Table S1. Construction of genomic libraries, generation and filtering of sequencing data used for genomic assembly

Genome sequencing platform	Library	Average length of read (bp)	Total length (Gb)	CLC preliminary assembly	Newbler preliminary assembly	Final assembly
Illumina	fragment size 200 bp; paired end	100	44.2	building basic contigs; connecting contigs	not used	not used
Illumina (filtered)*	fragment size 200 bp; paired end	100	5.33	not used	not used	building contigs; constructing scaffolds
Illumina (filtered)*	fragment size 200 bp; single end	100	2.05	not used	not used	building contigs
Illumina	fragment size 500 bp; paired end	100	26.9	extending contigs; connecting contigs	not used	not used
Illumina (filtered)*	fragment size 500 bp; paired end	80	2.30	not used	not used	building contigs; constructing scaffolds
Roche/454	shotgun; single end	316	8.33	extending contigs	building contigs	building contigs
Roche/454	fragment size 8 kb; paired end	158	5.69	extending contigs; connecting contigs	building contigs; constructing scaffolds	building contigs; constructing scaffolds
Roche/454	fragment size 8 kb; single end	235	2.50	extending contigs	building contigs	building contigs
Roche/454	fragment size 20kb; paired end	148	0.987	not used	building contigs; constructing scaffolds	building contigs; constructing scaffolds
Roche/454	fragment size 20kb; single end	229	0.587	not used	building contigs	building contigs
SOLiD	fragment size 2 kb; paired end	41	3.81	connecting contigs	not used	not used
SOLiD (filtered)*	fragment size 2 kb; paired end	50	0.0918	not used	not used	building contigs; constructing scaffolds

*The Illumina reads were filtered by removing the reads matching repetitive regions, whereas the SOLiD reads were filtered by keeping only the paired reads that were at least 50 bp in length.

Table S2. Scaffolds showing the associated genes anchored on to the respective linkage groups based on the reported molecular markers

	Linkage map-g1
Scaffold 445443	
	Serine-threonine protein kinase
	Conserved hypothetical protein
	Conserved hypothetical protein
	Conserved hypothetical protein
	Conserved hypothetical protein
	Conserved hypothetical protein
	Pyruvate kinase, putative
	Chitinase
	Hevamine
	Hypothetical protein
	Chitinase
	Conserved hypothetical protein
	Hypothetical protein
	Conserved hypothetical protein
	Protein dimerization, putative
	ATP binding protein, putative
	Conserved hypothetical protein
	Ubiquitin conjugating enzyme 2 (E2)
	Ethylene-responsive transcription factor, putative
	Conserved hypothetical protein
	Mitochondrial carrier protein, putative
	Conserved hypothetical protein
	Tetrahydrofolylpolyglutamate synthase, putative
	DNA binding protein, putative
	WRKY transcription factor, putative
	mHbCIRT9
	mHbCIRT319
	RNA polymerase sigma factor rpoD, putative
	Conserved hypothetical protein
Scaffold 365857	
	Nuclear movement protein nudc, putative
	Hypothetical protein
	Hypothetical protein
	Polygalacturonase non-catalytic subunit AroGP3 precursor, putative
	Predicted protein
	mHbCIRA274/380
	Cap binding protein, putative
	Cap binding protein, putative
	Hypothetical protein
	Hypothetical protein
	Thump domain protein, putative

	Thump domain protein, putative
	Hexokinase, putative
	Hexokinase, putative
	Leucine-rich repeat containing protein, putative
Scaffold 180784	
	Trithorax, putative
	Hypothetical protein
	Hypothetical protein
	Hypothetical protein
	ATP binding protein, putative
	Splicing factor 3a, putative
	Glutamate synthase, putative
	Glutamate synthase, putative
	Hypothetical protein
	Conserved hypothetical protein
	Receptor serine/threonine kinase, putative
	Hypothetical protein
	Brassinosteroid Insensitive 1-associated receptor kinase 1 precursor, putative
	Receptor serine/threonine kinase, putative
	Receptor serine/threonine kinase, putative
	Hypothetical protein
	Conserved hypothetical protein
	Brassinosteroid Insensitive 1-associated receptor kinase 1 precursor, putative
	Receptor serine/threonine kinase, putative
	Receptor serine/threonine kinase, putative
	Hypothetical protein
	mHbCIRA134
	Conserved hypothetical protein
	Conserved hypothetical protein
Scaffold 08981	
	hmct22
	hmct21
	Elongation factor 1-beta, putative
	ATP binding protein, putative
	ATP binding protein, putative
	ATP binding protein, putative
	Hypothetical protein
	Conserved oligomeric Golgi complex component, putative
	Conserved oligomeric Golgi complex component, putative
	Polcalcin Jun o, putative
	Cycloeucalenol cycloisomerase, putative
	Cycloeucalenol cycloisomerase, putative
	Leucine-rich repeat protein, putative
	Nucleolar protein nop56, putative
	Adenylate kinase 1, putative
	Aspartyl aminopeptidase, putative

	Predicted protein
	mHbCIRA2684
	Conserved hypothetical protein
Scaffold 175245	
	mHbCIRTAs2455
Scaffold 125722	
	mHbCIRTAs2557
	Hypothetical protein
Scaffold 416894	
	Conserved hypothetical protein
	Hypothetical protein
	Hypothetical protein
	mHbCIRA200
Scaffold 412180	
	Conserved hypothetical protein
	Conserved hypothetical protein
	Conserved hypothetical protein
	Glutamate decarboxylase, putative
	mHbCIRA 2748
	1-aminocyclopropane-1-carboxylate deaminase, putative
	1-aminocyclopropane-1-carboxylate deaminase, putative
	Conserved hypothetical protein
	Homeodomain-leucine zipper protein hd4
	Organic anion transporter, putative
	Organic anion transporter, putative
	Linkage map-g2
Scaffold 416254	
	Protein P21, putative
	Conserved hypothetical protein
	RNA polymerase II ctd phosphatase, putative
	Predicted protein
	Conserved hypothetical protein
	Predicted protein
	RNA binding protein, putative
	RNA binding protein, putative
	Hypothetical protein
	Serine carboxypeptidase, putative
	Predicted protein
	Pentatricopeptide repeat-containing protein, putative
	Pentatricopeptide repeat-containing protein, putative
	Conserved hypothetical protein
	Predicted protein
	ATP binding protein, putative
	ATP binding protein, putative
	mHbCIRA 2348
	Predicted protein

	Conserved hypothetical protein
	Histone-lysine n-methyltransferase, suvh, putative
	Conserved hypothetical protein
	RNA-binding protein, putative
	Hypothetical protein
	Conserved hypothetical protein
	AP2 domain transcription factor RAP2.3, putative
	AP2 domain transcription factor RAP2.3, putative
	Zinc finger protein, putative
	Predicted protein
	Ubiquinol-cytochrome C reductase iron-sulfur subunit, putative
	Aspartate semialdehyde dehydrogenase, putative
	Predicted protein
	Transaldolase, putative
	Cytochrome P450, putative
	Predicted protein
	Pentatricopeptide repeat-containing protein, putative
	Predicted protein
	Predicted protein
	Transferase, transferring glycosyl groups, putative
	Conserved hypothetical protein
	Conserved hypothetical protein
	40S ribosomal protein S27, putative
	Diphosphoinositol polyphosphate phosphohydrolase, putative
Scaffold 272663	
	Cationic amino acid transporter, putative
	Cationic amino acid transporter, putative
	BTB and MATH domain-containing protein, putative
	BTB and MATH domain-containing protein, putative
	Conserved hypothetical protein
	Conserved hypothetical protein
	Sterol regulatory element-binding protein site 2 protease, putative
	Set domain protein, putative
	LOB domain-containing protein, putative
	Histone ubiquitination proteins group (HUPB902)
	Conserved hypothetical protein
	Membrin, putative
	HSP90 co-chaperone, putative
	Conserved hypothetical protein
	BTB/POZ domain-containing protein KCTD9, putative
	BTB/POZ domain-containing protein KCTD9, putative
	Serine/threonine-protein kinase ripk4, putative
	Vitamin-b12 independent methionine synthase
	5-methyltetrahydropteroyltriglutamate
	Predicted protein
	Early nodulin 55-2 precursor, putative

	Early nodulin 55-2 precursor, putative
	Early nodulin 55-2 precursor, putative
	Early nodulin 55-2 precursor, putative
	Mavicyanin, putative
	Predicted protein
	Conserved hypothetical protein
	Annexin, putative
	Predicted protein
	Conserved hypothetical protein
	gSSR096
	Conserved hypothetical protein
	Conserved hypothetical protein
	Conserved hypothetical protein
	Hydrolase, hydrolyzing O-glycosyl compounds, putative
	Hydrolase, hydrolyzing O-glycosyl compounds, putative
	ATECP63, putative
	Syntaxin, putative
	Syntaxin, putative
	Predicted protein
	hmct4
	Conserved hypothetical protein
	Catalytic, putative
	Importin beta-3, putative
	mHbCIRA2534
	Importin beta-3, putative
	Conserved hypothetical protein
	Hypothetical protein
	Tubulin alpha chain, putative
	Eukaryotic translation initiation factor 4e type, putative
	Predicted protein
	Conserved hypothetical protein
	Conserved hypothetical protein
	Adenylsulfate kinase, putative
Scaffold 335127	
	AMP dependent ligase, putative
	AMP dependent ligase, putative
	Conserved hypothetical protein
	mHbCIRA 2368
	Transcription regulator, putative
	Transferase, putative
	Transferase, putative
	3'-N-debenzoyl-2'-deoxytaxol N-benzoyltransferase, putative
	Predicted protein
Scaffold 586014	
	mHbCIRA2734

Scaffold 59282	
	mHbCIRA2510
	Hypothetical protein
	Expressed protein, putative
	Blue copper protein precursor, putative
	Conserved hypothetical protein
	Hypothetical protein
	26S proteasome regulatory subunit S3, putative
	Predicted protein
	Predicted protein
	Predicted protein
	Predicted protein
	Hypothetical protein
Scaffold 421682	
	mHbCIRT2140
	DNA-binding protein MNB1B, putative
	Protein binding protein, putative
	Conserved hypothetical protein
	Predicted protein
	Vacuolar cation/proton exchanger 1a, putative
	Conserved hypothetical protein
	Hevea brasiliensis isolate SSH47 sequence
	Predicted protein
	Conserved hypothetical protein
	Ubiquitin-protein ligase, putative
	Ethylene-inducible protein (ER1)
	Symplekin, putative
	hmct40
	Predicted protein
Scaffold 349088	
	Hypothetical protein
	Predicted protein
	mHbCIRA2381
	mHbCIRA2326
	Conserved hypothetical protein
	Conserved hypothetical protein
Scaffold 222405	
	mHbCIRt283
	Linkage map-g3
Scaffold 174498	
	DNA-directed RNA polymerase, putative
	mHbCIRA278
Scaffold 453132	
	Predicted protein
	Hypothetical protein
	DNA-repair protein xrcc1, putative

	NMDA receptor-regulated protein, putative
	NMDA receptor-regulated protein, putative
	Ring finger protein, putative
	Cysteine protease, putative
	Cysteine protease, putative
	Hypothetical protein
	Myristoyl-acyl carrier protein thioesterase, chloroplast precursor, putative
	Myristoyl-acyl carrier protein thioesterase, chloroplast precursor, putative
	ATP-dependent transporter, putative
	Auxin-responsive protein IAA1, putative
	Hypothetical protein
	Hypothetical protein
	Predicted protein
	Glutathione S-transferase omega
	Oxalate/formate antiporter
	Aspartate aminotransferase, putative
	mHbCIRTAs2558
	Aspartate aminotransferase, putative
	Katanin p60 ATPase-containing subunit, putative
	gHbCIRA2415
	Katanin p60 ATPase-containing subunit
Scaffold 263548	
	gHbCIRA2516
	mHbCIRA156
	Transportin-3, putative
Scaffold 93599	
	Predicted protein
	Electron transporter, putative
	hmct21
	hmct22
	mHbCIRA2485
	Hypothetical Protein
Scaffold 305576	
	hmct22
	hmct21
	mHbCIRTAs2697
Scaffold 198002	
	Conserved Hypothetical Protein
	mHbCIRBAC123d05
	hmct43
	Conserved hypothetical protein
	Conserved hypothetical protein
Scaffold 181532	
	mHbCIRA2264
	Calreticulin-3-like

Scaffold 170728	
	Transcription factor RF2a, putative
	Electron transfer flavoprotein-ubiquinone oxidoreductase
	mHbCIRA2707
	Electron transfer flavoprotein-ubiquinone oxidoreductase, putative
	Predicted protein strictosidine synthase, putative
Scaffold 197224	
	Protein binding protein, putative
	Predicted protein
	Phospholipid:diacylglycerol acyltransferase 2 (PDAT2)
	RNA splicing protein mrs2, mitochondrial, putative
	mHbCIRA2749
	srpk, putative
	Linkage map-g4
Scaffold 131572	
	Ethylene-responsive element binding protein 1 (EREBP1)
	FAD NAD binding oxidoreductases, putative
	AP2/ERF domain-containing transcription factor (ERF43)
	Serine-threonine protein kinase, plant-type, putative
	mHbCIRA2706
	Predicted protein
	Auxin-repressed protein-like protein ARP1
	Ring finger protein, putative
Scaffold 138950	
	Receptor protein kinase CLAVATA1 precursor, putative
	Conserved hypothetical protein
	mHbCIRTA2157
	Conserved hypothetical protein
	mHbCIRT2091
	Conserved hypothetical protein
	Protein binding protein, putative
	Predicted protein
	Predicted protein
Scaffold 541370	
	mHbCIRA2766
Scaffold 430947	
	DNA repair protein reca, putative
	DNA repair protein reca, putative
	Nucleosome assembly protein, putative
	Hypothetical protein
	Regulatory protein NPR1, putative
	Hypothetical Protein
	Calmodulin binding protein, putative
	mHbCIRA385
	Hypothetical Protein
	Casein kinase, putative

	Conserved hypothetical protein
	Diacylglycerol acyltransferase 1 (DGAT-1)
	Dead box ATP-dependent RNA helicase, putative
	n-myristoyl transferase, putative
	DNA binding protein, putative
	Lycopene epsilon cyclase, chloroplast precursor, putative
	Lycopene epsilon cyclase, chloroplast precursor, putative
	Predicted protein
	Conserved hypothetical protein
Scaffold 287934	
	S-receptor kinase, putative
	L-ascorbate peroxidase 1, cytosolic, putative
	Conserved hypothetical protein
	grr1, plant, putative
	Conserved hypothetical protein
	Phopholipase d alpha, putative
	Hbtnr-50
	DNA binding protein, putative
	Multidrug resistance pump, putative
	Beta-glucosidase, putative
	RNA-dependent RNA polymerase, putative
	Xenotropic and polytropic murine leukemia virus receptor ids-4, putative
	Conserved hypothetical protein
	Predicted protein
	Conserved hypothetical protein
	Conserved hypothetical protein
	Triose phosphate chloroplast precursor, putative
	mbHCIRTAs2277
	ATPase n2b, putative
	Predicted protein
	ADP,ATP carrier protein, putative
	ADP,ATP carrier protein, putative
	Conserved hypothetical protein
	Cellulose synthase A catalytic subunit 6 [UDP-forming], putative
	Hbtnr-75
	Hbtnr-101
	Conserved hypothetical protein
	Conserved hypothetical protein
	Hypothetical protein
	Protein With Unknown Function
	tso1, putative
	Acyl-protein thioesterase, putative
	mHbCIRt93
	Peptidyl-prolyl cis-trans isomerase, putative
	Ammonium transporter, putative
	DNA (cytosine-5)-methyltransferase, putative

	Arabidopsis lyrata subsp. lyrata hypothetical protein
	Hypothetical protein
	Predicted Protein
	ran, putative
	Conserved hypothetical protein
	Ubiquinol-cytochrome C reductase complex 14 kda protein
	Potassium channel AKT6, putative
	Boron transporter, putative
	Conserved hypothetical protein
	WD-repeat protein, putative
	Conserved hypothetical protein
	Conserved hypothetical protein
	Conserved hypothetical protein
	Anthocyanidin synthase (ANS1)
	Glycerate dehydrogenase, putative
	Linkage map-g5
Scaffold 123369	
	Arginine/Serine-rich splicing factor, putative
	CCD1, putative
	FAD NAD binding oxidoreductases, putative
	Kinase, putative
	Kinase, putative
	Conserved hypothetical protein
	Predicted protein
	Ubiquitin-protein ligase, putative
	ORMDL, putative
	Predicted protein
	WD-repeat protein, putative
	mHbCIRa460
	Predicted protein (MYB201)
	Predicted protein
	Laccase, putative
	Laccase, putative
	Conserved hypothetical protein
	Beta-fructofuranosidase, putative
	Beta-fructofuranosidase, putative
	Beta-fructofuranosidase, putative
	Conserved hypothetical protein
	Conserved hypothetical protein
	Auxin response factor, putative
	Importin-alpha re-exporter, putative
	AP2/ERF domain-containing transcription factor (DREB56)
	Conserved hypothetical protein
	DNA binding protein, putative
	Predicted protein
	Flavonoid 3-hydroxylase, putative

gHbCIRA2737
Aspartic proteinase nepenthesin-1 precursor, putative
Ubiquitin ligase SINAT3, putative
Ubiquitin ligase SINAT3, putative
Dynamin, putative
Conserved hypothetical protein
Conserved hypothetical protein
Conserved hypothetical protein
Dopamine beta-monooxygenase, putative
Eukaryotic translation initiation factor 3 subunit, putative
Eukaryotic translation initiation factor 3 subunit, putative
gHbCIRT2636
Trithorax, putative
RING-H2 finger protein ATL3K, putative
RING-H2 finger protein ATL3K, putative
mbHCIRTAs 2559
Hypothetical protein
Beclin-1, putative
Predicted protein
Hypothetical protein
Cyclic nucleotide-gated ion channel, putative
Predicted protein
Dead box ATP-dependent RNA helicase, putative
Hypothetical protein
Triacylglycerol lipase, putative
Conserved hypothetical protein
Pentatricopeptide repeat-containing protein, putative
Chitinase, putative
Chitinase, putative
Histone H3 (HTR904)

Scaffold 274716

Pectinesterase-2 precursor, putative
Pectinesterase, putative
Pentatricopeptide repeat-containing protein, putative
Carboxypeptidase regulatory region-containing protein, putative
Carboxypeptidase regulatory region-containing protein, putative
Conserved hypothetical protein
Hypothetical protein
Conserved hypothetical protein
mHbCIRTAs2186
Kinase, putative
Enzyme inhibitor, putative
Protein binding protein, putative
Predicted protein
WRKY transcription factor 3

