

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
Polcalcine 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 <i>Hevea brasiliensis</i> 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 mHbCIRT2157 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
 Phospholipase 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 tya/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 dehydrogenase, 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
 Tetratricopeptide-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 <i>Hevea brasiliensis</i> 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

Irr 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

^aBLAST hits with E-value < 10⁻⁵ and 90% sequence identity cutoff^bData available as of October 2012^cIsotig sequences from <http://www4a.biotec.or.th/rubber/Download> (ref. 6)^dUnigenes from ref. 7^eAssembled 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	<i>Hevea brasiliensis</i>	<i>Ricinus communis</i>	<i>Populus trichocarpa</i>	<i>Arabidopsis thaliana</i>	<i>Eucalyptus grandis</i>	<i>Oryza sativa</i>	<i>Zea mays</i>
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
<i>Information and Storage and Processing</i>	
[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
<i>Cellular Processes and Signaling</i>	
[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
<i>Metabolism</i>	
[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
<i>Poorly Characterized</i>	
[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	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 cytidyltransferase	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/ Phosphoenolpyruvate-phosphatase	3.1.3.2/	18
HBM_contig670075_s281714c1_gene1		3.1.3.60	
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_contig1029566_s364163_gene1			
HBM_contig22381_s09035c12_gene1			
HBM_contig355008_s157135c8_gene2			
HBM_contig371266_s165213c7_gene4			
HBM_contig424017_s193270c32_gene1			
HBM_contig325046_s142945_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	5
HBM_contig225884_s100449c20_gene4			
HBM_contig385624_s172762c13_gene1			
HBM_contig419623_s190883c14_gene1			
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	5
HBM_contig287791_s126661c14_gene1			
HBM_contig319789_s140450c14_gene1			
HBM_contig351119_s155176c19_gene1			
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/	10
HBM_contig1038212_s365857c9_gene1		2.7.1.2	
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_contig313150_s137410c19_gene1			
HBM_contig1161306_s392766c6_gene1			
HBM_contig232867_s103635c14_gene1	β -fructofuranosidase/ Fructan β -fructosidase	3.2.1.26/	31
HBM_contig09843_s04035c2_gene1		3.2.1.80	
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_contig428152_s195531c24_gene1			
HBM_contig409303_s185263c11_gene1			
HBM_contig1341606_s442556_gene1			
HBM_contig1517170_gene1			
HBM_contig232864_s103635c11_gene1			
HBM_contig279165_s123369c14_gene1			
HBM_contig336326_s148152c9_gene1			
HBM_contig349207_s154257c6_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-polyisoprenylcistransferase	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_contig253780_s112770c3_gene1	Geranyl geranyl diphosphate synthase	2.5.1.29	7
HBM_contig1292487_s410603c7_gene1			
HBM_contig1298993_s412919c4_gene1			
HBM_contig550434_s255571_gene1			
HBM_contig324001_gene1			
HBM_contig124304_s54106c3_gene1			
HBM_contig324027_gene1			
HBM_contig1289171_s409884c2_gene1	Fructose-bisphosphate aldolase	4.1.2.13	9
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			
HBM_contig214134_s95238c3_gene1	Glucose 1-phosphate adenylyl transferase	2.7.7.27	5
HBM_contig285749_s125863c8_gene2			
HBM_contig391064_s175615c5_gene1			
HBM_contig418176_s190089c6_gene1			
HBM_contig743614_s296819c6_gene1			
HBM_contig1357958_s456977c6_gene3	Glucose-6-phosphate 1-dehydrogenase	1.1.1.49	2
HBM_contig276796_s122460c2_gene1			
HBM_contig339226_s149517c1_gene1	Glucose-6-phosphate 1-epimerase	5.1.3.15	2
HBM_contig1313987_s421061c3_gene1			
HBM_contig362889_s161039c11_gene1	Glucose-6-phosphate isomerase	5.3.1.9	1
HBM_contig1288678_s409802c20_gene2	Glyceraldehyde 3-phosphate dehydrogenase	1.2.1.12	11
HBM_contig1340694_s441737c10_gene1			
HBM_contig218121_s97036c9_gene1			
HBM_contig342711_s151221c4_gene1			
HBM_contig130132_s56830c9_gene1			
HBM_contig163761_s72322c28_gene1			
HBM_contig474498_s220352c2_gene1			
HBM_contig251675_s111894c5_gene1			
HBM_contig262609_s116600c13_gene1			
HBM_contig1295303_s411482c9_gene1			
HBM_contig410838_s186095c19_gene1			
HBM_contig342780_s151248c4_gene1	Glycogen (starch) phosphorylase	2.4.1.1	1
HBM_contig1290182_s410061c3_gene1	Hydroxymethyl glutaryl-CoA reductase	1.1.1.34	5
HBM_contig269042_s119264c2_gene1			

