3.5	similar to UniRef100_P93713 Cluster: PETHy;ZPT2-5
	DB922262	Cassava	4	similar to UniRef100_Q9LHE8 Cluster
	DB931629	Cassava	4	similar to UniRef100_Q9LHE8 Cluster
	TC2624	Cassava	4	similar to UniRef100_A0T2N9 Cluster: Neoxanthin cleavage enzyme-like protein
	DB937821	Cassava	4	UniRef100_P59229 Cluster: Vacuolar ATP synthase 16 kDa proteolipid subunit 4
	TC1265	Cassava	4	UniRef100_P59229 Cluster: Vacuolar ATP synthase 16 kDa proteolipid subunit 4
	DV131573	Leafy spurge	4	
	TC1007	Leafy spurge	4	homologue to UniRef100_A7Q4Z2 Cluster
	TC8099	Leafy spurge	4	similar to UniRef100_A7Q494 Cluster
	DV136929	Leafy spurge	4	weakly similar to UniRef100_Q12CS9 Cluster: Homoserine kinase
	DV126560	Leafy spurge	4	
	TC3480	Leafy spurge	4	similar to UniRef100_A7NVH8 Cluster

	EC604281	rubber tree	4	Y49C02 YLX600 Hevea brasiliensis cDNA clone Y49C02 5'
	EC600306	rubber tree	4	Y69A01 YLX600 Hevea brasiliensis cDNA clone Y69A01 5'
	GR305629	rubber tree	4	TPD_SSH_BC126 TPD responsive transcripts of Hevea brasiliensis (TPD affected bark) Hevea brasiliensis cDNA similar to unknown protein
	EC609905	rubber tree	4	LatexY13D12 YLX600 Hevea brasiliensis cDNA clone LatexY13D12 5', mRNA sequence

Target Acc.: target accession numbers. For the target genes predicted from rubber tree ESTs, the accession numbers are from Genbank. The accession numbers for the other targets are from *Euphorbia esula* (leafy spurge) DFCI gene index release 1 or *Manihot esculenta* (cassava) DFCI gene index release 1.

& Database: the database from which the targets were predicted.

* Expectation: the scores given by the target prediction program. In the 0-5 scale, a score of 0-2 represents a stringent cutoff. For all miRNAs except for hbr-cand18, the score range was set to 0-3 for the prediction. For hbr-cand18, the range was set to 0-4, since no targets were predicted in the 0-3 range.