Scaffold 127481	
	mHbCIRA36
Scaffold 297292	
	mHbCIRA 2745
	Carboxy-terminal kinesin, putative
	Carboxy-terminal kinesin, putative
	gHbCIRTAs2724
Scaffold 129112	
	mHbCIRA2509
	Serine-threonine protein kinase, plant-type, putative
Scaffold 25532	
	mHbCIRA2518
Scaffold 53705	
	Methylcobalamin:com methyltransferase, putative
	mHbCIRT2603
	Linkage map-g6
Scaffold 227539	
	mHbCIRa296
	ATP binding protein, putative
Scaffold 588071	
	Hypothetical protein
	Type II inositol 5-phosphatase, putative
	Beta-hexosaminidase, putative
	Predicted protein
	mHbCIRa 367
	Pentatricopeptide repeat-containing protein, putative
	Pentatricopeptide repeat-containing protein, putative
	Serine-threonine protein kinase, plant-type, putative
	Endo-1,4-beta-glucanase, putative
	Latex cyanogenic beta glucosidase
	Latex cyanogenic beta glucosidase
	Type II inositol 5-phosphatase, putative
	Predicted protein
	Pentatricopeptide repeat-containing protein, putative
	Type II inositol 5-phosphatase, putative
	Cohesin subunit rad21, putative
	mHbCIRa2391
	Splicing factor U2AF-associated protein, putative
	Latex cyanogenic beta glucosidase
	Type II inositol 5-phosphatase, putative
	Predicted protein
	Beta-hexosaminidase, putative
	Acetolactate synthase, putative
	Leucine zipper-ef-hand containing transmembrane protein, putative
	Cohesin subunit rad21, putative

Scaffold 163591	
	Signal recognition particle receptor subunit beta, putative
	Conserved hypothetical protein
	Conserved hypothetical protein
	Axial regulator YABBY4, putative
	Hypothetical protein
	ATP binding protein, putative
	Nucleic acid binding protein, putative
	Conserved hypothetical protein
	Conserved hypothetical protein
	Pyroglutamyl-peptidase I, putative
	Pentatricopeptide repeat-containing protein, putative
	Polygalacturonase precursor, putative
	mHbCIRa 170
	Polygalacturonase, putative
	Phosphatidylinositol 3-kinase class, putative
	Phosphatidylinositol 3-kinase class, putative
	Phosphatidylinositol 3-kinase class, putative
Scaffold 228549	
	Predicted protein (MYB)
	Predicted protein
	mHbCIRA2498
	ATATH13, putative
	Conserved hypothetical protein
	Conserved hypothetical protein
	Nuclease, putative
	Nucleoside transporter, putative
	Conserved hypothetical protein
	Conserved hypothetical protein
	Predicted protein
	Splicing endonuclease positive effector sen1, putative
	Conserved hypothetical protein
	Conserved hypothetical protein
	Glutaredoxin S12
	Monooxygenase, putative
	Monooxygenase, putative
	Myosin XI, putative
Scaffold 186880	
	mHbCIRA2398
Scaffold 187443	
	mHbCIRA2511
Scaffold 114815	
	Structural constituent of cell wall, putative
	Predicted protein
	Magnesium-dependent phosphatase 1-like
	ATP binding protein, putative

	Hypothetical protein
	Conserved hypothetical protein
	Conserved hypothetical protein
	Conserved hypothetical protein
	Conserved hypothetical protein
	Conserved hypothetical protein
	ATP binding protein, putative
	Cysteine-type endopeptidase, putative
	mHbCIRA2406
	ATP binding protein, putative
	ATP binding protein, putative
	Conserved hypothetical protein
	Hypothetical protein
	Conserved hypothetical protein
	Linkage map-g7
Scaffold 122409	
	Serine/threonine protein kinase, putative
	Ubiquitin-protein ligase, putative
	mHbCIRTAs2743
	Protein G10, putative
	ATP-binding cassette transporter, putative
	ATP-binding cassette transporter, putative
	Starch branching enzyme II, putative
	Starch branching enzyme II, putative
	gHbCIRA2758
	Conserved hypothetical protein
	Predicted protein
Scaffold 224310	
	mHbCIRA2708
Scaffold 146047	
	tRNA (guanine-n(7)-)-methyltransferase, putative
	Remorin, putative
	Pentatricopeptide repeat-containing protein, putative
	GTP-binding protein typa/bipa, putative
	mHbCIRA2429
	Predicted protein
	Calcium-dependent protein kinase (CDPK1)
Scaffold 238809	
	Conserved hypothetical protein
	Villin 1-4, putative
	g15mHbCIRA295
	Predicted protein
	Insulin-degrading enzyme, putative
Scaffold 416082	
	gHbCIRA2763

	Signal peptidase I, putative
	hmct21
Scaffold 463202	
	Predicted protein
	Proliferation-associated 2g4, putative
	Proliferation-associated 2g4, putative
	mHbCIRA2686
	Conserved hypothetical protein
	Glutaredoxin, grx, putative
	Glutaredoxin, grx, putative
Scaffold 519782	
	mHbCIRT2115
Scaffold 93102	
	Phospholipase C 3 precursor, putative
	Conserved hypothetical protein
	Protein binding protein, putative
	mHbCIRA2762
	Deoxyribonuclease, putative
	DNA-binding protein smubp-2, putative
	Conserved hypothetical protein
	Transcription regulator, putative
	Linkage map-g8
Scaffold 231182	
	mHbCIRA2442
	Conserved hypothetical protein
	Probable membrane-associated kinase regulator 1-like
Scaffold 161238	
	Ubiquitin-associated uba/ubx domain-containing protein, putative
	TBC1 domain family member
	DUF246 Domain-containing protein At1g04910-like
	Conserved hypothetical protein
	Pentatricopeptide repeat-containing protein, putative
	Anthranilate N-benzoyltransferase protein, putative
	Arp2/3 complex 20 kd subunit, putative
	Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein (NOV)
	mHbCIRa251
	Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein (NOV)
	Alkaline phytoceramidase, putative
	Methionine-tRNA synthetase, putative
	Beta-galactosidase, putative
	Conserved hypothetical protein
	Ubiquitin-protein ligase, putative
	Conserved hypothetical protein
	Non-imprinted in Prader-Willi/Angelman syndrome region protein, putative
	Conserved hypothetical protein
	Chaperone protein dnaJ 20, chloroplast precursor, putative

	hmct40
Scaffold 417274	
	Chromatin remodeling complex subunit (CHR952)
	mHbCIRT73
	Mom(plant), putative
	Hypothetical protein
	Mom(plant), putative
	Conserved hypothetical protein
	Glycosyltransferase, cazy family GT8
	Conserved hypothetical protein
Scaffold 354160	
	Nuclear inhibitor of protein phosphatase-1, putative
	Nuclear inhibitor of protein phosphatase-1, putative
	mHbCIRT686
	Nuclear inhibitor of protein phosphatase-1, putative
Scaffold 235226	
	Calcium ion binding protein, putative
	Glutamate receptor 2 plant, putative
	Hypothetical protein
	Glutamate receptor 2 plant, putative
	Predicted protein
	Predicted protein
	Homogentisate 1,2-dioxygenase, putative
	Hypothetical protein
	Ring finger protein, putative
	mHbCIRT2542
	RNA exonuclease, putative
Scaffold 328348	
	Processing protein PRP40, putative
	mHbCIRT2635
	Processing protein PRP40, putative
Scaffold 136822	
	Predicted protein
	mHbCIRa120
	Hypothetical protein
Scaffold 488663	
	mHbCIRT730
	Phospholipid:diacylglycerol acyltransferase 1-2 (PDAT1-2)
Scaffold 412100	
	Transcription factor, putative
	Transcription factor, putative
	Transcription factor, putative
	M630
	ATP-dependent clp protease ATP-binding subunit clpx, putative
	ATP-dependent clp protease ATP-binding subunit clpx, putative
	Transcription factor, putative

	Conserved hypothetical protein
	Predicted protein
	Nitrate transporter, putative
	Nitrate transporter, putative
	CDK-activating kinase
	cak1, putative
	Sugar transporter, putative
	Predicted protein
	Transcription factor, putative
	3-hydroxyacyl-CoA dehyrogenase, putative
	Conserved hypothetical protein
	Multidrug resistance pump, putative
	Multidrug resistance pump, putative
	Conserved hypothetical protein
	Aspartate aminotransferase, putative
	Predicted protein
	Hypothetical protein
	Cytoplasmic dynein light chain, putative
	Conserved hypothetical protein
	Hypothetical protein
	Pentatricopeptide repeat-containing protein, putative
	Linkage map-g9
Scaffold 89544	
	mHbCIRTA2244
	hmct40
	mHbCIRA2298
	DNA binding protein, putative
	Homeobox protein, putative
Scaffold 124084	
	Brassinosteroid Insensitive 1-associated receptor kinase 1 precursor, putative
	mHbCIRA2744
Scaffold 139710	
	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase, putative
	tRNA delta(2)-isopentenylpyrophosphate transferase, putative
	Lipid binding protein, putative
	Lysophosphatidic acid acyltransferase, putative
	Conserved hypothetical protein
	Conserved hypothetical protein
	Multidrug resistance pump, putative
	Multidrug resistance pump, putative
	4-hydroxy-3-methylbut-2-enyl diphosphate reductase
	NAD dependent epimerase/dehydratase, putative
	NAD dependent epimerase/dehydratase, putative
	S-adenosylmethionine-dependent methyltransferase, putative
	S-adenosylmethionine-dependent methyltransferase, putative
	mHbCIRa104

	Protein ariadne-1, putative
	Conserved hypothetical protein
	Non-symbiotic hemoglobin, putative
	Non-symbiotic hemoglobin, putative
	Conserved hypothetical protein
	Hypothetical protein
Scaffold 199300	
	mHbCIRA2689
Scaffold 412552	
	Predicted protein
	Transcriptional regulator SUPERMAN, putative
	mHbCIRTAs2178
	Transcriptional regulator SUPERMAN, putative
	Ethylene receptor, putative
	DNA binding protein, putative
	Protein transporter, putative
	Hypothetical protein
	DNA repair helicase rad5,16, putative
	DNA repair helicase rad5,16, putative
	Conserved hypothetical protein
	Conserved hypothetical protein
	Desacetoxyvindoline 4-hydroxylase, putative
	Outward rectifying K+ channel (KCO1)
	1-aminocyclopropane-1-carboxylate oxidase homolog 12-like
	Desacetoxyvindoline 4-hydroxylase, putative
	Conserved hypothetical protein
	Auxin-induced protein 5NG4, putative
	DNA binding protein, putative
	Predicted protein
Scaffold 411125	
	ATP binding protein, putative
	ATP binding protein, putative
	gHbCIRA2522
	mHbCIRA2432
	Eukaryotic translation initiation factor 2c, putative
	Eukaryotic translation initiation factor 2c, putative
Scaffold 128180	
	ATP binding protein, putative
	Conserved hypothetical protein
	Conserved hypothetical protein
	Zinc finger protein, putative
	Predicted protein
	Lipase
	Predicted protein
	Helicase, putative
	Receptor serine-threonine protein kinase, putative

	Receptor serine-threonine protein kinase, putative
	Glutaredoxin, grx, putative
	Acyl-coa binding protein, putative
	Anaphase promoting complex subunit, putative
	Anaphase promoting complex subunit, putative
	Predicted protein
	Tonneau, putative
	Serine/threonine protein kinase, putative
	Spo0B-associated GTP-binding protein, putative
	DNA binding protein, putative
	Nucleic acid binding protein, putative
	Always early, putative
	mHbCIRA2682
	Always early, putative
	AMP-activated protein kinase, gamma regulatory subunit, putative
	Hypothetical protein
	Hypothetical protein
	Pentatricopeptide repeat-containing protein, putative
	Flavonol synthase/flavanone 3-hydroxylase, putative
	Cullin-1, putative
	Plastid CUL1 (CUL1)
	Linkage map-g10
Scaffold 121193	
	mHbCIRA2408
Scaffold 431381	
	SAUR family protein (SAUR23)
	Calcium-dependent protein kinase, putative
	Calcium-dependent protein kinase, putative
	Calcium-dependent protein kinase, putative
	Conserved hypothetical protein
	mHbCIRA2767
	Conserved hypothetical protein
	gHbCIRA2510
	Predicted protein
	Predicted protein
	Conserved hypothetical protein
	Predicted protein
	hmac3
Scaffold 601618	
	Hbtnr-46
	Hbtnr-91
	Cytochrome P450, putative
	Cytochrome P450, putative
	Cytochrome P450, putative
	Heat shock protein binding protein
	Predicted protein

	gHbCIRA2317
	Amino acid binding protein, putative
	mHbCIRA2320
Scaffold 106428	
	mHbCIRA2425
Scaffold 297920	
	Protein ABIL2, putative
	Hypothetical protein
	Hypothetical protein
	Predicted protein
	Cdk8, putative
	Transcription factor, putative
	mHbCIRT2096
Scaffold 410607	
	Transducin/WD40 domain-containing protein-like protein (AT4G14310)
	Structural molecule, putative
	mHbCIRa214
	Kinesin heavy chain, putative
	Desiccation-associated protein (MTR_2g077860)
	Glycolipid transfer protein, putative
	Conserved hypothetical protein
	60S ribosomal protein L14, putative
	Protein phosphatase 2c, putative
	Conserved hypothetical protein
	Conserved hypothetical protein
	Kinesin light chain, putative
	Conserved hypothetical protein
	mHbCIRT2668
Scaffold 151685	
	mHbCIRA2316
	WRKY transcription factor, putative
Scaffold 168316	
	Sodium-bile acid cotransporter, putative
	mHbCIRA2388
Scaffold 237846	
	Vam6/Vps39-like protein-like
	Conserved hypothetical protein
	Conserved hypothetical protein
	Protein FAM96B, putative
	Transporter, putative
	Chitin-inducible gibberellin-responsive protein, putative
	Succinate dehydrogenase, putative
	Steroid 22-alpha hydroxylase (DWF4)
	Steroid 22-alpha hydroxylase (DWF4)
	Hypothetical protein
	ISWI chromatin remodeling complex ATPase ISW1, putative

	Conserved hypothetical protein
	U1 small nuclear ribonucleoprotein 70 kDa, putative
	maf protein, putative
	Somatic embryogenesis receptor kinase, putative
	Somatic embryogenesis receptor kinase, putative
	Somatic embryogenesis receptor kinase, putative
	Somatic embryogenesis receptor kinase, putative
	Conserved hypothetical protein
	Acidic leucine-rich nuclear phosphoprotein 32-related protein-like
	Sugar transporter, putative
	mHbCIRA2702
	Predicted protein
	hmct40
	Sugar transporter, putative
	Conserved hypothetical protein
	Glutamyl-trna synthetase 1, 2, putative
	TPR repeat-containing thioredoxin TTL1-like
	Tetratricopetide-repeat thioredoxin-like 4 protein (TTL4)
Scaffold 415719	
	ATP-binding cassette transporter, putative
	Conserved hypothetical protein
	Vacuolar cation/proton exchanger 1a, putative
	NudC domain-containing protein, putative
	Kinase, putative
	ATP binding protein, putative
	Conserved hypothetical protein
	Cyclophilin, putative
	Ubiquitin-protein ligase, putative
	Pyridoxin biosynthesis protein PDX1, putative
	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase, putative
	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase, putative
	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase, putative
	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase, putative
	Transcription factor, putative
	Conserved hypothetical protein
	Omega-3 fatty acid desaturase (Fad3)
	Omega-3 fatty acid desaturase, endoplasmic reticulum, putative
	Hypothetical protein
	Selt-like protein-like
	Serine-threonine protein kinase, plant-type, putative
	Tonoplast intrinsic protein, putative
	Predicted protein
	Alpha-galactosidase/alpha-n-acetylgalactosaminidase, putative
	Pentatricopeptide repeat-containing protein, putative
	Conserved hypothetical protein
	Putative integral membrane protein conserved region

	Conserved hypothetical protein
	Conserved hypothetical protein
	ATP-binding cassette transporter, putative
	Histone deacetylase, putative
	Histone deacetylase, putative
	Protein transport protein sec23, putative
	Protein transport protein sec23, putative
	mHbCIRTAs2196
	Protein transport protein sec23, putative
	Taz protein, putative
	Calmodulin binding protein, putative
	Gibberellin 3-beta-dioxygenase, putative
	Serine-threonine protein kinase, plant-type, putative
	Conserved hypothetical protein
	Cucumisin precursor, putative
	Cucumisin precursor, putative
	Conserved hypothetical protein
	Type 2 diacylglycerol acyltransferase (DGAT2)
	Type 2 diacylglycerol acyltransferase (DGAT2)
	FAR1-RELATED SEQUENCE 5-like
	FAR1-RELATED SEQUENCE 5-like
	Auxin:hydrogen symporter, putative
	Auxin:hydrogen symporter, putative
Scaffold 172714	
	Histidine-containing phosphotransfer protein, putative
	Serine-threonine protein kinase, plant-type, putative
	Pentatricopeptide repeat-containing protein, putative
	Bsu-protein phosphatase, putative
	Stromal antigen, putative
	Stromal antigen, putative
	NPL4-like protein 1-like
	GTPase activating protein, putative
	Conserved hypothetical protein
	RNA binding protein, putative
	U1 small nuclear ribonucleoprotein C, putative
	mHbCIRA157
	U1 small nuclear ribonucleoprotein C, putative
	F-box/kelch-repeat protein (MTR_2g015760)
	Conserved hypothetical protein
	Short chain alcohol dehydrogenase, putative
	Shikimate dehydrogenase, putative
	Predicted protein
	Transcription factor, putative
	Transcription factor, putative
	Serine endopeptidase degp2, putative
	Monooxygenase, putative

	Predicted protein
	Conserved hypothetical protein
Scaffold 284371	
	mHbCIRA2392
	Big map kinase/bmk, putative
Scaffold 429519	
	Hypothetical protein
	DNA binding protein, putative
	Ubiquitin-conjugating enzyme h, putative
	Chromo domain protein, putative
	Latex beta-cyanoalanine synthase
	Conserved hypothetical protein
	Hypothetical protein
	Conserved hypothetical protein
	Cytochrome p450, putative
	Sialin, putative
	Sialin, putative
	Ubiquitin-protein ligase, putative
	Minor histocompatibility antigen H13, putative
	Receptor protein kinase, putative
	Pentatricopeptide repeat-containing protein, putative
	Receptor protein kinase, putative
	Receptor protein kinase, putative
	Conserved hypothetical protein
	Conserved hypothetical protein
	Conserved hypothetical protein
	CRP, putative
	mHbCIRA2730
	Rop guanine nucleotide exchange factor, putative
	Pentatricopeptide repeat-containing protein, putative
	Pentatricopeptide repeat-containing protein, putative
	Gibberellin 20-oxidase, putative
	Transcription factor, putative
	Beta-amylase, putative
	Beta-amylase, putative
	Calmodulin-binding heat-shock protein, putative
	60S ribosomal protein L36e, putative
	Acyl-CoA thioesterase, putative
	Protein AFR, putative
	Conserved hypothetical protein
	Hypothetical protein
	DMT1 gene for chloroplast-resident DNA methyltransferase
	Receptor protein kinase, putative
	DNA binding protein, putative
	Kiwellin, putative
	Kiwellin, putative