HBM_contig411305_s186349c9_gene1			
HBM_contig454459_s209676c4_gene1			
HBM_contig382803_s171253_gene1			
HBM_contig1303558_s415149c3_gene1	Hydroxymethylglutaryl-CoA synthase	2.3.3.10	2
HBM_contig265284_s117727c3_gene4			
HBM_contig243087_s108198c7_gene1	Isocitrate dehydrogenase	1.1.1.42	3
HBM_contig821362_s316780c28_gene2			
HBM_contig354346_s156820c5_gene1			
HBM_contig501437_s233949c28_gene1	Isopentenyl-diphosphate delta-isomerase	5.3.3.2	3
HBM_contig326011_s143366_gene1			
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	16
HBM_contig1295328_s411484c1_gene1			
HBM_contig284161_s125295c10_gene2			
HBM_contig1297103_s412143c2_gene1			
HBM_contig1396318_s493516c3_gene2			
HBM_contig1431931_s528398_gene1			
HBM_contig1432076_s528536_gene1			
HBM_contig286272_s126079c2_gene1			
HBM_contig299478_s131426c5_gene2			
HBM_contig323068_s142068c15_gene2			
HBM_contig330011_s145212c19_gene2			
HBM_contig337779_s148815c3_gene1			
HBM_contig349947_s154583_gene1			
HBM_contig451347_s208034_gene1			
HBM_contig332061_s146156c4_gene2			
HBM_contig675650_s282628_gene1			
HBM_contig1324605_s428704c13_gene4	Malate dehydrogenase (decarboxylating)/	1.1.1.39/	19
HBM_contig285159_s125660c12_gene1	Malate dehydrogenase (oxaloacetate-decarboxylating)	1.1.1.40	
HBM_contig673366_s282240c3_gene1			
HBM_contig721178_s292728c3_gene1			
HBM_contig1297091_s412138c4_gene1			
HBM_contig1297092_s412138c5_gene1			
HBM_contig1302213_s414481c5_gene1			
HBM_contig1302214_s414481c6_gene1			
HBM_contig1324606_s428704c14_gene1			
HBM_contig1347612_s447769_gene1			
HBM_contig1356436_s455595c6_gene1			
HBM_contig1356437_s455595c7_gene1			
HBM_contig324268_s142597_gene1			
HBM_contig350581_s154926_gene1			
HBM_contig428410_s195673c1_gene1			
HBM_contig428411_s195673c2_gene1			
HBM_contig440660_s202264_gene1			
HBM_contig98998_s42626c10_gene1			

HBM_contig98999_s42626c11_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_contig205504_s91271c2_gene1	Monosaccharide transporter (MT)	na	30
HBM_contig253707_s112736c8_gene1			
HBM_contig377316_s168363c3_gene1			
HBM_contig392526_s176392c5_gene1			
HBM_contig395725_s178055_gene1			
HBM_contig408839_s185016_gene1			
HBM_contig446109_s205232c1_gene1			
HBM_contig446110_s205232c2_gene2			
HBM_contig1301388_s414043_gene1			
HBM_contig1323260_s427655_gene1			
HBM_contig1109905_s381969_gene1			
HBM_contig429984_s196523_gene1			
HBM_contig1321698_s426518c5_gene1			
HBM_contig1301003_s413843c6_gene1			
HBM_contig1301009_s413843c12_gene3			
HBM_contig1314924_s421675c8_gene1			
HBM_contig1317114_s423241_gene1			
HBM_contig1327193_s430716c2_gene1			
HBM_contig1377511_s475352_gene1			
HBM_contig1382478_s480117c3_gene1			
HBM_contig1450478_s546338_gene1			
HBM_contig1487136_s577425c10_gene1			
HBM_contig1487136_s577425c10_gene2			
HBM_contig242138_s107781c4_gene2			
HBM_contig291717_s128069c7_gene1			
HBM_contig317671_s139551c2_gene1			
HBM_contig325647_s143203_gene1			
HBM_contig374965_s167091_gene1			
HBM_contig422653_s192531_gene1			
HBM_contig459400_s212319c13_gene1			
HBM_contig303759_s133310c8_gene1	NADP-dependent glyceraldehyde-3-phosphatedehydrogenase	1.2.1.9	1
HBM_contig1354496_s453822c10_gene2	Oxoglutarate:malate antiporter (OMT)	na	4
HBM_contig231307_s102930c15_gene1			
HBM_contig302254_s132663c8_gene1			
HBM_contig728764_s293779c7_gene1			
HBM_contig1302285_s414518c3_gene1	Dicarboxylate/Tricarboxylate carrier protein (DTC)	na	1
HBM_contig1305977_s416315c19_gene1	Phosphoglucomutase	5.4.2.2	2
HBM_contig422634_s192523c3_gene2			
HBM_contig747716_s298021c22_gene1	Phosphoglycerate kinase	2.7.2.3	2

HBM_contig747717_s298021c23_gene1			
HBM_contig323198_s142103c44_gene1	Phosphoglycerate mutase	5.4.2.1	3
HBM_contig349580_s154385c27_gene1			
HBM_contig389245_s174714c12_gene1			
HBM_contig433979_s198650c9_gene1	Phosphomevalonatekinase	2.7.4.2	3
HBM_contig227302_s101115c1_gene1			
HBM_contig297356_s130487_gene1			
HBM_contig295239_s129579c5_gene1	Phosphopyruvate hydratase (enolase)	4.2.1.11	1
HBM_contig1289256_s409900_gene1	Oligo-1,6-glucosidase	3.2.1.10	2
HBM_contig298771_s131111c1_gene1			
HBM_contig1290187_s410061c8_gene3	Pyrophosphate--fructose-6-phosphate 1-phosphotransferase	2.7.1.90	2
HBM_contig334050_s147096c2_gene1			
HBM_contig433980_s198650c10_gene1	Pyruvate dehydrogenase	1.2.4.1	9
HBM_contig1301528_s414125c2_gene1			
HBM_contig1311068_s419250c5_gene1			
HBM_contig30266_s12350c4_gene1			
HBM_contig475200_s220734_gene1			
HBM_contig280867_s123996_gene1			
HBM_contig1317715_s423641c13_gene1			
HBM_contig1317714_s423641c12_gene1			
HBM_contig1295434_s411511c6_gene1			
HBM_contig101953_s43997c3_gene2	Dihydrolipoyllysine-residue acetyl transferase	2.3.1.12	4
HBM_contig299370_s131382_gene1			
HBM_contig397018_s178729c12_gene1			
HBM_contig402074_s181422c8_gene1			
HBM_contig1026725_s363504c2_gene2	Pyruvate kinase	2.7.1.40	8
HBM_contig1297534_s412313c2_gene1			
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_gene1			
HBM_contig306687_s134504c10_gene1			
HBM_contig332846_s146521c1_gene1			
HBM_contig943860_s342523c1_gene1			
HBM_contig1289127_s409874c9_gene1			
HBM_contig1318935_s424517c31_gene1			
HBM_contig1348382_s448422c18_gene1	Phosphoenolpyruvate carboxykinase	4.1.1.49	5
HBM_contig309950_s135961c7_gene1			
HBM_contig320759_s140923c1_gene1			
HBM_contig350988_s155107c19_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	3
HBM_contig470957_s218510c13_gene2			
HBM_contig363653_s161426_gene1			
HBM_contig227922_s101408c5_gene1	Pyruvate decarboxylase	4.1.1.1	3
HBM_contig1381025_s478729c8_gene1			
HBM_contig369579_s164395c1_gene1			
HBM_contig213287_s94844c20_gene1	Aldehyde dehydrogenase	1.2.1.3	6
HBM_contig325083_s142963_gene1			
HBM_contig259895_s115401c4_gene1			
HBM_contig380725_s170152c1_gene1			
HBM_contig1375260_s473175c20_gene2			
HBM_contig378330_s168914c2_gene2			
HBM_contig378047_s168772_gene1	Alcohol dehydrogenase	1.1.1.1	7
HBM_contig1292937_s410710c5_gene1			
HBM_contig1314460_s421368c3_gene1			
HBM_contig1354880_s454167c4_gene1			
HBM_contig1354881_s454167c5_gene1			