	Synaptotagmin, putative
	Actin depolymerizing factor, putative
	KDEL motif-containing protein 1 precursor, putative
	KDEL motif-containing protein 1 precursor, putative
	Double-stranded RNA-specific adenosine deaminase
	tRNA-specific adenosine deaminase 1-like
	Remorin, putative
	R2R3-MYB transcription factor, putative
	gHbCIRA2741
	Dead box ATP-dependent RNA helicase, putative
	Acetyl-coenzyme A carboxylase carboxyl transferase alpha, putative
	Conserved hypothetical protein
	Linkage map-g11
Scaffold 492213	
	mHbCIRBAC83E19
Scaffold 201737	
	Calmodulin binding protein, putative
	mHbCIRTAs2260
Scaffold 280583	
	mHbCIRa268
Scaffold 158826	
	mHbCIRA2736
	fkbp-rapamycin associated protein, putative
Scaffold 45077	
	ADP-ribosylation factor, putative
	mHbCIRA2536
	Transcription factor, putative
Scaffold 25873	
	mHbCIRA297
Scaffold 438547	
	mHbCIRa2535
	Glycoprotein 3-alpha-l-fucosyltransferase A, putative
	Molybdopterin-binding, putative
	Molybdopterin-binding, putative
	Linkage map-g12
Scaffold 130216	
	Hedgehog receptor, putative
	mHbCIRA2484
Scaffold 451604	
	SAB, putative
	SAB, putative
	SAB, putative
	SAB, putative
	SAB, putative
	GATA transcription factor, putative

	GATA transcription factor, putative
	UDP-glucosyltransferase, putative
	UDP-glucosyltransferase, putative
	Conserved hypothetical protein
	Conserved hypothetical protein
	Conserved hypothetical protein
	Conserved hypothetical protein
	Conserved hypothetical protein
	map3k delta-1 protein kinase, putative
	Predicted protein
	Conserved hypothetical protein
	Protein VERNALIZATION-INSENSITIVE, putative
	Protein VERNALIZATION-INSENSITIVE, putative
	Cytochrome P450, putative
	Cytochrome P450, putative
	DNA binding protein, putative
	DNA binding protein, putative
	Argininosuccinate lyase, putative
	Argininosuccinate lyase, putative
	mHbCIRT2085
	Conserved hypothetical protein
	Conserved hypothetical protein
	Conserved hypothetical protein
	Conserved hypothetical protein
Scaffold 114620	
	mHbCIRTAs2698
	Mitogen-activated protein kinase kinase kinase
Scaffold 224948	
	Hydrolase, putative
	Disease resistance protein RPP13, putative
	mHbCIRT2588
	Serine/threonine-protein kinase cx32, putative
	Dead box ATP-dependent RNA helicase, putative
	SAUR family protein (SAUR28)
Scaffold 185123	
	mHbCIRA2715
Scaffold 193057	
	Pentatricopeptide repeat-containing protein, putative
	Protein phosphatase methylesterase, putative
	Protein phosphatase methylesterase, putative
	Phosphoprotein phosphatase
	Cytochrome P450, putative
	Cytochrome P450, putative
	Tubulin-specific chaperone E, putative
	Tubulin-specific chaperone E, putative
	Conserved hypothetical protein

	Conserved hypothetical protein
	Conserved hypothetical protein
	Conserved hypothetical protein
	Conserved hypothetical protein
	mHbCIRA2405
	Ubiquitin ligase protein, lrsam1, putative
	Hypothetical protein
	Chlorophyll A/B binding protein, putative
	Linkage map-g13
Scaffold 323928	
	Conserved hypothetical protein
	Serine-threonine protein kinase, plant-type, putative
	DNA-binding protein MNB1B, putative
	Hypothetical protein
	DNA-binding protein MNB1B, putative
	Conserved hypothetical protein
	Predicted protein
	DNA repair helicase rad5,16, putative
	Aspartic proteinase nepenthesin-1 precursor, putative
	Aspartic proteinase nepenthesin-1 precursor, putative
	Protein arginine n-methyltransferase, putative
	Protein arginine n-methyltransferase, putative
	Mitochondrial import receptor subunit tom40, putative
	Mitochondrial import receptor subunit tom40, putative
	Reticulocalbin-2 precursor, putative
	mHbCIRa140
	Reticulocalbin-2 precursor, putative
	DNA binding protein, putative
	DNA binding protein, putative
	Conserved hypothetical protein
	Conserved hypothetical protein
	Glucose regulated repressor protein, putative
	Protein-s isoprenylcysteine O-methyltransferase, putative
	Conserved hypothetical protein
	Transmembrane protein 53-like
	Glycerol-3-phosphate dehydrogenase, putative
	Cytokinin dehydrogenase, putative
	Cytokinin dehydrogenase, putative
	Silene conica chromosome 76 mitochondrion sequence
	Glycine max protein IQ-DOMAIN 14-like
	N-acetyltransferase, putative
	Conserved hypothetical protein
	Hypothetical protein
	Hypothetical protein
	Nucleotide pyrophosphatase/phosphodiesterase, putative
	Transcription factor, putative

	Predicted protein
	Disease resistance response protein, putative
	Conserved hypothetical protein
	Conserved hypothetical protein
	Conserved hypothetical protein
	Conserved hypothetical protein
	Short chain alcohol dehydrogenase, putative
	Predicted protein
	O-methyltransferase, putative
	CC-NBS-LRR resistance protein
Scaffold 123832	
	Conserved hypothetical protein
	Nucleoporin NUP53, putative
	Hypothetical protein
	Conserved hypothetical protein
	Cell division cycle protein 27 homolog B-like
	Predicted protein
	DNA binding protein, putative
	DNA binding protein, putative
	mHbCIRA2394
	Conserved hypothetical protein
	Hypothetical protein
	Casein kinase, putative
	Casein kinase, putative
	Conserved hypothetical protein
	Conserved hypothetical protein
Scaffold 207081	
	Katanin p60 ATPase-containing subunit, putative
	mHbCIRA2415
	Katanin p60 ATPase-containing subunit, putative
Scaffold 411742	
	mHbCIRA2523
	Hypothetical protein
Scaffold 411971	
	Ethylene-insensitive3 protein, putative
	mHbCIRA2508
	hmct21
Scaffold 411167	
	Phenylalanine ammonia-lyase, putative
	Hypothetical protein
	Carbonic anhydrase, putative
	Conserved hypothetical protein
	mHbCIRA2757
	Bel1 homeotic protein, putative
	Conserved hypothetical protein

Scaffold 148311	
	mHbCIRTAs2456
	Linkage map-g14
Scaffold 416127	
	Predicted protein
	mHbCIRa282
Scaffold 501411	
	mHbCIRA2435
Scaffold 156035	
	Conserved hypothetical protein
	Hypothetical protein
	Protein binding protein, putative
	Conserved hypothetical protein
	Glycine-rich RNA-binding protein, putative
	Hypothetical protein
	Hypothetical protein
	Phosphoserine phosphatase, putative
	ATP synthase f1, gamma subunit, putative
	Mitochondrial carrier protein, putative
	Hypothetical protein
	Histone deacetylase hda1, putative
	mHbCIRA2545
	hmct21
	Hypothetical protein
	Hydrolase, hydrolyzing O-glycosyl compounds, putative
Scaffold 126947	
	Alpha-n-acetylglucosaminidase, putative
	Alpha-n-acetylglucosaminidase, putative
	Betaine-aldehyde dehydrogenase
	Betaine-aldehyde dehydrogenase
	Mannose-1-phosphate guanyltransferase, putative
	Pentatricopeptide repeat-containing protein, putative
	Cell division cycle, putative
	Two-component sensor protein histidine protein kinase, putative
	Actin binding protein, putative
	Lipase, putative
	Conserved hypothetical protein
	Microtubule-associated protein TORTIFOLIA1, putative
	Conserved hypothetical protein
	DNA binding protein, putative
	Hevea brasiliensis isolate SSH16
	Conserved hypothetical protein
	mHbCIRA2423
	Predicted protein
	Hypothetical protein
	Hypothetical protein

	Hypothetical protein
	Predicted protein
	5-formyltetrahydrofolate cyclo-ligase, putative
	5-formyltetrahydrofolate cyclo-ligase, putative
	Rhicadhesin receptor precursor, putative
	DNA binding protein, putative
	GTR20
	Conserved hypothetical protein
	R2R3-MYB transcription factor, putative
	Galactosyltransferase, putative
	Predicted protein
	Predicted protein
	ATP binding protein, putative
	ATP binding protein, putative
	ATP binding protein, putative
	tRNA ligase, putative
	tRNA ligase, putative
	tRNA ligase, putative
	HIPL1 protein precursor, putative
	Epstein-Barr nuclear antigen, putative
	Predicted protein
	Conserved hypothetical protein
	Conserved hypothetical protein
	LOB domain-containing protein, putative
	Conserved hypothetical protein
	ACR24
Scaffold 409802	
	Brassinosteroid insensitive 1-associated receptor kinase 1 precursor
	Protein bem46, putative
	Protein tipD, putative
	Conserved hypothetical protein
	Cysteine protease, putative
	Hypothetical protein
	Predicted protein
	Conserved hypothetical protein
	Predicted protein
	Nucleic acid binding protein, putative
	Nucleic acid binding protein, putative
	Nucleic acid binding protein, putative
	Predicted protein
	Transferase, transferring glycosyl groups, putative
	Transferase, transferring glycosyl groups, putative
	Esterase precursor, putative
	Ubiquitin-protein ligase, putative
	Elongator complex protein, putative
	Predicted protein

	Sentrin/sumo-specific protease, putative
	Predicted protein
	Ubiquinone biosynthesis protein coq-8, putative
	Hypothetical protein
	Nucleoside diphosphate kinase, putative
	DELLA protein RGL1, putative
	Anthranilate N-benzoyltransferase protein, putative
	Anthranilate N-benzoyltransferase protein, putative
	Conserved hypothetical protein
	Glyceraldehyde 3-phosphate dehydrogenase, putative
	Conserved hypothetical protein
	Conserved hypothetical protein
	Predicted protein
	Bromodomain-containing protein, putative
	Bromodomain-containing protein, putative
	Predicted protein
	Conserved hypothetical protein
	mHbCIRA2504
	AMP dependent CoA ligase, putative
Scaffold 120605	
	mHbCIRTA2452
	Conserved hypothetical protein
	Linkage map-g15
Scaffold 169399	
	Hypothetical protein
	Sodium-bile acid cotransporter, putative
	mHbCIRa289
	Bromodomain-containing protein, putative
	mHbCIRA2391
	Predicted protein
	Bromodomain-containing protein, putative
	Hypothetical protein
	Transmembrane receptor, putative
	Hypothetical protein
	Hypothetical protein
Scaffold 134709	
	Nucleic acid binding protein, putative
	Nucleic acid binding protein, putative
	Protein kinase APK1B, chloroplast precursor, putative
	Predicted protein
	mHbCIRT2086
	Hypothetical protein
Scaffold 435366	
	Conserved hypothetical protein
	Protein binding protein, putative
	Protein binding protein, putative

	Protein binding protein, putative
	Serine carboxypeptidase, putative
	mHbCIRA2483
	mHbCIRA2391
	mHbCIRA314
	Sterol regulatory element-binding protein site 2 protease, putative
Scaffold 129826	
	mHbCIRTAs2709
Scaffold 43997	
	NAD dehydrogenase, putative
	NAD dehydrogenase, putative
	Conserved hypothetical protein
	Predicted protein
	mHbCIRA2391
	Predicted protein
	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase, putative
	mHbCIRA2510
	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase, putative
	MTA/SAH nucleosidase, putative
	hmct53
	Hbtnr-71
	mHbCIRt182
	gHbCIRA2685
	3-Phosphoinositide-dependent protein kinase-1, putative
	3-Phosphoinositide-dependent protein kinase-1, putative
Scaffold 42633	
	Conserved hypothetical protein
	Lipid binding protein, putative
	Conserved hypothetical protein
	Predicted protein
	mHbCIRA2697
	mHbCIRa390
	hmct21
	hmct22
	Serine-threonine protein kinase, plant-type, putative
Scaffold 254588	
	Hypothetical protein
	Pentatricopeptide repeat-containing protein, putative
	Two-component system sensor histidine kinase/response regulator, putative
	Hypothetical protein
	Leucine-rich repeat-containing protein 2, lrrc2, putative
	Leucine-rich repeat-containing protein 2, lrrc2, putative
	Leucine-rich repeat-containing protein 2, lrrc2, putative
	ATP binding protein, putative
	Conserved hypothetical protein
	Conserved hypothetical protein

	Conserved hypothetical protein
	RING-H2 finger protein ATL3C, putative
	Transcription factor RF2b, putative
	Dihydropteroate synthase, putative
	Predicted protein
	Predicted protein
	mHbCIRA2391
	Hypothetical protein
	mHbCIRTA2157
	hmct40
	Hypothetical protein
	Hypothetical protein
	mHbCIRa095
	ATP binding protein, putative
	Mn-superoxide dismutase (SODMn) gene
	Conserved hypothetical protein
	Predicted protein
	Aspartic proteinase nepenthesin-1 precursor, putative
Scaffold 119584	
	Dead box ATP-dependent RNA helicase, putative
	Hypothetical protein
	Hypothetical protein
	mHbCIRA2492
	Predicted protein
	mHbCIRA2492
	mHbCIRTA2157
	Linkage map-g16
Scaffold 154109	
	Signal recognition particle receptor subunit beta, putative
	mHbCIRTAs2225
Scaffold 134200	
	hmct40
	Paramyosin, putative
	Cytochrome P450, putative
	Afc, putative
	Pentatricopeptide repeat-containing protein, putative
	Alpha-galactosidase/alpha-n-acetylgalactosaminidase, putative
	mHbCIRA131
	Alpha-L-fucosidase 2 precursor, putative
	Alpha-L-fucosidase 2 precursor, putative
	Protein phosphatase 2c, putative
	ATP binding protein, putative
	Conserved hypothetical protein
	Protein phosphatase 2c, putative
	Cytochrome P450, putative

	Serine/threonine-protein kinase bri1, putative
	ATP binding protein, putative
	Suppressor of ty, putative
	Predicted protein
	Cysteine desulfuration protein sufe, putative
	Cytochrome P450, putative
	Hypothetical protein
Scaffold 251160	
	Axial regulator YABBY4, putative
	mHbCIRA2407
Scaffold 177599	
	Hypothetical protein
	Heat shock protein 70 (HSP70)-interacting protein, putative
	Predicted protein
	Alcohol dehydrogenase, putative
	mHbCIRA097
	Nucleotide binding protein, putative
	Predicted protein
Scaffold 158956	
	mHbCIRA2765
	Ribonuclease z, chloroplast, putative
	Ribonuclease z, chloroplast, putative
Scaffold 307979	
	Hbtnr-17
	mHbCIRA275
	Beta-1,3-galactosyltransferase sqv-2, putative
Scaffold 420218	
	MADs box protein, putative
	mHbCIRA2396
Scaffold 234640	
	mHbCIRA179
	Linkage map-g17
Scaffold 121986	
	mHbCIRTs2188
Scaffold 413909	
	gHbCIRTAs2720
	Conserved hypothetical protein
	Conserved hypothetical protein
	Conserved hypothetical protein
	Glucan endo-1,3-beta-glucosidase precursor, putative
	mHbCIRA2414
	Hypothetical protein
	Conserved hypothetical protein
	Conserved hypothetical protein
	DUF26 domain-containing protein 1 precursor, putative
	Conserved hypothetical protein

	Nucleic acid binding protein, putative
	Nucleic acid binding protein, putative
	Calcium ion binding protein, putative
	Ubiquitin-conjugating enzyme, putative
	hmac2
	hmct21
	gHbCIRA2511
Scaffold 418287	
	hmct12
	mHbCIRA2425
	Beta-ketoacyl-ACP synthase I
	mHbCIRa344
	mHbCIRa78
	Conserved hypothetical protein
	Urease accessory protein ureG, putative
	DNA replication licensing factor MCM3, putative
	Beta-ketoacyl-ACP synthase I
Scaffold 433878	
	Pectinesterase (MTR_3g010770)
	Coatomer gamma subunit, putative
	mHbCIRT140
	Guanine nucleotide-binding protein beta, putative
	Glucan endo-1,3-beta-glucosidase precursor, putative
	mHbCIRA2418-2
	Adenylyl cyclase-associated protein, putative
	Cytochrome P450 3A27 putative
	Serine/threonine-protein kinase PBS1, putative
	Hypothetical protein
	Predicted protein
	2-Hydroxyacid dehydrogenase, putative
	Conserved hypothetical protein
	Predicted protein
	NADH-ubiquinone oxidoreductase 1, chain, putative
	Phenylalanyl-trna synthetase beta chain, putative
	Phenylalanyl-trna synthetase beta chain, putative
	Conserved hypothetical protein
	lrr receptor protein kinase, putative
	Hypothetical protein
	DNA binding protein, putative
	Hypothetical protein
	Hypothetical protein
	Predicted protein
	Predicted protein
	Acyltransferase, putative
	Hypothetical protein

Scaffold 133200	
	mHbCIRT2447
Scaffold 521115	
	mHbCIRA2391
	Oligopeptide transporter, putative
	Cadmium-induced protein AS8, putative
	mHbCIRA2387
	Predicted protein
	mHbCIRTA2157
	hmac3
	Linkage map-g18
Scaffold 122775	
	Multidrug resistance protein ABC transporter family
	Multidrug resistance protein ABC transporter family
	Mitochondrial translational initiation factor, putative
	Ubiquitin ligase protein cop1, putative
	Ubiquitin ligase protein cop1, putative
	Predicted protein
	Predicted protein
	Hypothetical protein
	Ubiquitin-conjugating enzyme E2, putative
	Predicted protein
	Aldose 1-epimerase, putative
	Beta-1,3-galactosyltransferase sqv-2, putative
	50S ribosomal protein L18, chloroplast precursor, putative
	mHbCIRT2113
	Predicted protein
Scaffold 174767	
	mHbCIRA2197
Scaffold 108198	
	Glutathione s-transferase, putative
	Conserved hypothetical protein
	Conserved hypothetical protein
	Conserved hypothetical protein
	Conserved hypothetical protein
	DNA binding protein, putative
	UTP-glucose-1-phosphate uridylyltransferase, putative
	UTP-glucose-1-phosphate uridylyltransferase, putative
	NADP-specific isocitrate dehydrogenase, putative
	Glutamate decarboxylase, putative
	Conserved hypothetical protein
	nnp-1 protein, putative
	Predicted protein
	Conserved hypothetical protein
	Conserved hypothetical protein

	Conserved hypothetical protein
	Transcription factor, putative
	Predicted protein
	Nonsense-mediated decay protein, putative
	mHbCIRA2422
	Importin beta-3, putative
	Oxidoreductase, putative
	Conserved hypothetical protein
	Zinc finger protein, putative
	Receptor protein kinase, putative
Scaffold 155107	
	Amine oxidase, putative
	O-linked n-acetylglucosamine transferase, ogt, putative
	O-linked n-acetylglucosamine transferase, ogt, putative
	N-acetylglucosamine kinase, putative
	N-acetylglucosamine kinase, putative
	mHbCIRA463
	Conserved hypothetical protein
	Serine/threonine-protein kinase PBS1, putative
	Serine/threonine-protein kinase PBS1, putative
	Small nucleolar RNA-associated protein 14 homolog A-like
	protein kinase, putative
	F-box/leucine rich repeat protein, putative
	F-box/leucine rich repeat protein, putative
	Transcription initiation factor TFIID subunit
	Conserved hypothetical protein
	Hypothetical protein
	Phosphoenolpyruvate carboxylase
Scaffold 181819	
	mHbCIRA320
Scaffold 436803	
	Protein with unknown function
	Transcription factor, putative
	Serine/threonine-protein kinase cx32, putative
	Serine/threonine-protein kinase cx32, putative
	Dihydrodipicolinate synthase, putative
	Nucellin, putative
	Disease resistance response protein, putative
	Suppressor of actin, putative
	mHbCIRA2482
	Catalase (cat)
	Hypothetical protein
	Plant ubiquilin, putative
	SSR P2-D6-2
	Cyclin B, putative
	Predicted protein

	GTP binding protein, putative
	GTP binding protein, putative
	Predicted protein
	Hypothetical protein
	Isocitrate dehydrogenase, putative
Scaffold 155502	
	Hypothetical protein
	mHbCIRA2409
Scaffold 577425	
	Sodium-dependent phosphate transport protein, putative
	mHbCIRTAs2217
	Cytochrome P450, putative
	Conserved hypothetical protein
	Predicted protein
	Josephin-2, putative
	Predicted protein
	Catalytic, putative
	Catalytic, putative
	Predicted protein
	Conserved hypothetical protein
	Conserved hypothetical protein
	Sugar transporter, putative
	Predicted protein
	Predicted protein
	DNA binding protein, putative
	phosphatidylinositol n-acetylglucosaminyltransferase subunit p, putative
	conserved hypothetical protein
	mHbCIRA2391
Scaffold 410482	
	mHbCIRT373
	Hypothetical protein
	mHbCIRT2391
	Serine-threonine protein kinase, plant-type, putative
	Serine-threonine protein kinase, plant-type, putative
	Serine-threonine protein kinase, plant-type, putative
	ATP binding protein, putative
Scaffold 513701	
	DNA mismatch repair protein mlh1, putative
	DNA mismatch repair protein mlh1, putative
	DNA mismatch repair protein mlh1, putative
	Dead box ATP-dependent RNA helicase, putative
	ACR37
	mHbCIRT1067
	Hydrolase, putative
	Hypothetical protein
	Prefoldin-related ke2-like protein

Scaffold 128818	
	Conserved hypothetical protein
	mHbCIRA2439
	Conserved hypothetical protein
	Conserved hypothetical protein
	Conserved hypothetical protein
	Serine-threonine protein kinase, plant-type, putative
Scaffold 467142	
	mHbCIRTAs 2744
	Aspartate kinase, putative
Scaffold 336055	
	mHbCIRA288
Scaffold 308928	
	mHbCIRTAs 2271
	Sterol desaturase, putative

Table S3. Main classes of repeat elements in the *H. brasiliensis* genome assembly

Class	Types	Total repeats (%)
DNA transposons	En-Spm	0.61
	MuDR	0.45
	hAT-Tag1	0.21
	hAT-Ac	0.14
	hAT-Tip100	0.09
	Helitron	0.01
	Others	0.05
Retrotransposons	LTR/Gypsy	38.20
	LTR/Copia	7.38
	LTR/Caulimovirus	0.39
	LINE/ RTE-BovB	0.97
	LINE/ L1	0.34
	LINE/CR1	0.05
	LINE/ R1	0.02
	SINE	0.01
	Others	0.18
Satellite		0.02
Simple repeat		0.64
Unknown		50.24

Table S4. Summary statistics of gene models predicted by seven programs

	EVM	AUGUSTUS	FGENESH	GENEID	GENEMARK HMME	GLIMMER HMM	SNAP
Number of models	68,955	48,087	62,020	65,851	65,669	65,902	59,591
Total number of bases	47,978,108	41,396,159	47,897,431	39,074,868	44,307,210	30,116,191	41,503,482
Average ORF length (bp)	696	861	772	593	675	457	696

Table S5. Comparison of publicly available *H. brasiliensis* transcripts with the genome

Resource	Accession No.	*Hevea* clone	No. Sequences	No. Aligned[a]	% Aligned
NCBI dbEST[b]	Various	Primarily (>90%) RRIM600	37,826	36,786	97.25
BIOTEC, Thailand[c]	N/A	RRIM600	28,300	28,237	99.78
NCBI GEO[d]	GSE26514	RY7-33-97	48,768	45,640	93.59
NCBI TSA[e]	JR344291-JR366936	RY7-33-97	22,646	20,589	90.92
Total			**137,540**	**131,252**	**95.43**

[a] BLAST hits with E-value < 10^{-5} and 90% sequence identity cutoff

[b] Data available as of October 2012

[c] Isotig sequences from http://www4a.biotec.or.th/rubber/Download (ref. 6)

[d] Unigenes from ref. 7

[e] Assembled transcripts from ref. 10

Table S6. General features of the transcriptome assembly

Number of contigs	73,060
Mean length of contigs (bp)	1,173
Length of the largest contig (bp)	15,597
Number of contigs aligned to the genome (>90% sequence identity)	72,644
Number of contigs with NR alignment	55,154
Number of unique GI accession IDs	19,788
Number of contigs with matching protein coverage of 80-100%	18,571
Number of unique GIs with matching protein coverage of 80-100%	10,161
Number of contigs with matching protein coverage of 50-80%	13,198
Number of unique GIs with matching protein coverage of 50-80%	6,593

Table S7. Functional annotation of predicted proteins for *H. brasiliensis*

Protein databases	Number of proteins
NR alignment	52,968
KEGG alignment	52,825
KOG/COG assignment	33,472
EC assignment	16,779
KO assignment	28,488
GO assignment	26,816
InterPro signature	41,743

Table S8. Comparison of KOG functions across various sequenced plant genomes

KOG Functions	*Hevea brasiliensis*	*Ricinus communis*	*Populus trichocarpa*	*Arabidopsis thaliana*	*Eucalyptus grandis*	*Oryza sativa*	*Zea mays*
INFORMATION STORAGE AND PROCESSING							
[J] Translation, ribosomal structure and biogenesis	1236	663	1129	1068	1207	1109	2290
[A] RNA processing and modification	1067	547	999	940	1023	976	1814
[K] Transcription	1459	826	1619	1618	1608	1508	2419
[L] Replication, recombination and repair	661	314	654	504	595	486	853
[B] Chromatin structure and dynamics	377	183	348	349	323	284	578
CELLULAR PROCESSES AND SIGNALING							
[D] Cell cycle control, cell division, chromosome partitioning	627	300	537	565	593	495	969
[Y] Nuclear structure	122	40	80	72	60	62	128
[V] Defense mechanisms	274	136	261	180	334	280	370
[T] Signal transduction mechanisms	5216	1959	4288	2837	6806	4006	4857
[M] Cell wall/membrane/envelope biogenesis	464	202	366	288	478	365	589
[N] Cell motility	7	2	3	5	4	6	2
[Z] Cytoskeleton	1092	404	826	701	1046	697	1333
[W] Extracellular structures	116	55	115	66	81	73	91
[U] Intracellular trafficking, secretion, and vesicular transport	1496	638	1276	1142	1367	1188	2210
[O] Posttranslational modification, protein turnover, chaperones	2886	1486	2691	2396	3227	2726	4451
METABOLISM							
[C] Energy production and conversion	1119	657	973	749	1555	982	1585
[G] Carbohydrate transport and metabolism	1665	804	1354	1102	1817	1336	1993
[E] Amino acid transport and metabolism	1119	613	962	809	1266	1011	1565
[F] Nucleotide transport and metabolism	299	157	232	215	243	281	475
[H] Coenzyme transport and metabolism	289	159	239	212	292	235	393
[I] Lipid transport and metabolism	1178	638	1038	832	1478	963	1635
[P] Inorganic ion transport and metabolism	902	433	848	590	963	673	1045
[Q] Secondary metabolites biosynthesis, transport and catabolism	1470	768	1171	785	2007	1018	1289
POORLY CHARACTERIZED							
[R] General function prediction only	3493	1834	3085	2790	4156	3023	4499
[S] Function unknown	1449	723	1388	1163	1675	1282	2240

Table S9. Pfam domains in the *H. brasiliensis* genome. Only the most abundant domains (≥10 hits) are listed.

Pfam Domain	Hits
Leucine Rich Repeat	7259
Ankyrin repeat	1030
EF hand	657
GTPase of unknown function	534
ABC transporter	518
ATPase family associated with various cellular activities (AAA)	433
Binding-protein-dependent transport system inner membrane component	348
ATP synthase A chain	319
Cytochrome P450	292
7 transmembrane receptor (rhodopsin family)	290
Cytochrome C and Quinol oxidase polypeptide I	283
DEAD/DEAH box helicase	211
Elongation factor Tu GTP binding domain	188
Helicase conserved C-terminal domain	147
Homeobox domain	134
FAD dependent oxidoreductase	129
alpha/beta hydrolase fold	128
haloacid dehalogenase-like hydrolase	114
Elongation factor Tu domain 2	103
Glycosyl transferases group 1	93
CBS domain pair	82
His Kinase A (phosphoacceptor) domain	80
4Fe-4S binding domain	78
Aminotransferase class I and II	78
Calcineurin-like phosphoesterase	74
ATP synthase alpha/beta family, nucleotide-binding domain	69
Alcohol dehydrogenase GroES-like domain	63
Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase	55
Acetyltransferase (GNAT) family	52
AMP-binding enzyme	52
Cytochrome b(C-terminal)/b6/petD	52
4Fe-4S iron sulfur cluster binding proteins, NifH/frxC family	41
Aldehyde dehydrogenase family	41
Glycosyl transferase family 2	39
Cytochrome b(N-terminal)/b6/petB	32
Cytochrome C oxidase subunit II, transmembrane domain	32
HAMP domain	30
Elongation factor Tu C-terminal domain	27
Bacterial regulatory helix-turn-helix protein, lysR family	24
ATP synthase alpha/beta family, beta-barrel domain	23
Bacterial regulatory helix-turn-helix proteins, AraC family	21
Bacterial regulatory proteins, gntR family	18
gag gene protein p24 (core nucleocapsid protein)	18
Helix-turn-helix	18
Bacterial regulatory proteins, tetR family	15
gag gene protein p17 (matrix protein)	15

Table S10. Predicted subcellular localization of *H. brasiliensis* gene models based on SignalP 3.0 analysis

Localization Site	Hits	GO Cellular Component ID
Chloroplast	1699	0005576, 0009543, 0009507
Extracellular	1367	0005618
Plasma Membrane	554	0005886
Vacuolar Membrane	368	0005774(2)
Cytosol	286	0005829
Nuclear	249	0005634
Endoplasmic Reticulum	56	0005783
Mitochondria	47	0005739
Golgi Apparatus	12	0005794(1)
Peroxisome	5	0005777(2)
Total	**4643**	

Table S11. tRNA types found in the *H. brasiliensis* genome

tRNA type	Number	Number of Introns
Ala	37	1
Arg	50	
Asn	24	
Asp	29	
Cys	17	
Gln	19	
Glu	33	
Gly	58	
His	16	
Ile	33	
Leu	59	1
Lys	40	
Met	47	11
Phe	27	
Pro	14	
Ser	62	
Thr	42	
Trp	13	
Tyr	21	17
Val	40	
Pseudo	32	3
Sup	12	
Undet	4	
Total	**729**	**33**

Table S12. Gene Ontology (GO) analysis of *Hevea* specific genes. Only the most abundant GO terms (≥10 hits) are listed.

GO terms	Hits	Description
GO:0005524	746	ATP binding
GO:0000166	409	Nucleotide binding
GO:0004672	374	Protein kinase activity
GO:0006468	374	Protein phosphorylation
GO:0006915	335	Apoptosis
GO:0006952	325	Defense response
GO:0004674	294	Protein serine/threonine kinase activity
GO:0003676	278	Nucleic acid binding
GO:0016301	232	Kinase activity
GO:0016740	225	Transferase activity
GO:0003677	204	DNA binding
GO:0016491	198	Oxidoreductase activity
GO:0008270	189	Zinc ion binding
GO:0055114	189	Oxidation-reduction process
GO:0016020	185	Membrane
GO:0016787	171	Hydrolase activity
GO:0016021	150	Integral to membrane
GO:0008152	130	Metabolic process
GO:0007165	122	Signal transduction
GO:0004888	111	Transmembrane signaling receptor activity
GO:0031224	111	Intrinsic to membrane
GO:0045087	111	Innate immune response
GO:0032440	107	2-alkenal reductase[NAD(p)] activity
GO:0017111	103	Nucleoside-triphosphatase activity
GO:0003824	101	Catalytic activity
GO:0015074	101	DNA integration
GO:0004721	92	Phosphoprotein phosphatase activity
GO:0004872	86	Receptor activity
GO:0005488	85	Binding
GO:0003723	79	RNA binding
GO:0005634	76	Nucleus
GO:0003964	74	RNA-directed DNA polymerase activity
GO:0006278	63	RNA-dependent DNA replication
GO:0005529	51	Sugar binding
GO:0045449	49	Regulation of transcription, DNA-dependent
GO:0004715	48	Non-membrane spanning protein tyrosine kinase
GO:0046872	48	Metal ion binding
GO:0006508	47	Proteolysis
GO:0005975	44	Carbohydrate metabolic process
GO:0006355	37	Regulation of transcription, DNA-dependent
GO:0004713	36	Protein tyrosine kinase activity
GO:0016310	36	Phosphorylation
GO:0004553	35	Hydrolase activity, hydrolyzing O-glycosyl
GO:0004523	34	Ribonuclease H activity
GO:0005506	34	Iron ion binding
GO:0004709	33	MAP kinase kinase kinase activity
GO:0005622	33	Intracellular
GO:0048544	33	Recognition of pollen
GO:0004497	30	Monooxygenase activity
GO:0020037	29	Heme binding
GO:0005509	27	Calcium ion binding
GO:0009055	27	Electron carrier activity
GO:0043169	26	Cation binding
GO:0006350	25	Transcription, DNA-dependent
GO:0016758	25	Transferase activity, transferring hexosyl groups
GO:0016798	25	Hydrolase activity, acting on glycosyl bonds

GO:0046983	23	Protein dimerization activity
GO:0016829	22	Lyase activity
GO:0016757	21	Transferase activity, transferring glycosyl groups
GO:0005737	20	Cytoplasm
GO:0055085	20	Transmembrane transport
GO:0000287	19	Magnesium ion binding
GO:0000785	19	Chromatin
GO:0003682	19	Chromatin binding
GO:0004190	19	Aspartic-type endopeptidase activity
GO:0006333	19	Chromatin assembly or disassembly
GO:0004697	18	Protein kinase C activity
GO:0008233	16	Peptidase activity
GO:0006351	14	Transcription, DNA-dependent
GO:0008353	14	RNA polymerase II carboxy-terminal domain kinase activity
GO:0000160	13	Two-component signal transduction system (phosphorelay)
GO:0047213	13	Anthocyanidin 3-O-glucosyltransferase activity
GO:0004714	12	Transmembrane receptor protein tyrosine kinase activity
GO:0005525	12	GTP binding
GO:0008236	12	Serine-type peptidase activity
GO:0003700	11	Sequence-specific DNA binding transcription factor activity
GO:0004252	11	Serine-type endopeptidase activity
GO:0004568	11	Chitinase activity
GO:0006032	11	Chitin catabolic process
GO:0016998	11	Cell wall macromolecule catabolic process
GO:0050660	11	Flavin adenine dinucleotide binding
GO:0006810	10	Transport
GO:0008168	10	Methyltransferase activity
GO:0032259	10	Methylation
GO:0044237	10	Cellular metabolic process
GO:0050662	10	Coenzyme binding

Table S13. InterPro domains within the *Hevea* specific lineage. Only the most abundant domains (≥10 hits) are listed.

InterPro ID	Hits	Domain Description
IPR001611	846	Leucine-rich repeat
IPR017442	178	Serine/threonine-protein kinase-like domain
IPR002885	124	Pentatricopeptide repeat
IPR001245	110	Serine-threonine/tyrosine-protein kinase
IPR002182	110	NB-ARC
IPR013210	86	Leucine-rich repeat-containing N-terminal, type 2
IPR002110	54	Ankyrin repeat
IPR000157	49	Toll-Interleukin receptor
IPR005162	49	Retrotransposon gag protein
IPR001128	35	Cytochrome P450
IPR004158	30	Protein of unknown function DUF247, plant
IPR001480	24	Bulb-type lectin domain
IPR013242	23	Retroviral aspartyl protease
IPR005508	22	Protein of unknown function DUF313
IPR002902	20	Gnk2-homologous domain
IPR003340	20	Transcriptional factor B3
IPR004252	18	Transposase, Ptta/En/Spm, plant
IPR003656	17	Zinc finger, BED-type predicted
IPR000626	16	Ubiquitin
IPR021820	16	S-locus receptor kinase, C-terminal
IPR001810	15	F-box domain, cyclin-like
IPR002213	15	UDP-glucuronosyl/UDP-glucosyltransferase
IPR000858	13	S-locus glycoprotein
IPR000504	12	RNA recognition motif domain
IPR001878	12	Zinc finger, CCHC-type
IPR003676	12	Auxin responsive SAUR protein
IPR005630	12	Terpene synthase, metal-binding domain
IPR013695	12	Wall-associated kinase
IPR001153	11	Barwin
IPR005123	11	Oxoglutarate/iron-dependent oxygenase
IPR023210	11	NADP-dependent oxidoreductase domain
IPR001360	10	Glycoside hydrolase, family 1
IPR011713	10	Leucine-rich repeat 3

Table S14. Pfam domains within the *Hevea* specific lineage. Only the most abundant domains (≥10 hits) are listed.