HBM_contig427387_s195110c1_gene1			
HBM_contig1292652_s410638c8_gene2			
HBM_contig63343_s26589c5_gene1	l-lactate dehydrogenase	1.1.1.27	2
HBM_contig1254051_s405310c12_gene1			
HBM_contig202157_s89781c2_gene1	Acetyl-CoA ligase	6.2.1.1	2
HBM_contig770884_s304118c4_gene1			
HBM_contig403677_s182258c2_gene1	Trehalose phosphatase	3.1.3.12	9
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_contig1352489_s452038_gene1	4-hydroxy-3-methylbut-2-enyl-diphosphate synthase	1.17.7.1	3
HBM_contig328275_s144399c2_gene1			
HBM_contig433089_s198173c7_gene1			
HBM_contig1289509_s409944c2_gene1	Sucrose -fructosyltransferase	2.4.1.99	3
HBM_contig1324950_s428974c9_gene1			
HBM_contig1345306_s445741c4_gene1			
HBM_contig1288687_s409803c1_gene1	Sucrose phosphate phosphatase	3.1.3.24	2
HBM_contig272605_s120794c27_gene1			
HBM_contig757629_s300436c6_gene1	Sucrose phosphate synthase	2.4.1.14	4
HBM_contig771203_s304239c15_gene1			
HBM_contig1463859_s558603c4_gene1			
HBM_contig355822_s157485c2_gene1			
HBM_contig01226_s00535c7_gene1	Sucrose synthase	2.4.1.13	8
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			
HBM_contig47165_s19567c3_gene2	Sucrose transporter (SUT)	na	7
HBM_contig1289974_s410033c6_gene1			
HBM_contig332408_s146322c13_gene1			
HBM_contig332409_s146322c14_gene1			
HBM_contig380380_s169971_gene1			
HBM_contig397588_s179019c30_gene3			
HBM_contig654533_s279397c2_gene1			
HBM_contig346208_s152843c5_gene1	Transaldolase	2.2.1.2	2
HBM_contig1305835_s416254c32_gene5			
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.-	4
HBM_contig1323470_s427819c4_gene1			
HBM_contig1013854_s360717c11_gene3			
HBM_contig1299176_s413002_gene1			

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_contig323068_s142068c15_gene2	10	2.69E-94	100
HBM_contig470957_s218510c13_gene2	27	2.72E-112	100
HBM_contig380725_s170152c1_gene1	11	6.63E-105	100
HBM_contig362889_s161039c11_gene1	2	2.43E-24	98
HBM_contig1297534_s412313c2_gene1	8	4.63E-133	98
HBM_contig348246_s153791c8_gene2	27	7.26E-105	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_contig340487_s150149c5_gene1	6	8.66E-111	96
HBM_contig756485_s300037c2_gene5	5	1.23E-109	96
HBM_contig251675_s111894c5_gene1	30	1.83E-101	96
HBM_contig218121_s97036c9_gene1	36	1.00E-124	95
HBM_contig163761_s72322c28_gene1	35	5.62E-94	95
HBM_contig324268_s142597_gene1	5	2.70E-23	95
HBM_contig770884_s304118c4_gene1	18	6.89E-53	95
HBM_contig339478_s149632c15_gene2	21	1.00E-117	94
HBM_contig1288678_s409802c20_gene2	37	4.02E-122	94
HBM_contig342711_s151221c4_gene1	37	3.20E-119	94
HBM_contig410838_s186095c19_gene1	30	2.94E-103	94
HBM_contig1301528_s414125c2_gene1	7	1.99E-47	94
HBM_contig328275_s144399c2_gene1	9	6.93E-126	94
HBM_contig433089_s198173c7_gene1	9	1.37E-125	94
HBM_contig1302790_s414786c2_gene1	8	7.77E-118	93
HBM_contig147570_s64869c11_gene1	16	2.14E-114	93
HBM_contig522414_s243848c9_gene1	23	5.14E-135	93
HBM_contig1303558_s415149c3_gene1	22	8.27E-106	93
HBM_contig330011_s145212c19_gene2	3	1.73E-122	93
HBM_contig675650_s282628_gene1	11	1.46E-103	93
HBM_contig428411_s195673c2_gene1	8	9.40E-54	93
HBM_contig1302285_s414518c3_gene1	39	2.12E-98	93
HBM_contig294978_s129482c1_gene1	8	1.78E-96	93
HBM_contig346208_s152843c5_gene1	5	1.51E-112	93
HBM_contig1307528_s417190c7_gene1	7	1.17E-52	92
HBM_contig343183_s151438c5_gene1	4	1.09E-60	92
HBM_contig289576_s127312c17_gene3	9	5.65E-115	92
HBM_contig907698_s335276c27_gene1	10	3.22E-113	92
HBM_contig1289171_s409884c2_gene1	23	3.97E-135	92
HBM_contig180992_s80187c5_gene1	21	1.66E-131	92
HBM_contig130132_s56830c9_gene1	35	1.47E-120	92
HBM_contig821362_s316780c28_gene2	5	1.07E-105	92
HBM_contig337779_s148815c3_gene1	4	4.96E-109	92

HBM_contig295239_s129579c5_gene1	22	3.95E-127	92
HBM_contig1317714_s423641c12_gene1	4	2.61E-72	92
HBM_contig1305835_s416254c32_gene5	7	1.71E-111	92
HBM_contig1299176_s413002_gene1	8	3.01E-97	92
HBM_contig1326688_s430296c2_gene2	10	6.66E-89	91
HBM_contig217879_s96943c3_gene1	9	4.76E-88	91
HBM_contig484019_s225263c9_gene1	13	1.91E-110	91
HBM_contig1340694_s441737c10_gene1	36	8.63E-119	91
HBM_contig326011_s143366_gene1	7	8.30E-79	91
HBM_contig320759_s140923c1_gene1	8	1.17E-127	91
HBM_contig382299_s170997c9_gene2	4	1.16E-130	90
HBM_contig290988_s127806c2_gene1	2	9.62E-11	90
HBM_contig1339227_s440512c5_gene3	22	1.09E-130	90
HBM_contig418176_s190089c6_gene1	5	8.17E-103	90
HBM_contig411305_s186349c9_gene1	8	1.02E-96	90
HBM_contig454459_s209676c4_gene1	17	2.33E-93	90
HBM_contig354346_s156820c5_gene1	7	3.22E-95	90
HBM_contig1324605_s428704c13_gene4	7	5.58E-106	90
HBM_contig1356436_s455595c6_gene1	3	2.92E-39	90
HBM_contig747716_s298021c22_gene1	11	3.21E-108	90
HBM_contig136768_s59843c7_gene1	10	4.18E-111	90
HBM_contig297371_s130496_gene1	15	7.42E-89	89
HBM_contig1352768_s452278c9_gene1	2	7.10E-123	89
HBM_contig303742_s133305c3_gene1	3	1.25E-122	89
HBM_contig323410_s142207c17_gene1	5	2.93E-123	89
HBM_contig1322658_s427165c3_gene3	22	1.09E-129	89
HBM_contig284161_s125295c10_gene2	10	1.93E-107	89
HBM_contig451347_s208034_gene1	9	4.82E-53	89
HBM_contig1297091_s412138c4_gene1	9	3.28E-75	89
HBM_contig747717_s298021c23_gene1	8	5.19E-87	89
HBM_contig350988_s155107c19_gene1	9	9.17E-126	89
HBM_contig378330_s168914c2_gene2	12	4.61E-103	89
HBM_contig1292937_s410710c5_gene1	38	4.70E-106	89
HBM_contig1354881_s454167c5_gene1	22	3.46E-96	89
HBM_contig1292652_s410638c8_gene2	34	6.96E-104	89
HBM_contig354344_s156820c3_gene1	12	1.65E-97	89
HBM_contig425247_s193932c4_gene2	2	5.80E-124	88
HBM_contig257034_s114160c16_gene1	13	4.10E-114	88
HBM_contig743614_s296819c6_gene1	5	7.80E-103	88
HBM_contig474498_s220352c2_gene1	10	7.74E-101	88
HBM_contig269042_s119264c2_gene1	9	1.60E-106	88
HBM_contig1293296_s410821c9_gene1	10	3.69E-107	88
HBM_contig286272_s126079c2_gene1	4	2.03E-117	88
HBM_contig303759_s133310c8_gene1	10	6.79E-100	88
HBM_contig1290187_s410061c8_gene3	19	2.89E-63	88
HBM_contig1311068_s419250c5_gene1	6	1.13E-71	88