Pfam ID	Hits	Domain Description
PF00560	846	LRR_1
PF00069	178	Pkinase
PF01535	124	PR
PF00931	110	NB-ARC
PF07714	110	Pkinase_Tyr
PF08263	86	LRRNT_2
PF00023	54	Ank
PF01582	49	TIR
PF03732	49	Retrotrans_gag
PF00067	35	p450
PF03140	30	Domain of unknown function
PF01453	24	D-mannose binding lectin
PF08284	23	Retroviral aspartyl protease
PF03754	22	Domain of unknown function (DUF313)
PF01657	20	Domain of unknown function
PF02362	20	B3 domain
PF03004	18	Plant transposase (Ptta/En/Spm family)
PF02892	17	ED zinc finger
PF00240	16	Ubiquitin
PF11883	16	Domain of unknown function
PF00201	15	Glucuronosyltransferase
PF00646	15	F-box protein
PF00954	13	S-locus glycoprotein family
PF00076	12	RNA recognition motif
PF00098	12	Zinc finger
PF02519	12	Auxin responsive protein
PF03936	12	Terpene synthase family, metal binding domain
PF08488	12	Wall-associated kinase
PF00248	11	Aldo-keto reductase
PF00967	11	Barwin domain
PF03171	11	2OG-Fe(II) oxygenase superfamily
PF00232	10	Glycoside hydrolase family 1
PF07725	10	Leucine Rich Repeat

Table S15. KOG analysis of *Hevea* specific genes

KOG Functions	**Counts**
Information and Storage and Processing	
[J] Translation, ribosomal structure and biogenesis	27
[A] RNA processing and modification	18
[K] Transcription	21
[L] Replication, recombination and repair	30
[B] Chromatin structure and dynamics	10
Cellular Processes and Signaling	
[D] Cell cycle control, cell division, chromosome partitioning	17
[Y] Nuclear structure	2
[V] Defense mechanisms	16
[T] Signal transduction mechanisms	603
[M] Cell wall/membrane/envelope biogenesis	29
[N] Cell motility	0
[Z] Cytoskeleton	116
[W] Extracellular structures	11
[U] Intracellular trafficking, secretion, and vesicular transport	13
[O] Posttranslational modification, protein turnover, chaperones	89
Metabolism	
[C] Energy production and conversion	48
[G] Carbohydrate transport and metabolism	74
[E] Amino acid transport and metabolism	38
[F] Nucleotide transport and metabolism	2
[H] Coenzyme transport and metabolism	12
[I] Lipid transport and metabolism	32
[P] Inorganic ion transport and metabolism	22
[Q] Secondary metabolites biosynthesis, transport and catabolism	80
Poorly Characterized	
[R] General function prediction only	140
[S] Function unknown	67

Table S16. Rubber biosynthesis related genes in the *H. brasiliensis* genome. Shading indicates the transcript has been validated from leaf and/or latex cDNA pools.

Gene model	**Gene name**	**EC No.**	**Members**
HBM _contig317144 _s139324c15 _gene2	1,4-alpha-glucan branching enzyme	2.4.1.18	1
HBM_contig1307528_s417190c7_gene1	1-deoxy-D-xylulose-5-phosphate isomeroreductase	1.1.1.267	2
HBM_contig343183_s151438c5_gene1			
HBM_contig1288739_s409811c4_gene1	1-deoxyxylulose-5-phosphate synthase	2.2.1.7	7
HBM_contig529416_s246980c14_gene1			
HBM_contig199115_s88445_gene1			
HBM_contig366145_s162700_gene1			
HBM_contig979245_s352662c2_gene3			
HBM_contig1343951_s444526c6_gene1			
HBM_contig1404580_s501548c30_gene1			
HBM_contig1289901_s410013c1_gene1	2,1-fructan:2,1-fructan 1-fructosyltransferase/levansucrase	2.4.1.10	2
HBM_contig1297666_s412376_gene1			
HBM_contig1326688_s430296c2_gene2	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	4.6.1.12	2
HBM_contig217879_s96943c3_gene1			
HBM_contig1339539_s440773c5_gene3	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	2.7.7.60	2
HBM_contig229209_s101968_gene1			
HBM _contig382299 _s170997c9 _gene2	2-oxoglutaratedehydrogenase	1.2.4.2	1
HBM _contig395100 _s177727c26 _gene1	4-alpha-glucanotransferase	2.4.1.25	1
HBM_contig1308223_s417615c21_gene1	4-diphosphocytidyl-2-C-methyl-d-erythritol kinase	2.7.1.148	2
HBM_contig302280_s132669c17_gene1			
HBM_contig318055_s139710c8_gene1	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	1.17.1.2	3
HBM_contig276900_s122507c5_gene1			
HBM_contig297371_s130496_gene1			
HBM _contig1074439 _s372022c11 _gene1	6-phosphofructokinase	2.7.1.11	5
HBM _contig1164696 _s393417c29 _gene2			
HBM _contig396545 _s178492 _gene1			
HBM _contig434052 _s198679c8 _gene2			
HBM _contig945098 _s342802c4 _gene3			
HBM _contig1302790 _s414786c2 _gene1	6-phosphogluconate dehydrogenase	1.1.1.44	3
HBM _contig1374823 _s472809c3 _gene1			
HBM _contig289576 _s127312c17 _gene3			
HBM _contig368493 _s163834c3 _gene1	6-phosphogluconolactonase	3.1.1.31	1
HBM _contig338536 _s149176c3 _gene1	Acetyl-CoA C-acetyltransferase	2.3.1.9	3
HBM_contig407283_s184142c3_gene1			
HBM_contig440778_s202339_gene1			
HBM _contig298278 _s130904c3 _gene3	Acid phosphatase	3.1.3.2	12
HBM _contig670075 _s281714c1 _gene1			
HBM _contig134158 _s58687c27 _gene1			
HBM _contig355008 _s157135c8 _gene1			
HBM _contig438518 _s201108c18 _gene1			
HBM _contig1494088 _s582224c2 _gene2			

HBM _contig323185 _s142103c31 _gene1			
HBM _contig348258 _s153791c20 _gene1			
HBM _contig1409221 _s506095c5 _gene3			
HBM _contig1016681 _s361260c5 _gene1			
HBM _contig431766 _s197470c4 _gene1			
HBM _contig1409222 _s506095c6 _gene1			
HBM _contig147570 _s64869c11 _gene1	Aconitate hydratase	4.2.1.3	2
HBM _contig907698 _s335276c27 _gene1			
HBM _contig1292498 _s410603c18 _gene2	Aldose 1-epimerase	5.1.3.3	2
HBM _contig1318907 _s424517c3 _gene1			
HBM _contig318329 _s139806c20 _gene1	Alpha, alpha-trehalase	3.2.1.28	2
HBM_contig1318212_s423994c4_gene1			
HBM _contig285982 _s125966c2 _gene2	Alpha-amylase	3.2.1.1	2
HBM _contig393825 _s177072c1 _gene1			
HBM _contig1022739 _s362558c6 _gene2	Alpha-glucosidase	3.2.1.20	2
HBM _contig286418 _s126148c2 _gene1			
HBM _contig1357960 _s456977c8 _gene3	ATP citrate synthase	2.3.3.8	4
HBM _contig298249 _s130891c6 _gene1			
HBM _contig340487 _s150149c5 _gene1			
HBM _contig756485 _s300037c2 _gene5			
HBM_contig1038211_s365857c8_gene3	Hexokinase/Glucokinase	2.7.1.1/ 2.7.1.2	14
HBM_contig1038212_s365857c9_gene1			
HBM_contig1161305_s392766c5_gene2			
HBM_contig1302222_s414481c14_gene1			
HBM_contig1348390_s448422c26_gene1			
HBM_contig264692_s117484c7_gene1			
HBM_contig274496_s121527c2_gene1			
HBM_contig355900_s157502c9_gene1			
HBM _contig1302222 _s414481c14 _gene1			
HBM _contig1348390 _s448422c26 _gene1			
HBM _contig264692 _s117484c7 _gene1			
HBM _contig274496 _s121527c2 _gene1			
HBM _contig313150 _s137410c19 _gene1			
HBM _contig355900 _s157502c9 _gene1			
HBM _contig1289509 _s409944c2 _gene1	β-fructofuranosidase/ Fructan β-fructosidase	3.2.1.26/ 3.2.1.80	34
HBM _contig1303515 _s415144c5 _gene1			
HBM _contig1324950 _s428974c9 _gene1			
HBM _contig1345306 _s445741c4 _gene1			
HBM _contig1352768 _s452278c9 _gene1			
HBM _contig1357953 _s456977c1 _gene1			
HBM _contig232810 _s103616c2 _gene3			
HBM _contig232867 _s103635c14 _gene1			
HBM _contig299515 _s131427c8 _gene1			
HBM _contig303742 _s133305c3 _gene1			
HBM _contig336329 _s148152c12 _gene1			

HBM _contig425247 _s193932c4 _gene2			
HBM_contig09843_s04035c2_gene1			
HBM_contig1030687_s364424c2_gene1			
HBM_contig1030688_s364424c3_gene1			
HBM_contig1119081_s384118c2_gene1			
HBM_contig1119082_s384118c3_gene1			
HBM_contig1303515_s415144c5_gene1			
HBM_contig1308208_s417615c6_gene2			
HBM_contig1352768_s452278c9_gene1			
HBM_contig1357953_s456977c1_gene1			
HBM_contig232810_s103616c2_gene3			
HBM_contig279164_s123369c13_gene5			
HBM_contig283350_s124975c7_gene1			
HBM_contig299515_s131427c8_gene1			
HBM_contig303742_s133305c3_gene1			
HBM_contig323410_s142207c17_gene1			
HBM_contig326170_s143445_gene1			
HBM_contig336323_s148152c6_gene1			
HBM_contig336327_s148152c10_gene2			
HBM_contig336329_s148152c12_gene1			
HBM_contig369602_s164404_gene1			
HBM_contig425247_s193932c4_gene2			
HBM_contig819355_s316235_gene1			
HBM _contig1322037 _s426750c3 _gene1	Carbonate dehydratase	4.2.1.1	5
HBM _contig1352352 _s451908c3 _gene2			
HBM _contig285737 _s125861c3 _gene1			
HBM _contig343186 _s151438c8 _gene1			
HBM _contig383816 _s171800 _gene1			
HBM _contig366916 _s163044c2 _gene1	Citrate (Si) synthase	2.3.3.1	1
HBM_contig1289286_s409907c6_gene1	Rubber cis-polyprenylcistransferase	2.5.1.20	3
HBM_contig272314_s120676_gene1			
HBM_contig919895_s338071c2_gene1			
HBM _contig257034 _s114160c16 _gene1	Dihydrolipoamide dehydrogenase	1.8.1.4	4
HBM _contig316009 _s138773 _gene1			
HBM _contig393998 _s177156c10 _gene1			
HBM _contig484019 _s225263c9 _gene1			
HBM_contig1311115_s419277c5_gene1	Dimethylallyltranstransferase	2.5.1.1	2
HBM_contig526985_s245906c4_gene1			
HBM _contig656003 _s279612c2 _gene3	Diphosphomevalonate decarboxylase	4.1.1.33	3
HBM_contig1061580_s369994_gene1			
HBM_contig1294315_s411141c4_gene1			
HBM _contig1305637 _s416164c2 _gene1	Farnesyl diphosphate synthase	2.5.1.10	4
HBM_contig657916_s279871c2_gene2			
HBM_contig290987_s127806c1_gene1			
HBM_contig290988_s127806c2_gene1			

HBM _contig1311115 _s419277c5 _gene1 HBM_contig253780_s112770c3_gene1 HBM_contig1292487_s410603c7_gene1 HBM_contig1298993_s412919c4_gene1 HBM_contig550434_s255571_gene1 HBM_contig324001_gene1 HBM_contig324027_gene1	Geranyl geranyl diphosphate synthase	2.5.1.29	7
HBM _contig1289171 _s409884c2 _gene1 HBM _contig1303826 _s415277c9 _gene1 HBM _contig1322658 _s427165c3 _gene3 HBM _contig1339227 _s440512c5 _gene3 HBM _contig180992 _s80187c5 _gene1 HBM _contig316188 _s138852c6 _gene2 HBM _contig320635 _s140865c2 _gene1 HBM _contig339478 _s149632c15 _gene2 HBM _contig522414 _s243848c9 _gene1	Fructose-bisphosphate aldolase	4.1.2.13	9
HBM _contig214134 _s95238c3 _gene1 HBM _contig285749 _s125863c8 _gene2 HBM _contig391064 _s175615c5 _gene1 HBM _contig418176 _s190089c6 _gene1 HBM _contig743614 _s296819c6 _gene1	Glucose 1-phosphate adenyl transferase	2.7.7.27	5
HBM _contig1357958 _s456977c6 _gene3 HBM _contig276796 _s122460c2 _gene1	Glucose-6-phosphate 1-dehydrogenase	1.1.1.49	2
HBM_contig339226_s149517c1_gene1 HBM_contig1313987_s421061c3_gene1	Glucose-6-phosphate 1-epimerase	5.1.3.15	2
HBM_contig362889_s161039c11_gene1	Glucose-6-phosphate isomerase	5.3.1.9	1
HBM _contig1288678 _s409802c20 _gene2 HBM _contig1340694 _s441737c10 _gene1 HBM _contig218121 _s97036c9 _gene1 HBM _contig342711 _s151221c4 _gene1 HBM _contig130132 _s56830c9 _gene1 HBM _contig163761 _s72322c28 _gene1 HBM _contig474498 _s220352c2 _gene1	Glyceraldehyde 3-phosphate dehydrogenase	1.2.1.12	7
HBM _contig342780 _s151248c4 _gene1	Glycogen (starch) phosphorylase	2.4.1.1	1
HBM _contig1290182 _s410061c3 _gene1 HBM _contig269042 _s119264c2 _gene1 HBM _contig411305 _s186349c9 _gene1 HBM _contig454459 _s209676c4 _gene1 HBM_contig382803_s171253_gene1	Hydroxymethyl glutaryl-CoA reductase	1.1.1.34	5
HBM _contig1303558 _s415149c3 _gene1 HBM_contig265284_s117727c3_gene4	Hydroxymethylglutaryl-CoA synthase	2.3.3.10	2
HBM _contig243087 _s108198c7 _gene1 HBM _contig354346 _s156820c5 _gene1	Isocitrate dehydrogenase	1.1.1.42	2
HBM _contig501437 _s233949c28 _gene1 HBM_contig326011_s143366_gene1	Isopentenyl-diphosphate delta-isomerase	5.3.3.2	3

HBM_contig284636_s125486_gene1			
HBM _contig01222 _s00535c3 _gene1	L-malate hydro-lyase/ fumarate hydratase	4.2.1.2	1
HBM_contig1293296_s410821c9_gene1	Malate dehydrogenase	1.1.1.37	10
HBM_contig1295328_s411484c1_gene1			
HBM_contig284161_s125295c10_gene2			
HBM_contig332061_s146156c4_gene2			
HBM_contig675650_s282628_gene1			
HBM _contig1293296 _s410821c9 _gene1			
HBM _contig1295328 _s411484c1 _gene1			
HBM _contig284161 _s125295c10 _gene2			
HBM _contig332061 _s146156c4 _gene2			
HBM _contig675650 _s282628 _gene1			
HBM_contig1324605_s428704c13_gene4	Malate dehydrogenase (decarboxylating)/ Malate dehydrogenase (oxaloacetate-decarboxylating)	1.1.1.39/ 1.1.1.40	7
HBM _contig285159 _s125660c12 _gene1			
HBM _contig673366 _s282240c3 _gene1			
HBM _contig721178 _s292728c3 _gene1			
HBM_contig285159_s125660c12_gene1			
HBM_contig673366_s282240c3_gene1			
HBM_contig721178_s292728c3_gene1			
HBM_contig1295671_s411600c1_gene1	Mevalonate kinase	2.7.1.36	2
HBM_contig1300792_s413756c8_gene1			
HBM_contig819783_s316335c3_gene1	Mitochondrial dicarboxylate carrier protein (DIC)	na	3
HBM_contig278880_s123280_gene1			
HBM_contig362882_s161039c4_gene3			
HBM_contig325647_s143203_gene1	Monocarboxylate porter (MCP)	na	1
HBM_contig113175_s49095c7_gene1	Monosaccharide transporter (MT)	na	24
HBM_contig1289350_s409914c30_gene1			
HBM_contig1293510_s410890c6_gene1			
HBM_contig1294848_s411334c2_gene2			
HBM_contig205504_s91271c2_gene1			
HBM_contig246731_s109760c5_gene1			
HBM_contig253707_s112736c8_gene1			
HBM_contig300103_s131701_gene1			
HBM_contig301843_s132492c5_gene1			
HBM_contig335154_s147607c4_gene1			
HBM_contig338935_s149375c12_gene1			
HBM_contig369354_s164271_gene1			
HBM_contig377316_s168363c3_gene1			
HBM_contig383251_s171496c1_gene1			
HBM_contig383942_s171864_gene1			
HBM_contig392526_s176392c5_gene1			
HBM_contig395725_s178055_gene1			
HBM_contig408839_s185016_gene1			
HBM_contig414079_s187868_gene1			
HBM_contig446109_s205232c1_gene1			