HBM_contig1310976_s419196c4_gene1	5	6.73E-111	88
HBM_contig281038_s124058c3_gene2	5	8.27E-111	88
HBM_contig1290182_s410061c3_gene1	9	2.08E-90	87
HBM_contig243087_s108198c7_gene1	5	7.55E-102	87
HBM_contig285159_s125660c12_gene1	8	1.43E-123	87
HBM_contig1344950_s445443c5_gene5	14	3.55E-51	87
HBM_contig1311114_s419277c4_gene1	11	1.90E-46	87
HBM_contig1343951_s444526c6_gene1	9	8.48E-82	86
HBM_contig945098_s342802c4_gene3	16	1.12E-112	86
HBM_contig419623_s190883c14_gene1	6	1.34E-63	86
HBM_contig298249_s130891c6_gene1	7	4.29E-107	86
HBM_contig1305637_s416164c2_gene1	4	5.90E-104	86
HBM_contig382803_s171253_gene1	10	4.62E-104	86
HBM_contig01222_s00535c3_gene1	3	4.14E-91	86
HBM_contig1295328_s411484c1_gene1	10	6.91E-105	86
HBM_contig334050_s147096c2_gene1	9	1.38E-121	86
HBM_contig227922_s101408c5_gene1	4	3.99E-44	86
HBM_contig434052_s198679c8_gene2	16	8.92E-116	85
HBM_contig407283_s184142c3_gene1	4	1.70E-59	85
HBM_contig440778_s202339_gene1	17	2.69E-57	85
HBM_contig501437_s233949c28_gene1	7	2.25E-95	85
HBM_contig278880_s123280_gene1	51	1.65E-46	85
HBM_contig349580_s154385c27_gene1	4	6.90E-104	85
HBM_contig304780_s133706c10_gene2	4	2.42E-98	85
HBM_contig272605_s120794c27_gene1	3	9.23E-26	85
HBM_contig01226_s00535c7_gene1	8	8.19E-119	85
HBM_contig1061580_s369994_gene1	5	5.86E-53	84
HBM_contig1324606_s428704c14_gene1	3	1.22E-13	84
HBM_contig402074_s181422c8_gene1	9	1.53E-58	84
HBM_contig1381025_s478729c8_gene1	8	2.76E-71	84
HBM_contig1339539_s440773c5_gene3	2	2.63E-53	83
HBM_contig318055_s139710c8_gene1	16	4.62E-120	83
HBM_contig276900_s122507c5_gene1	4	5.90E-101	83
HBM_contig338536_s149176c3_gene1	20	6.37E-111	83
HBM_contig656003_s279612c2_gene3	6	5.54E-90	83
HBM_contig1294315_s411141c4_gene1	5	9.78E-28	83
HBM_contig1303826_s415277c9_gene1	26	1.49E-119	83
HBM_contig262609_s116600c13_gene1	30	1.00E-76	83
HBM_contig1302213_s414481c5_gene1	10	2.24E-121	83
HBM_contig819783_s316335c3_gene1	53	1.76E-57	83
HBM_contig1312636_s420192c3_gene1	5	1.40E-96	83
HBM_contig213287_s94844c20_gene1	3	5.18E-109	83
HBM_contig1254051_s405310c12_gene1	8	7.39E-101	83
HBM_contig1125285_s385576c12_gene1	8	4.61E-51	83
HBM_contig1013854_s360717c11_gene3	7	4.13E-85	83
HBM_contig124304_s54106c3_gene1	11	1.00E-65	82

HBM_contig316188_s138852c6_gene2	22	5.59E-115	82
HBM_contig320635_s140865c2_gene1	23	2.35E-116	82
HBM_contig1295303_s411482c9_gene1	30	2.37E-79	82
HBM_contig349947_s154583_gene1	9	6.84E-32	82
HBM_contig673366_s282240c3_gene1	9	2.10E-123	82
HBM_contig721178_s292728c3_gene1	8	3.99E-105	82
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HBM_contig302280_s132669c17_gene1	4	9.39E-68	81
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HBM_contig316009_s138773_gene1	15	4.26E-90	81
HBM_contig285749_s125863c8_gene2	8	2.54E-89	81
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HBM_contig943860_s342523c1_gene1	5	2.89E-35	79
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HBM_contig529416_s246980c14_gene1	9	7.77E-79	78
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HBM_contig283350_s124975c7_gene1	3	9.10E-109	78
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HBM_contig380380_s169971_gene1	9	3.19E-81	78
HBM_contig1357960_s456977c8_gene3	8	3.48E-104	77
HBM_contig265284_s117727c3_gene4	6	7.87E-61	77
HBM_contig299478_s131426c5_gene2	7	3.21E-86	77
HBM_contig428410_s195673c1_gene1	9	3.16E-49	77
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HBM_contig1038212_s365857c9_gene1	3	1.41E-32	76
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HBM_contig355900_s157502c9_gene1	2	1.26E-53	76
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HBM_contig385624_s172762c13_gene1	1	3.56E-52	71
HBM_contig350581_s154926_gene1	3	8.71E-51	71
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HBM_contig1294277_s411129_gene1	4	3.20E-29	69
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HBM_contig09843_s04035c2_gene1	4	5.80E-73	67
HBM_contig550434_s255571_gene1	13	2.98E-25	67
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HBM_contig306687_s134504c10_gene1	5	1.38E-41	67
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HBM_contig314926_s138259_gene1	12	1.29E-35	43
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HBM_contig1291168_s410297_gene2	9	1.43E-34	42
HBM_contig323185_s142103c31_gene1	4	1.69E-23	40
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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
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HBM_contig451554_s208132c13_gene1	1	9.18E-06	26
HBM_contig353116_s156220_gene1	2	2.09E-07	26

^aTBLASTN hits with E-value < 10⁻⁵

^bIn 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

	<i>Hevea</i>	<i>Ricinus</i>	<i>Populus</i>	<i>Arabidopsis</i>	<i>Oryza</i>	<i>Selaginella</i>
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 comparison to other sequenced genomes

Predicted Protein	<i>Hevea</i>	<i>Populus</i>	<i>Papaya</i>	<i>Arabidopsis</i>	<i>Oryza</i>
<i>Without LRRs</i>					
TIR-NBS	17	10	2	21	3
CC-NBS	134	19	2	5	7
NBS	350	49	17	1	45
<i>With LRRs</i>					
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)	<i>Hevea</i>	<i>Ricinus</i>	<i>Populus</i>	<i>Arabidopsis</i>	<i>Oryza</i>	<i>Selaginella</i>
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	Monooxygenase
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 peroxidase
HBM_contig252939_s112426c6_gene2	Zeamatin precursor
HBM_contig262953_s116732c1_gene1	Mitogen-activated protein kinase 2
HBM_contig263035_s116770c1_gene1	Flavine-containing monooxygenase
HBM_contig264998_s117599_gene1	Rhcadhesin 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 binding 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	<i>Hevea</i>	<i>Ricinus</i>	<i>Populus</i>	<i>Arabidopsis</i>	<i>Oryza</i>	<i>Selaginella</i>
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	<i>Hevea</i>	<i>Ricinus</i>	<i>Populus</i>	<i>Arabidopsis</i>	<i>Oryza</i>	<i>Selaginella</i>
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 monooxygenases	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	<i>Hevea</i>	<i>Populus</i>	<i>Arabidopsis</i>
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	<i>Hevea</i>	<i>Arabidopsis</i>
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
CrtIso	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