HBM_contig446110_s205232c2_gene2 HBM_contig656790_gene1 HBM_contig757308_s300336c4_gene2 HBM_contig766992_s302901c1_gene1			
HBM _contig303759 _s133310c8 _gene1	NADP-dependentglyceraldehyde-3-phosphatedehydrogenase	1.2.1.9	1
HBM_contig1354496_s453822c10_gene2 HBM_contig231307_s102930c15_gene1 HBM_contig302254_s132663c8_gene1 HBM_contig728764_s293779c7_gene1 HBM _contig1354496 _s453822c10 _gene2 HBM _contig231307 _s102930c15 _gene1 HBM _contig302254 _s132663c8 _gene1	Oxoglutarate:malate antiporter (OMT)	na	7
HBM_contig1302285_s414518c3_gene1	Dicarboxylate/Tricarboxylate carrier protein (DTC)	na	1
HBM_contig1029566_s364163_gene1 HBM_contig1289192_s409889c5_gene1 HBM_contig134158_s58687c27_gene1 HBM_contig22381_s09035c12_gene1 HBM_contig325046_s142945_gene1	Phosphoenolpyruvate-phosphatase	3.1.3.60	5
HBM_contig1305977_s416315c19_gene1 HBM _contig422634 _s192523c3 _gene2	Phosphoglucomutase	5.4.2.2	2
HBM _contig747716 _s298021c22 _gene1	Phosphoglycerate kinase	2.7.2.3	1
HBM _contig323198 _s142103c44 _gene1 HBM _contig349580 _s154385c27 _gene1 HBM _contig389245 _s174714c12 _gene1	Phosphoglycerate mutase	5.4.2.1	3
HBM _contig433979 _s198650c9 _gene1 HBM_contig227302_s101115c1_gene1 HBM_contig297356_s130487_gene1	Phosphomevalonatekinase	2.7.4.2	3
HBM _contig295239 _s129579c5 _gene1	Phosphopyruvate hydratase (enolase)	4.2.1.11	1
HBM_contig1289256_s409900_gene1 HBM_contig298771_s131111c1_gene1	Oligo-1,6-glucosidase	3.2.1.10	2
HBM _contig1290187 _s410061c8 _gene3 HBM _contig334050 _s147096c2 _gene1	Pyrophosphate--fructose-6-phosphate 1-phosphotransferase	2.7.1.90	2
HBM _contig433980 _s198650c10 _gene1 HBM _contig1301528 _s414125c2 _gene1 HBM _contig1311068 _s419250c5 _gene1 HBM _contig30266 _s12350c4 _gene1 HBM _contig1290757 _s410195c9 _gene1 HBM _contig1294128 _s411073c7 _gene1	Pyruvate dehydrogenase	1.2.4.1	6
HBM_contig101953_s43997c3_gene2 HBM_contig299370_s131382_gene1 HBM_contig397018_s178729c12_gene1 HBM_contig402074_s181422c8_gene1	Dihydrolipoyllysine-residue acetyl transferase	2.3.1.12	4
HBM _contig1026725 _s363504c2 _gene2 HBM _contig1297534 _s412313c2 _gene1	Pyruvate kinase	2.7.1.40	8

HBM _contig1304126 _s415411c3 _gene1			
HBM _contig1344950 _s445443c5 _gene5			
HBM _contig136768 _s59843c7 _gene1			
HBM _contig290846 _s127748c7 _gene1			
HBM _contig383462 _s171609c3 _gene1			
HBM _contig294978 _s129482c1 _gene1			
HBM _contig114975 _s49906c13 _gene1	Ribose 5-phosphate isomerase A	5.3.1.6	3
HBM _contig1312636 _s420192c3 _gene1			
HBM _contig346662 _s153048c28 _gene3			
HBM _contig304780 _s133706c10 _gene2	Ribulose-phosphate 3-epimerase	5.1.3.1	1
HBM_contig1314787_s421584c1_gene1	Rubber elongation factor (REF)	na	12
HBM_contig1314789_s421584c3_gene1			
HBM_contig1352860_s452368_gene1			
HBM_contig1432969_s529413_gene1			
HBM_contig210302_s93430_gene1			
HBM_contig246314_s109563_gene1			
HBM_contig285004_s125605_gene1			
HBM_contig289068_s127107_gene1			
HBM_contig331924_s146093c6_gene1			
HBM_contig331929_s146093c11_gene1			
HBM_contig420863_s191570c9_gene1			
HBM_contig953976_gene1			
HBM_contig1291168_s410297_gene2	Small rubber particle protein (SRPP)	na	10
HBM_contig1314791_s421584c5_gene1			
HBM_contig1351062_s450759c14_gene1			
HBM_contig1445641_s541695c60_gene1			
HBM_contig314926_s138259_gene1			
HBM_contig331920_s146093c2_gene1			
HBM_contig331921_s146093c3_gene1			
HBM_contig331923_s146093c5_gene1			
HBM_contig364556_s161856_gene1			
HBM_contig878396_gene1			
HBM _contig164849 _s72856c4 _gene2	Starch synthase	2.4.1.21	7
HBM_contig230057_s102351c21_gene 1			
HBM_contig306687_s134504c10_gene 1			
HBM_contig332846_s146521c1_gene 1			
HBM_contig943860_s342523c1_gene 1			
HBM_contig1289127_s409874c9_gene 1			
HBM_contig1318935_s424517c31_gene 1			
HBM _contig1348382 _s448422c18 _gene1	Phosphoenolpyruvate carboxykinase	4.1.1.49	3
HBM _contig309950 _s135961c7 _gene1			
HBM _contig329252 _s144873c5 _gene3			
HBM _contig290756 _s127709c10 _gene1	Succinate dehydrogenase	1.3.5.1	2
HBM _contig509596 _s237846c7 _gene1			
HBM_contig348246_s153791c8_gene2	Succinyl-CoA ligase	6.2.1.5	2

HBM_contig363653_s161426_gene1			
HBM_contig227922_s101408c5_gene1 HBM_contig369579_s164395c1_gene1	Pyruvate decarboxylase	4.1.1.1	2
HBM_contig213287_s94844c20_gene1 HBM_contig325083_s142963_gene1 HBM_contig378330_s168914c2_gene2	Aldehyde dehydrogenase	1.2.1.3	3
HBM_contig378047_s168772_gene1 HBM_contig1292652_s410638c8_gene2	Alcohol dehydrogenase	1.1.1.1	2
HBM_contig63343_s26589c5_gene1 HBM_contig1254051_s405310c12_gene1	l-lactate dehydrogenase	1.1.1.27	2
HBM_contig202157_s89781c2_gene1 HBM_contig770884_s304118c4_gene1	Acetyl-CoA ligase	6.2.1.1	2
HBM_contig403677_s182258c2_gene1 HBM_contig1289511_s409944c4_gene3 HBM_contig371632_s165417c5_gene1 HBM_contig1324951_s428974c10_gene1 HBM_contig1420163_s516850c9_gene1 HBM_contig451554_s208132c13_gene1 HBM_contig353116_s156220_gene1 HBM_contig431760_s197468c3_gene3 HBM_contig1288955_s409848c4_gene1 HBM_contig1332985_s435332c13_gene1	Trehalose phosphatase	3.1.3.12	10
HBM_contig1352489_s452038_gene1 HBM_contig328275_s144399c2_gene1 HBM_contig433089_s198173c7_gene1	4-hydroxy-3-methylbut-2-enyl-diphosphate synthase	1.17.7.1	3
HBM_contig1289509_s409944c2_gene1 HBM_contig1345306_s445741c4_gene1	Sucrose -fructosyltransferase	2.4.1.99	2
HBM _contig1288687 _s409803c1 _gene1 HBM_contig272605_s120794c27_gene1	Sucrose phosphate phosphatase	3.1.3.24	2
HBM _contig757629 _s300436c6 _gene1 HBM_contig771203_s304239c15_gene1 HBM_contig1463859_s558603c4_gene1 HBM_contig355822_s157485c2_gene1	Sucrose phosphate synthase	2.4.1.14	4
HBM _contig01226 _s00535c7 _gene1 HBM_contig1310976_s419196c4_gene1 HBM_contig281038_s124058c3_gene2 HBM_contig395231_s177780c5_gene1 HBM_contig513220_s239591c6_gene3 HBM_contig314089_s137872_gene1 HBM_contig1294277_s411129_gene1 HBM_contig281039_s124058c4_gene1	Sucrose synthase	2.4.1.13	8
HBM _contig47165 _s19567c3 _gene2 HBM_contig1109905_s381969_gene1 HBM_contig1289974_s410033c6_gene1 HBM_contig1299594_s413194c9_gene1	Sucrose transporter (SUT)	na	14

HBM_contig1301388_s414043_gene1			
HBM_contig1323260_s427655_gene1			
HBM_contig332408_s146322c13_gene1			
HBM_contig332409_s146322c14_gene1			
HBM_contig380380_s169971_gene1			
HBM_contig429984_s196523_gene1			
HBM_contig43409_s17931_gene1			
HBM_contig47165_s19567c3_gene2			
HBM_contig654533_s279397c2_gene1			
HBM _contig205504 _s91271c2 _gene1			
HBM _contig346208 _s152843c5 _gene1	Transaldolase	2.2.1.2	1
HBM _contig1125285 _s385576c12 _gene1	Transketolase	2.2.1.1	2
HBM _contig324592 _s142744 _gene1			
HBM _contig277898 _s122911c5 _gene1	Trehalose-6-phosphate synthase	2.4.1.15	2
HBM_contig273515_s121147c18_gene2			
HBM _contig1317309 _s423378c2 _gene1	Triosephosphate isomerase	5.3.1.1	2
HBM _contig1364363 _s462960c8 _gene1			
HBM _contig354344 _s156820c3 _gene1	UTP-glucose-1-phosphateuridylyltransferase	2.7.7.9	1
HBM_contig1356982_s456101_gene1	Undecaprenyl-diphosphate synthase	2.5.1.31	5
HBM_contig379004_s169268c2_gene1			
HBM_contig1329326_s432359c2_gene3			
HBM_contig379006_s169268c4_gene1			
HBM_contig232787_s103605c15_gene1			
HBM_contig1311114_s419277c4_gene1	Galtase	2.4.1.-	5
HBM_contig1323470_s427819c4_gene1			
HBM_contig1013854_s360717c11_gene3			
HBM_contig1299176_s413002_gene1			
HBM_contig1311113_s419277c3_gene2			

Table S17. Rubber biosynthesis related genes of *H. brasiliensis* in comparison to *Parthenium argentatum* (guayule) ESTs

Gene model	**No. of EST hits**[a]	**Lowest E-value**[b]	**Greatest identity %**[b]
HBM_contig1297534_s412313c2_gene1	8	4.63E-133	98
HBM_contig362889_s161039c11_gene1	2	2.43E-24	98
HBM_contig1352489_s452038_gene1	5	1.67E-35	97
HBM_contig1288739_s409811c4_gene1	9	3.72E-95	96
HBM_contig1374823_s472809c3_gene1	7	3.57E-88	96
HBM_contig301843_s132492c5_gene1	5	4.19E-85	96
HBM_contig340487_s150149c5_gene1	6	8.66E-111	96
HBM_contig756485_s300037c2_gene5	5	1.23E-109	96
HBM_contig1357960_s456977c8_gene3	44	8.16E-124	95
HBM_contig163761_s72322c28_gene1	35	5.62E-94	95
HBM_contig770884_s304118c4_gene1	18	6.89E-53	95
HBM_contig1288678_s409802c20_gene2	37	4.02E-122	94
HBM_contig1301528_s414125c2_gene1	7	1.99E-47	94
HBM_contig328275_s144399c2_gene1	9	6.93E-126	94
HBM_contig339478_s149632c15_gene2	21	1.00E-117	94
HBM_contig342711_s151221c4_gene1	37	3.20E-119	94
HBM_contig433089_s198173c7_gene1	9	1.37E-125	94
HBM_contig766992_s302901c1_gene1	6	1.06E-83	94
HBM_contig1302285_s414518c3_gene1	39	2.12E-98	93
HBM_contig1302790_s414786c2_gene1	8	7.77E-118	93
HBM_contig147570_s64869c11_gene1	16	2.14E-114	93
HBM_contig294978_s129482c1_gene1	8	1.78E-96	93
HBM_contig338935_s149375c12_gene1	5	9.15E-77	93
HBM_contig346208_s152843c5_gene1	11	6.42E-113	93
HBM_contig522414_s243848c9_gene1	23	5.14E-135	93
HBM_contig675650_s282628_gene1	11	1.46E-103	93
HBM_contig1289171_s409884c2_gene1	23	3.97E-135	92
HBM_contig1299176_s413002_gene1	22	2.30E-98	92
HBM_contig130132_s56830c9_gene1	35	1.47E-120	92
HBM_contig1307528_s417190c7_gene1	7	1.17E-52	92
HBM_contig180992_s80187c5_gene1	21	1.66E-131	92
HBM_contig289576_s127312c17_gene3	9	5.65E-115	92
HBM_contig295239_s129579c5_gene1	22	3.95E-127	92
HBM_contig343183_s151438c5_gene1	4	1.09E-60	92
HBM_contig907698_s335276c27_gene1	10	3.22E-113	92
HBM_contig1326688_s430296c2_gene2	10	6.66E-89	91
HBM_contig1340694_s441737c10_gene1	36	8.63E-119	91
HBM_contig217879_s96943c3_gene1	9	4.76E-88	91
HBM_contig326011_s143366_gene1	7	8.30E-79	91
HBM_contig484019_s225263c9_gene1	13	1.91E-110	91
HBM_contig1324605_s428704c13_gene4	7	5.58E-106	90
HBM_contig1339227_s440512c5_gene3	22	1.09E-130	90

HBM_contig136768_s59843c7_gene1	10	4.18E-111	90
HBM_contig290988_s127806c2_gene1	2	9.62E-11	90
HBM_contig354346_s156820c5_gene1	7	3.22E-95	90
HBM_contig382299_s170997c9_gene2	4	1.16E-130	90
HBM_contig411305_s186349c9_gene1	8	1.02E-96	90
HBM_contig418176_s190089c6_gene1	5	8.17E-103	90
HBM_contig454459_s209676c4_gene1	17	2.33E-93	90
HBM_contig743614_s296819c6_gene1	15	1.76E-107	90
HBM_contig1292652_s410638c8_gene2	34	6.96E-104	89
HBM_contig1322658_s427165c3_gene3	22	1.09E-129	89
HBM_contig1352768_s452278c9_gene1	2	7.10E-123	89
HBM_contig284161_s125295c10_gene2	10	1.93E-107	89
HBM_contig297371_s130496_gene1	15	7.42E-89	89
HBM_contig303742_s133305c3_gene1	3	1.25E-122	89
HBM_contig323410_s142207c17_gene1	5	2.93E-123	89
HBM_contig354344_s156820c3_gene1	12	1.65E-97	89
HBM_contig378330_s168914c2_gene2	12	4.61E-103	89
HBM_contig1290187_s410061c8_gene3	19	2.89E-63	88
HBM_contig1293296_s410821c9_gene1	10	3.69E-107	88
HBM_contig1310976_s419196c4_gene1	5	6.73E-111	88
HBM_contig1311068_s419250c5_gene1	6	1.13E-71	88
HBM_contig257034_s114160c16_gene1	13	4.10E-114	88
HBM_contig269042_s119264c2_gene1	9	1.60E-106	88
HBM_contig281038_s124058c3_gene2	5	8.27E-111	88
HBM_contig303759_s133310c8_gene1	10	6.79E-100	88
HBM_contig425247_s193932c4_gene2	2	5.80E-124	88
HBM_contig474498_s220352c2_gene1	10	7.74E-101	88
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HBM_contig1311114_s419277c4_gene1	11	1.90E-46	87
HBM_contig1344950_s445443c5_gene5	14	3.55E-51	87
HBM_contig243087_s108198c7_gene1	5	7.55E-102	87
HBM_contig285159_s125660c12_gene1	8	1.43E-123	87
HBM_contig01222_s00535c3_gene1	3	4.14E-91	86
HBM_contig1295328_s411484c1_gene1	10	6.91E-105	86
HBM_contig1305637_s416164c2_gene1	4	5.90E-104	86
HBM_contig1343951_s444526c6_gene1	9	8.48E-82	86
HBM_contig227922_s101408c5_gene1	4	3.99E-44	86
HBM_contig298249_s130891c6_gene1	7	4.29E-107	86
HBM_contig334050_s147096c2_gene1	9	1.38E-121	86
HBM_contig382803_s171253_gene1	10	4.62E-104	86
HBM_contig945098_s342802c4_gene3	16	1.12E-112	86
HBM_contig01226_s00535c7_gene1	8	8.19E-119	85
HBM_contig272605_s120794c27_gene1	3	9.23E-26	85
HBM_contig278880_s123280_gene1	51	1.65E-46	85
HBM_contig304780_s133706c10_gene2	4	2.42E-98	85
HBM_contig349580_s154385c27_gene1	4	6.90E-104	85

HBM_contig407283_s184142c3_gene1	4	1.70E-59	85
HBM_contig434052_s198679c8_gene2	16	8.92E-116	85
HBM_contig440778_s202339_gene1	17	2.69E-57	85
HBM_contig501437_s233949c28_gene1	7	2.25E-95	85
HBM_contig1061580_s369994_gene1	5	5.86E-53	84
HBM_contig1074439_s372022c11_gene1	16	2.14E-114	84
HBM_contig300103_s131701_gene1	6	7.80E-33	84
HBM_contig402074_s181422c8_gene1	9	1.53E-58	84
HBM_contig1125285_s385576c12_gene1	8	4.61E-51	83
HBM_contig113175_s49095c7_gene1	7	1.04E-36	83
HBM_contig1254051_s405310c12_gene1	8	7.39E-101	83
HBM_contig1289350_s409914c30_gene1	8	1.31E-32	83
HBM_contig1294315_s411141c4_gene1	5	9.78E-28	83
HBM_contig1303558_s415149c3_gene1	25	1.78E-117	83
HBM_contig1303826_s415277c9_gene1	26	1.49E-119	83
HBM_contig1312636_s420192c3_gene1	5	1.40E-96	83
HBM_contig1339539_s440773c5_gene3	2	2.63E-53	83
HBM_contig213287_s94844c20_gene1	3	5.18E-109	83
HBM_contig276900_s122507c5_gene1	4	5.90E-101	83
HBM_contig318055_s139710c8_gene1	16	4.62E-120	83
HBM_contig338536_s149176c3_gene1	20	6.37E-111	83
HBM_contig43409_s17931_gene1	14	2.25E-85	83
HBM_contig656003_s279612c2_gene3	6	5.54E-90	83
HBM_contig819783_s316335c3_gene1	53	1.76E-57	83
HBM_contig114975_s49906c13_gene1	10	6.08E-100	82
HBM_contig316188_s138852c6_gene2	22	5.59E-115	82
HBM_contig320635_s140865c2_gene1	23	2.35E-116	82
HBM_contig323198_s142103c44_gene1	3	1.43E-97	82
HBM_contig63343_s26589c5_gene1	8	4.23E-98	82
HBM_contig673366_s282240c3_gene1	9	2.10E-123	82
HBM_contig721178_s292728c3_gene1	8	3.99E-105	82
HBM_contig1294128_s411073c7_gene1	11	3.54E-28	81
HBM_contig285749_s125863c8_gene2	8	2.54E-89	81
HBM_contig302280_s132669c17_gene1	4	9.39E-68	81
HBM_contig314089_s137872_gene1	7	5.06E-26	81
HBM_contig316009_s138773_gene1	15	4.26E-90	81
HBM_contig369579_s164395c1_gene1	3	6.98E-66	81
HBM_contig1289192_s409889c5_gene1	4	5.09E-50	80
HBM_contig1299594_s413194c9_gene1	18	3.10E-88	80
HBM_contig1304126_s415411c3_gene1	10	6.68E-106	80
HBM_contig1404580_s501548c30_gene1	7	1.93E-78	80
HBM_contig279164_s123369c13_gene5	3	3.59E-63	80
HBM_contig377316_s168363c3_gene1	9	1.39E-92	80
HBM_contig290846_s127748c7_gene1	10	1.05E-105	79
HBM_contig378047_s168772_gene1	37	4.09E-72	79
HBM_contig392526_s176392c5_gene1	11	2.15E-91	79

HBM_contig943860_s342523c1_gene1	5	2.89E-35	79
HBM_contig1290757_s410195c9_gene1	10	1.39E-29	78
HBM_contig202157_s89781c2_gene1	10	4.11E-45	78
HBM_contig283350_s124975c7_gene1	3	9.10E-109	78
HBM_contig299370_s131382_gene1	7	4.62E-59	78
HBM_contig380380_s169971_gene1	9	3.19E-81	78
HBM_contig529416_s246980c14_gene1	9	7.77E-79	78
HBM_contig1364363_s462960c8_gene1	8	3.48E-104	77
HBM_contig265284_s117727c3_gene4	6	7.87E-61	77
HBM_contig1038212_s365857c9_gene1	3	1.41E-32	76
HBM_contig274496_s121527c2_gene1	2	3.50E-53	76
HBM_contig30266_s12350c4_gene1	7	1.66E-70	76
HBM_contig355900_s157502c9_gene1	2	1.26E-53	76
HBM_contig1302222_s414481c14_gene1	2	6.06E-53	75
HBM_contig433979_s198650c9_gene1	4	3.18E-51	75
HBM_contig1289974_s410033c6_gene1	7	3.90E-61	74
HBM_contig1318907_s424517c3_gene1	13	1.30E-54	74
HBM_contig332409_s146322c14_gene1	3	3.50E-07	74
HBM_contig1295671_s411600c1_gene1	5	7.97E-38	73
HBM_contig264692_s117484c7_gene1	4	1.58E-38	73
HBM_contig290987_s127806c1_gene1	5	7.29E-73	73
HBM_contig393998_s177156c10_gene1	12	1.89E-74	73
HBM_contig420863_s191570c9_gene1	11	4.77E-50	73
HBM_contig1317309_s423378c2_gene1	5	3.38E-95	72
HBM_contig414079_s187868_gene1	13	1.14E-81	72
HBM_contig513220_s239591c6_gene3	4	1.41E-90	72
HBM_contig657916_s279871c2_gene2	8	5.12E-86	72
HBM_contig232787_s103605c15_gene1	15	2.81E-62	71
HBM_contig1288687_s409803c1_gene1	4	3.57E-64	70
HBM_contig1300792_s413756c8_gene1	4	1.56E-38	70
HBM_contig227302_s101115c1_gene1	3	7.09E-48	70
HBM_contig329252_s144873c5_gene3	3	5.29E-85	70
HBM_contig366145_s162700_gene1	4	9.31E-68	70
HBM_contig397018_s178729c12_gene1	3	3.88E-13	70
HBM_contig757308_s300336c4_gene2	8	3.82E-72	70
HBM_contig1294277_s411129_gene1	4	3.20E-29	69
HBM_contig1294848_s411334c2_gene2	7	1.46E-49	69
HBM_contig1311115_s419277c5_gene1	16	1.93E-37	69
HBM_contig1323470_s427819c4_gene1	10	3.58E-91	69
HBM_contig1348382_s448422c18_gene1	1	1.84E-84	69
HBM_contig1357953_s456977c1_gene1	3	1.64E-79	69
HBM_contig309950_s135961c7_gene1	4	1.68E-83	69
HBM_contig362882_s161039c4_gene3	33	3.01E-30	69
HBM_contig281039_s124058c4_gene1	2	1.44E-28	68
HBM_contig395231_s177780c5_gene1	3	2.68E-88	68
HBM_contig654533_s279397c2_gene1	8	2.04E-65	68

HBM_contig09843_s04035c2_gene1	4	5.80E-73	67
HBM_contig1026725_s363504c2_gene2	5	8.11E-65	67
HBM_contig1308223_s417615c21_gene1	3	5.26E-69	67
HBM_contig1324950_s428974c9_gene1	38	2.67E-86	67
HBM_contig1332985_s435332c13_gene1	3	1.57E-90	67
HBM_contig306687_s134504c10_gene1	5	1.38E-41	67
HBM_contig332061_s146156c4_gene2	7	8.04E-72	67
HBM_contig363653_s161426_gene1	6	3.47E-28	67
HBM_contig550434_s255571_gene1	13	2.98E-25	67
HBM_contig1345306_s445741c4_gene1	32	1.01E-76	66
HBM_contig1351062_s450759c14_gene1	10	1.95E-09	66
HBM_contig273515_s121147c18_gene2	7	2.38E-91	66
HBM_contig335154_s147607c4_gene1	5	1.60E-42	66
HBM_contig1289509_s409944c2_gene1	32	3.70E-74	65
HBM_contig1305977_s416315c19_gene1	4	1.58E-62	65
HBM_contig299515_s131427c8_gene1	5	3.92E-80	64
HBM_contig332846_s146521c1_gene1	5	3.84E-70	64
HBM_contig396545_s178492_gene1	12	2.32E-88	64
HBM_contig1030688_s364424c3_gene1	6	2.80E-75	63
HBM_contig1119081_s384118c2_gene1	5	7.00E-76	63
HBM_contig276796_s122460c2_gene1	5	2.19E-81	63
HBM_contig919895_s338071c2_gene1	5	7.52E-44	63
HBM_contig369602_s164404_gene1	3	7.71E-14	62
HBM_contig1329326_s432359c2_gene3	9	2.21E-62	61
HBM_contig246731_s109760c5_gene1	5	2.11E-48	61
HBM_contig325046_s142945_gene1	5	3.10E-56	61
HBM_contig47165_s19567c3_gene2	7	1.13E-55	61
HBM_contig1303515_s415144c5_gene1	8	1.12E-79	60
HBM_contig1352860_s452368_gene1	15	6.45E-15	60
HBM_contig379006_s169268c4_gene1	15	1.48E-61	60
HBM_contig383462_s171609c3_gene1	11	2.71E-72	60
HBM_contig1308208_s417615c6_gene1	13	4.54E-10	59
HBM_contig272314_s120676_gene1	8	8.30E-23	59
HBM_contig325083_s142963_gene1	2	6.21E-65	59
HBM_contig332408_s146322c13_gene1	8	1.76E-42	59
HBM_contig1289286_s409907c6_gene1	10	9.39E-48	58
HBM_contig232867_s103635c14_gene1	32	3.83E-65	58
HBM_contig253780_s112770c3_gene1	3	1.78E-17	58
HBM_contig364556_s161856_gene1	10	3.95E-56	58
HBM_contig369354_s164271_gene1	5	1.80E-32	58
HBM_contig446109_s205232c1_gene1	7	1.22E-69	58
HBM_contig878396_gene1	9	9.53E-12	58
HBM_contig1030687_s364424c2_gene1	5	5.68E-13	57
HBM_contig246314_s109563_gene1	12	1.50E-17	57
HBM_contig285737_s125861c3_gene1	8	6.96E-37	57
HBM_contig324592_s142744_gene1	3	5.30E-29	57

HBM_contig368493_s163834c3_gene1	5	2.31E-65	57
HBM_contig379004_s169268c2_gene1	7	6.53E-56	57
HBM_contig395725_s178055_gene1	3	1.38E-09	57
HBM_contig819355_s316235_gene1	25	1.89E-59	57
HBM_contig286418_s126148c2_gene1	12	3.38E-35	56
HBM_contig336329_s148152c12_gene1	32	1.07E-70	56
HBM_contig422634_s192523c3_gene1	8	4.66E-47	56
HBM_contig1292487_s410603c7_gene1	11	6.86E-41	55
HBM_contig253707_s112736c8_gene1	12	9.16E-69	55
HBM_contig331923_s146093c5_gene1	12	1.48E-48	55
HBM_contig348258_s153791c20_gene1	5	1.32E-20	55
HBM_contig383816_s171800_gene1	8	6.39E-51	55
HBM_contig979245_s352662c2_gene3	3	2.90E-20	55
HBM_contig205504_s91271c2_gene1	10	1.70E-66	54
HBM_contig391064_s175615c5_gene1	4	1.40E-42	54
HBM_contig1314787_s421584c1_gene1	11	3.93E-19	53
HBM_contig1323260_s427655_gene1	7	4.52E-65	53
HBM_contig1352352_s451908c3_gene2	9	5.74E-49	53
HBM_contig289068_s127107_gene1	13	2.44E-15	53
HBM_contig313150_s137410c19_gene1	3	1.80E-33	53
HBM_contig331921_s146093c3_gene1	9	2.31E-20	53
HBM_contig331924_s146093c6_gene1	10	1.65E-22	53
HBM_contig331929_s146093c11_gene1	14	1.74E-21	53
HBM_contig429984_s196523_gene1	11	7.07E-65	53
HBM_contig757629_s300436c6_gene1	5	1.48E-08	53
HBM_contig1022739_s362558c6_gene2	12	8.39E-37	52
HBM_contig343186_s151438c8_gene1	10	2.09E-55	52
HBM_contig134158_s58687c27_gene1	6	1.10E-38	51
HBM_contig1357958_s456977c6_gene3	4	7.03E-59	51
HBM_contig22381_s09035c12_gene1	2	1.50E-39	51
HBM_contig1314789_s421584c3_gene1	10	9.51E-24	50
HBM_contig1356982_s456101_gene1	7	7.60E-12	50
HBM_contig230057_s102351c21_gene1	4	7.89E-50	50
HBM_contig336327_s148152c10_gene1	7	6.58E-06	50
HBM_contig348246_s153791c8_gene1	5	6.54E-48	49
HBM_contig526985_s245906c4_gene1	10	3.28E-44	49
HBM_contig1322037_s426750c3_gene1	9	2.23E-35	48
HBM_contig1445641_s541695c60_gene1	13	1.13E-28	48
HBM_contig325647_s143203_gene1	10	3.19E-55	48
HBM_contig336323_s148152c6_gene1	15	8.39E-33	48
HBM_contig408839_s185016_gene1	13	3.68E-07	48
HBM_contig431766_s197470c4_gene1	8	2.73E-37	48
HBM_contig1016681_s361260c5_gene1	5	6.90E-38	47
HBM_contig1494088_s582224c2_gene2	4	4.49E-28	47
HBM_contig771203_s304239c15_gene1	3	5.61E-08	47
HBM_contig1109905_s381969_gene1	7	2.84E-17	45

HBM_contig1348390_s448422c26_gene1	3	4.27E-25	45
HBM_contig331920_s146093c2_gene1	22	9.62E-30	45
HBM_contig355008_s157135c8_gene1	4	9.30E-36	45
HBM_contig1314791_s421584c5_gene1	12	2.24E-35	44
HBM_contig1409221_s506095c5_gene3	2	5.04E-39	44
HBM_contig164849_s72856c4_gene2	4	7.03E-20	44
HBM_contig1409222_s506095c6_gene1	2	1.05E-33	43
HBM_contig314926_s138259_gene1	12	1.29E-35	43
HBM_contig1291168_s410297_gene2	9	1.43E-34	42
HBM_contig446110_s205232c2_gene1	7	6.70E-08	42
HBM_contig323185_s142103c31_gene1	4	1.69E-23	40
HBM_contig1119082_s384118c3_gene1	1	4.23E-26	37
HBM_contig1289127_s409874c9_gene1	1	1.50E-38	36
HBM_contig1288955_s409848c4_gene1	2	7.10E-06	35
HBM_contig1311113_s419277c3_gene1	6	5.30E-09	35
HBM_contig403677_s182258c2_gene1	3	2.00E-07	34
HBM_contig1289511_s409944c4_gene3	3	1.15E-07	33
HBM_contig1318935_s424517c31_gene1	3	7.59E-18	32
HBM_contig371632_s165417c5_gene1	4	5.42E-08	29
HBM_contig1420163_s516850c9_gene1	1	1.88E-08	26
HBM_contig353116_s156220_gene1	2	2.09E-07	26
HBM_contig451554_s208132c13_gene1	1	9.18E-06	26

[a] TBLASTN hits with E-value < 10^{-5}

[b] In cases where multiple hits occur, the reported value is for the top hit

Table S18. Lignocellulose biosynthetic genes of *H. brasiliensis* in comparison to other sequenced genomes

	Hevea	***Ricinus***	***Populus***	***Arabidopsis***	***Oryza***	***Selaginella***
Lignin synthesis related genes						
PAL	4	4	5	4	6	1
C4H	7	1	2	1	2	-
4CL	4	3	3	4	5	2
HCT	6	1	1	1	2	3
COMT	10	46	41	17	49	17
C3H	6	2	3	1	2	-
CCoAOMT	3	3	2	1	1	2
CCR	3		3	2	3	
F5H	2	1	3	1	1	-
CAD	5	10	24	9	20	9
Cellulose synthesis related genes						
CesA	36	13	28	10	20	6
COBRA	10	6	4	1	9	2
SuSy	8	5	7	6	5	-
FRA2	4	1	2	1	1	1
KOR	7	3	4	3	3	1
α-L-fucosidases	12	23	38	25	67	45

Table S19. Putative NBS-coding R genes of *H. brasiliensis* in comparsion to other sequenced genomes

Predicted Protein	***Hevea***	***Populus***	***Papaya***	***Arabidopsis***	***Oryza***
Without LRRs					
TIR-NBS	17	10	2	21	3
CC-NBS	134	19	2	5	7
NBS	350	49	17	1	45
With LRRs					
TIR-NBS-LRR	25	64	6	93	0
CC-NBS-LRR	45	119	4	51	160
NBS-LRR	47	90	23	3	304
Total	**618**	**351**	**54**	**174**	**519**

Table S20. Pathogenesis-related proteins of *H. brasiliensis* in comparison with other genomes

Pathogenesis-Related Proteins (PRs)	***Hevea***	***Ricinus***	***Populus***	***Arabidopsis***	***Oryza***	***Selaginella***
Pr1	12	7	16	10	10	3
Pr2	22	61	125	95	96	60
Pr3	7	9	23	14	19	23
Pr4	27	3	8	1	5	1
Pr5	17	26	42	22	40	18
Pr6	5	4	20	6	-	-
Pr8	14	8	14	1	31	8
Pr10	11	38	34	26	2	5
Lectins	32	48	64	102	127	16
Total	**147**	**204**	**346**	**277**	**330**	**134**

Table S21. Systemic acquired resistance (SAR) and hypersensitive response (HR) related genes found in the *H. brasiliensis* genome

Gene Model	**Gene name**
HBM_contig06421_s02656c2_gene2	Metallothionein
HBM_contig1037845_s365794c13_gene3	Non race-specific disease resistance 1
HBM_contig105575_s45633c21_gene1	F-box protein
HBM_contig1074434_s372022c6_gene1	Serine-threonine protein kinase
HBM_contig117141_s50884c14_gene1	Ethylene insensitive 3-like protein
HBM_contig1288682_s409802c24_gene1	Bromodomain-containing protein
HBM_contig1288976_s409852c2_gene2	Glycerol kinase
HBM_contig1289068_s409864c2_gene2	WRKY-like transcription
HBM_contig1289631_s409964c4_gene2	Alternative oxidase 2
HBM_contig1290638_s410161c14_gene1	Xanthine dehydrogenase 1
HBM_contig1291402_s410361c4_gene2	Serine/threonine protein kinase PSB1
HBM_contig1291889_s410454c6_gene1	Monoxygenase
HBM_contig1292364_s410573c2_gene1	Oxalate oxidase
HBM_contig1292450_s410594c2_gene1	Zinc finger protein
HBM_contig1292626_s410633c16_gene1	Lipoxygenase
HBM_contig1295205_s411448c4_gene2	Skp1-Cullin–F-box protein
HBM_contig1295495_s411532c6_gene1	Protein 5'->3' exoribonuclease, AIN1
HBM_contig1295989_s411738c1_gene1	Peroxidase 17
HBM_contig1296639_s411971c1_gene1	Early ethylene-responsive genes
HBM_contig1296662_s411975c11_gene2	Acyl-protein thioesterase
HBM_contig1296871_s412049c3_gene1	Omega-3 fatty acid desaturase, FAD8
HBM_contig1298013_s412552c3_gene1	Ethylene response sensor 2
HBM_contig1300802_s413756c18_gene1	Mitogen-activated protein kinase kinase kinase 2
HBM_contig1304427_s415555c19_gene4	Isochorismate synthase 1
HBM_contig1304763_s415719c13_gene1	Omega-3 fatty acid desaturase
HBM_contig1307472_s417170c13_gene1	Dimethylaniline monooxygenase
HBM_contig1308601_s417813c25_gene1	Serine/threonine-protein kinase CTR1
HBM_contig1315631_s422196c17_gene1	Mitogen activated protein1
HBM_contig1324775_s428843c2_gene1	Allene oxide synthase
HBM_contig1325708_s429519c25_gene2	Calmodulin-binding heat-shock protein,
HBM_contig1327523_s430947c6_gene1	Regulatory protein NPR1
HBM_contig1328657_s431840c3_gene3	Wall-associated receptor kinase 2
HBM_contig1333064_s435374c4_gene1	Enhanced disease susceptibility 1
HBM_contig1340690_s441737c6_gene1	DNA binding protein GT-1
HBM_contig1341105_s442084c7_gene1	Beta glucosidase
HBM_contig1342092_s442954c9_gene2	Phospholipase
HBM_contig1345388_s445788c3_gene1	Zeaxanthin epoxidase (1.14.13.90)
HBM_contig1347991_s448099c5_gene1	Hydroxynitrile lyase
HBM_contig1422110_s518739c4_gene1	Serine/threonine protein kinase
HBM_contig1465004_s559611c14_gene2	Pectate lyase
HBM_contig173710_s76922c5_gene1	CCoAMT; caffeoyl-CoA O-methyltransferase
HBM_contig17421_s07081c9_gene1	Heat shock protein

HBM_contig188767_s83719c8_gene1	cytochrome P450 probable ent-kaurenoic acid oxidase
HBM_contig200851_s89231c10_gene1	Receptor protein kinase
HBM_contig226693_s100838c4_gene1	Serine/threonine phosphatase
HBM_contig228172_s101510c3_gene3	Brassinosteroid insensitive 1
HBM_contig238412_s106118_gene1	Eukaryotic translation initiation factor 2c
HBM_contig242210_s107817c13_gene1	Glutathione peroxidas
HBM_contig252939_s112426c6_gene2	Zeamatin precursor
HBM_contig262953_s116732c1_gene1	Mitogen-activated protein kinase 2
HBM_contig263035_s116770c1_gene1	Flavine-containing monoxygenase
HBM_contig264998_s117599_gene1	Rhicadhesin receptor precursor
HBM_contig265562_s117837_gene1	Coronatine-insensitive 1
HBM_contig274137_s121393c1_gene1	Leucine-rich repeat-containing protein
HBM_contig274142_s121393c6_gene1	OUT domain protein
HBM_contig283262_s124944c9_gene1	Brassinosteroid insensitive 1 associated receptor kinase 1
HBM_contig285476_s125769c6_gene1	Ethylene receptor 2
HBM_contig296913_s130307_gene1	Ethylene-responsive transcription factor
HBM_contig315927_s138736c1_gene1	Pathogenesis-related protein 1
HBM_contig322575_s141866c13_gene1	Mitogen activated kinase-like protein
HBM_contig322635_s141887c15_gene2	Sphingoid base Hydroxylase 1
HBM_contig329111_s144804_gene1	Nucleoporin
HBM_contig333187_s146668c1_gene1	Disease resistance protein
HBM_contig339286_s149545c5_gene1	Latex beta-cyanoalanine synthase
HBM_contig341044_s150417c9_gene4	2-nitropropane dioxygenase family
HBM_contig346636_s153048c2_gene1	Map3k delta-1 protein kinase
HBM_contig349742_s154477c6_gene1	Disease resistance protein 2
HBM_contig351365_s155313c3_gene2	Poly(rC)-binding protein
HBM_contig369959_s164591c6_gene1	ethylene-responsive element bining factor 5
HBM_contig39977_s16454c9_gene1	Transcription factor HBP-1b
HBM_contig406858_s183928c16_gene1	APX1 (ascorbate peroxidase 1)
HBM_contig406860_s183928c18_gene1	Mitogen-activated protein kinase
HBM_contig409421_s185323_gene1	WRKY transcription factor, putative
HBM_contig423248_s192871c2_gene2	Calmodulin
HBM_contig423596_s193057c15_gene1	Ubiquitin ligase
HBM_contig427107_s194975c3_gene1	Mitogen-activated protein kinase kinase
HBM_contig442498_s203277c4_gene1	Stearoyl-acyl-carrier protein desaturase
HBM_contig455602_s210290c11_gene1	Ethylene receptor 1
HBM_contig469575_s217788c5_gene2	Phytoalexin deficient4
HBM_contig483419_s224948c2_gene1	Disease resistance protein 8
HBM_contig494277_s230381c9_gene2	GH3 family protein
HBM_contig509911_s237995c8_gene1	Copine
HBM_contig523425_s244330_gene1	Transcription factor MYC2
HBM_contig536436_s250034c21_gene1	Jasmonate-insensitive 3
HBM_contig549096_s255049c1_gene2	DNA-damage-inducible protein
HBM_contig644472_s277880c1_gene1	Mitogen-activated protein kinase kinase kinase1
HBM_contig701896_s287934c9_gene1	Ein3-binding f-box protein 3
HBM_contig732471_s294373c14_gene3	Ethylene- insensitive 4

HBM_contig73508_s31074c6_gene1	Gamma-glutamylcysteine synthetase
HBM_contig735668_s295000c2_gene1	Catalytic/ glucuronoxylan glucuronosyltransferase
HBM_contig764172_s302159c11_gene1	Mitogen-activated protein kinase kinase 2
HBM_contig764172_s302159c11_gene2	protein phosphatase 2C
HBM_contig821365_s316780c31_gene1	Ethylene-insensitive protein 2
HBM_contig829332_s318669c4_gene1	ABL Interactor-Like Protein 2
HBM_contig863487_s324777c6_gene2	S-phase kinase-associated protein 1
HBM_contig958308_s346865c1_gene1	Phospholipase d beta

Table S22. Latex allergens in the *H. brasiliensis* genome

Allergen type	**Names and contig number**
Hevb 1	**Rubber elongation factor (REF)**
	HBM_contig1314787_s421584c1_gene1
	HBM_contig1314789_s421584c3_gene1
	HBM_contig1352860_s452368_gene1
	HBM_contig1432969_s529413_gene1
	HBM_contig210302_s93430_gene1
	HBM_contig246314_s109563_gene1
	HBM_contig285004_s125605_gene1
	HBM_contig289068_s127107_gene1
	HBM_contig331924_s146093c6_gene1
	HBM_contig331929_s146093c11_gene1
	HBM_contig420863_s191570c9_gene1
	HBM_contig953976_gene1
Hevb 2	**β-1,3-glucanase**
	HBM_contig1053939_gene1
	HBM_contig1288699_s409805c4_gene6
	HBM_contig1288700_s409805c5_gene2
	HBM_contig1331601_s434259_gene1
	HBM_contig1383052_s480661_gene1
	HBM_contig1383052_s480661_gene2
	HBM_contig1493847_gene1
	HBM_contig1542420_gene1
	HBM_contig181937_s80601_gene1
	HBM_contig484011_s225263c1_gene1
	HBM_contig49288_s20505_gene1
Hevb 3	**Small rubber particle**
	HBM_contig1291168_s410297_gene2
	HBM_contig1314791_s421584c5_gene1
	HBM_contig1351062_s450759c14_gene1
	HBM_contig1445641_s541695c60_gene1
	HBM_contig878396_gene1
	HBM_contig364556_s161856_gene1
	HBM_contig331921_s146093c3_gene1
	HBM_contig331923_s146093c5_gene1
	HBM_contig314926_s138259_gene1
	HBM_contig331920_s146093c2_gene1
Hevb 4	**Lecithinase homolog**
	HBM_contig367975_s163585_gene1
	HBM_contig1311038_s419233c1_gene1
	HBM_contig1302448_s414608_gene1
	HBM_contig128030_s55849c2_gene1
	HBM_contig128029_s55849c1_gene1

Hevb 5	**Latex major allergen** HBM_contig279320_s123416c2_gene1
Hevb 6	**Hevein** HBM_contig1099636_s379205_gene1 HBM_contig1326398_s430072_gene1 HBM_contig1332655_s435061c1_gene1 HBM_contig1404480_s501478_gene1 HBM_contig1438942_s535269_gene1 HBM_contig1463769_s558530_gene1 HBM_contig1485741_s576443_gene1 HBM_contig1487445_s577627_gene1 HBM_contig1511743_gene1 HBM_contig1523411_s597290_gene1 HBM_contig1544593_s603451_gene1 HBM_contig1551202_s604715_gene1 HBM_contig1580472_gene1 HBM_contig293053_s128596c1_gene1 HBM_contig36291_gene1coding HBM_contig795181_s310723_gene1
Hevb 7	**Patatin-like** HBM_contig274460_s121513c2_gene1 HBM_contig269214_s119330c6_gene1 HBM_contig604530_s271122c2_gene1 HBM_contig1301350_s414027c3_gene2 HBM_contig1301351_s414027c4_gene1
Hevb 8	**Profilin** HBM_contig415131_s188411_gene1 HBM_contig1330838_s433634_gene1 HBM_contig367050_s163105c2_gene1 HBM_contig1164698_s393417c31_gene3 HBM_contig1074430_s372022c2_gene1 HBM_contig1329259_s432305_gene1
Hevb 9	**Enolase** HBM_contig260697_s115748c12_gene HBM_contig295239_s129579c5_gene1 HBM_contig319636_s140387c5_gene1 HBM_contig383573_s171660c8_gene1
Hevb 10	**Superoxide dismutase (Mn)** HBM_contig1380717_s478448c12_gene1 HBM_contig1299900_s413337c4_gene3
Hevb 11	**Chitinase** HBM_contig1331506_s434174c2_gene1 HBM_contig1374580_s472577_gene1 HBM_contig1434962_s531376_gene1 HBM_contig376395_s167879c1_gene1 HBM_contig380563_s170073_gene1

	HBM_contig412336_s186887c8_gene1
	HBM_contig594755_gene1
	HBM_contig782692_s307260_gene1
	HBM_contig951921_s344934c1_gene1
	HBM_contig952555_gene1
	HBM_contig980709_s353149_gene1
Hevb 12	**Lipid transfer precursor**
	HBM_contig323161_s142103c7_gene3
	HBM_contig349554_s154385c1_gene1
Hevb 13	**Esterase**
	HBM_contig371165_s165162c13_gene1
	HBM_contig371163_s165162c11_gene3
	HBM_contig1317196_s423303_gene1
	HBM_contig134028_s58638_gene1
	HBM_contig899653_s333225_gene1
	HBM_contig371167_s165162c15_gene1
	HBM_contig370747_s164953c24_gene1
	HBM_contig371169_s165162c17_gene1
	HBM_contig464308_s214932_gene1
Hevb 14	**Hevamine**
	HBM_contig1389101_s486528c4_gene1
	HBM_contig1371073_s469275_gene1
	HBM_contig1344950_s445443c5_gene6
	HBM_contig1321967_s426707c2_gene2
	HBM_contig1310281_s418802c6_gene1
	HBM_contig1303495_s415132_gene1

Table S23. Non-latex allergens in the *H. brasiliensis* genome

Non-latex allergen	**Gene model**
Pollen allergen	HBM_contig623408_s274630c9_gene1
	HBM_contig1074430_s372022c2_gene2
α-expansin	HBM_contig289660_s127337c2_gene1
	HBM_contig311528_s136675c1_gene1
	HBM_contig1291975_s410466c42_gene1
	HBM_contig1369889_s468147_gene1
	HBM_contig302755_s132887_gene1
	HBM_contig350467_s154865_gene1
	HBM_contig350403_s154837_gene1
	HBM_contig446231_s205297_gene1
β-expansin	HBM_contig903040_s334087c9_gene1
	HBM_contig818284_s315950c3_gene1
Isoflavone reductase	HBM_contig334692_s147398c6_gene1
	HBM_contig252987_s112426c54_gene1
	HBM_contig1305222_s415946c2_gene1
	HBM_contig212170_s94313_gene1

Table S24. Transcription factors present in *H. brasiliensis* in comparison to other sequenced plant genomes

Transcription Factors	***Hevea***	***Ricinus***	***Populus***	***Arabidopsis***	***Oryza***	***Selaginella***
bHLH	752	121	226	194	178	85
MYB	570	63	212	159	124	41
C3H	470	36	69	56	50	36
G2-like	461	33	74	55	56	32
WRKY	445	60	119	89	116	25
MYB_related	397	99	104	85	94	63
NAC	336	97	182	135	166	38
ERF	246	94	176	132	143	68
HD-ZIP	182	31	67	56	46	14
C2H2	164	69	115	104	91	44
AP2	139	18	30	25	27	16
TALE	139	16	35	23	28	5
HSF	136	19	32	27	44	14
B3	122	41	116	71	55	24
ARR-B	116	11	21	16	9	9
MADS-box	112	50	116	156	108	20
NF-YB	106	14	22	19	14	9
GATA	97	19	46	31	32	11
GRAS	96	48	114	36	77	89
SBP	88	15	32	18	20	16
WOX	78	11	20	17	12	13
LBD	63	34	59	43	42	21
CO-like	62	9	16	19	11	7
ZF-HD	62	11	24	17	15	15
YABBY	58	6	13	8	15	1
ARF	56	17	53	35	34	29
NF-YC	52	11	16	15	15	7
TCP	38	22	35	32	27	9
GRF	37	14	19	10	22	6
HB-other	37	10	15	8	15	15
CAMTA	34	5	9	8	8	12
E2F/DP	25	6	10	12	9	7
Nin-like	25	10	49	20	19	22
RAV	25	4	4	6	4	3
Trihelix	24	34	60	33	32	45
DBB	23	7	16	12	11	6
BES1	16	5	14	11	5	10
HB-PHD	15	2	4	2	1	2
Whirly	11	2	4	4	2	2
CPP	10	6	19	10	20	8
FAR1	9	21	54	20	71	0
GeBP	9	6	11	29	24	4

BBR/BPC	7	5	16	17	7	2
SAP	7	1	1	1	0	2
EIL	6	4	8	6	12	10
Dof	5	25	48	45	39	41
LFY	3	1	1	1	2	4
bZIP	2	51	106	101	99	39
NZZ/SPL	2	0	2	1	0	2
S1Fa-like	2	1	2	4	3	0
NF-X1	1	2	5	2	3	4
Total	**5978**	**1297**	**2621**	**2036**	**2057**	**1007**

Table S25. Genes involved in phytohormone metabolism, signaling and regulatory events represented in the *H. brasiliensis* genome

Biological Processes	***Hevea***	***Ricinus***	***Populus***	***Arabidopsis***	***Oryza***	***Selaginella***
Auxin Homeostasis And Signaling						
TIR1/AFB auxin receptor protein PintaTIR1	11	3	6	4	3	1
Auxin response factors	20	19	43	25	33	14
Aux/IAA repressors	6	18	35	29	35	4
Auxin binding proteins	6	1	1	1	2	1
PIN auxin efflux carriers	16	7	18	7	6	4
AUX1/LAX auxin influx transporters	12	4	8	4	5	3
YUCCA/FLOOZY monoxygenases	13	4	5	7	2	2
Class II GH3 IAA amidosynthetases	11	5	9	17	8	1
IRL1/ILL IAA amidohydrolases	18	7	12	7	11	2
Small Auxin-Up RNA (SAUR)	21	9	99	81	56	28
Topless/Topless Related	17	6	11	5	3	2
TAA/TAR (Tryptophan Aminotransferase-/Related)	6	1	1	1	-	-
Total	*157*	*84*	*248*	*188*	*164*	*62*
Cytokinin Biosynthetic Pathway						
Adenylate Isopentenyltransferase/ Adenosine Phosphate-Isopentenyltransferases (Ipts)	8	5	8	8	10	-
Trans-Zeatin Riboside Monophosphate Phosphoribohydrolase (LOG)	21	34	31	20	32	4
Adenosine Kinase (AK)	11	1	2	2	2	1
Adenine Phosphoribosyltransferase (APRT)	10	4	4	5	6	1
CKX/ Cytokinin Oxidase/ Dehydrogenase	13	6	9	7	11	1
Zeatin O-Glucosyltransferase	37	70	149	60	148	15
Total	*100*	*120*	*203*	*102*	*209*	*22*
Gibberellin Biosynthetic Pathway						
CYP88A	8	1	2	2	1	2
GA20ox (17)	5	1	2	2	1	-
GA3ox	1	2	-	1	-	-
GA2ox	9	5	4	2	2	-
GA7ox	1	-	-	1	-	-
GID	4	36	67	20	70	18
DELLA	5	2	4	5	1	1
GASA	7	14	21	15	6	6
SPINDLY	1	1	2	1	1	-
Total	*41*	*62*	*102*	*49*	*82*	*27*
Ethylene Biosynthesis						
s-adenosylmethionine synthetase	9	5	9	7	10	5
1-aminocyclopropane-1-carboxylate deaminase	3	1	1	1	1	1
1ACC synthase	5	7	12	13	6	4
1-aminocyclopropane-1-carboxylate oxidase	13	8	17	22	12	4
Ethylene Receptor	6	16	13	6	13	7
constitutive triple response-1	11	2	3	1	2	1
ethylene insensitive 2	5	1	2	1	2	2
ethylene responsive factor (ERF)	246	92	172	117	121	39
Ethylene overproducer 1 (ETO1)	4	3	8	4	5	4
Total	*302*	*135*	*237*	*172*	*172*	*67*

Jasmonic Acid Metabolic Pathway						
Lox (Lipoxygenase)	10	14	26	6	24	34
Aos (Allene oxide synthase)	4	2	9	2	5	17
Aoc (allene oxide cyclase)	5	2	3	4	1	2
Opr7	13	10	12	10	11	14
Total	*32*	*28*	*50*	*22*	*41*	*67*
Brassinosteroid Signaling						
DET2- probable steroid reductase	2	1	1	1	2	1
CYP90B1, DWF4	4	1	2	1	1	-
CYP90A1, CPD	7	1	2	1	2	1
CYP90C1, ROT3	8	1	1	1	-	-
CYP85A1, BR6OX1	4	1	3	2	1	-
CYP90D1, D1	3	1	2	1	2	2
CYP85A2	7	1	3	2	1	-
Total	*35*	*7*	*14*	*9*	*9*	*4*
Salicylic Acid Associated Genes						
PAL	5	7	6	4	13	2
PBS3	2	1	2	3	2	2
3-phosphoshikimate 1-carboxyvinyltransferase (EPSP synthase)	3	2	3	3	1	4
Total	*10*	*10*	*11*	*10*	*16*	*8*
Nitric Oxide Related Genes						
Nos	4	1	1	1	1	2
SOD	9	8	16	18	14	14
Cat (Catalase)	7	2	4	7	6	10
Total	*20*	*11*	*21*	*26*	*21*	*26*

Table S26. Circadian clock and light signaling gene families from *Hevea* in comparison to *Populus* and *Arabidopsis*

Gene name	*Hevea*	*Populus*	*Arabidopsis*
PRR/CCT	11	8	7
ZTL/FKF1	10	5	3
CCA1/LHY	11	4	3
RVE/ERP1	8	3	5
PHOT	13	3	2
ELF3	7	2	1
GI (Gigantea)	5	2	1
SRR1	24	2	2
ELF4	2	5	4
TIC/TKL	4	2	1
TEJ	2	2	1
PHY	7	5	5
CRY/cryptochrome/photolyase	9	5	3
PIF/PIL	8	5	6
Casein kinase	18	15	16
COP	2	1	1
SPA	4	2	2
HY5/HYH	5	2	1
DET	2	2	1
FUSCA	2	2	1
Total	**154**	**77**	**66**

Table S27. Major genes involved in carotenoid biosynthesis in *H. brasiliensis* and *A. thaliana*

Gene Name	**Gene Description**	***Hevea***	***Arabidopsis***
GGPPS	Geranylgeranyl diphosphate synthase	6	13
IDI	Isopentenyl diphosphate isomerase	3	2
PSY	Phytoene synthase	5	1
PDS	Phytoene desaturase	9	1
ZDS	Zeta-carotene desaturase	2	1
Crtlso	Carotene isomerase	2	1
LCYb	Lycopene β-cyclase	2	1
LCYe	Lycopene epsilon cyclase	3	1
CHYeP450	Carotenoid epsilon ring 3-hydroxylase of the cytochrome P450 type	2	1
CHYbP450	Carotene beta-ring hydroxylase/ oxygen binding	3	1
CHYb	Carotenoid beta-ring 3-hydroxylase	5	2
ZEP	Zeaxanthin epoxidase	2	1
VDE	Violaxanthin de-epoxidase	2	1
NSY	Neoxanthin synthase	2	1
Total		**48**	**28**