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Unique Features of the Loblolly Pine (*Pinus taeda* L.) Megagenome Revealed Through Sequence Annotation

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ABSTRACT The largest genus in the conifer family Pinaceae is *Pinus*, with over 100 species. The size and complexity of their genomes (~20–40 Gb, $2n = 24$) have delayed the arrival of a well-annotated reference sequence. In this study, we present the annotation of the first whole-genome shotgun assembly of loblolly pine (*Pinus taeda* L.), which comprises 20.1 Gb of sequence. The MAKER-P annotation pipeline combined evidence-based alignments and *ab initio* predictions to generate 50,172 gene models, of which 15,653 are classified as high confidence. Clustering these gene models with 13 other plant species resulted in 20,646 gene families, of which 1554 are predicted to be unique to conifers. Among the conifer gene families, 159 are composed exclusively of loblolly pine members. The gene models for loblolly pine have the highest median and mean intron lengths of 24 fully sequenced plant genomes. Conifer genomes are full of repetitive DNA, with the most significant contributions from long-terminal-repeat retrotransposons. In depth analysis of the tandem and interspersed repetitive content yielded a combined estimate of 82%.

L OBLLOLY pine is a long-lived, diploid member ($2n = 24$) of the genus *Pinus*, one of >100 species worldwide. The natural range of this primarily outcrossing tree extends over a large portion of the southeastern United States. Loblolly

pine is extensively cultivated in this region for timber and pulpwood, with plantations growing on >30 million hectares and producing ~18% of the world's industrial roundwood (Prestemon and Abt 2002). Loblolly pine's preference for mild, wet climates has made it a model for ecological considerations relating to carbon sequestration in coastal plain plantations (Noormets *et al.* 2010). The plant biomass on these plantations is thought to contribute to a negative accumulation of atmospheric CO₂ (Johnsen *et al.* 2001). This species is also under investigation as a potential source of sustainable, renewable energy, both as an independent source of terpenoids in liquid biofuels and as an intercropping species with other established sources, such as switchgrass (Briones *et al.* 2013; Westbrook *et al.* 2013). The economic and ecological importance of this species has led to several long-term breeding programs and large-scale

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Annotation of the genome is presented through the TreeGenes database (Wegrzyn *et al.* 2008). It is distributed both via Gbrowse (Stein *et al.* 2002) and WebApollo (<http://code.google.com/p/apollo-web/>). In addition, flat file access to the FASTA sequences of the genome and transcriptome, annotations, and gff3 files are available through the database FTP site (http://loblolly.ucdavis.edu/bipod/ftp/Genome_Data/genome/pinerefseq/Pita/). A masked version of the genome based on the PIER library 2.0 is available for download at the same location.

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studies that have addressed questions about the genetic diversity and adaptive capabilities (Brown *et al.* 2004; Eckert *et al.* 2010).

In the absence of an affordable and capable technology to generate and assemble a conifer genome, previous investigations have relied on other techniques to generate sequence for basic and applied research in pine genetics. For non-model organisms with large and complex genomes, transcriptome resources provide valuable sequence for gene discovery and annotation, as well as for comparative genomics. In loblolly pine, these were first generated with >300,000 Sanger-sequenced expressed sequence tags (ESTs) and later as *de novo* assemblies from next-generation sequencing technologies (Allona *et al.* 1998; Kirst *et al.* 2003; Cairney *et al.* 2006; Lorenz *et al.* 2006, 2012). Large-scale resequencing of the first ESTs and subsequent genotyping of single nucleotide polymorphisms in large populations expanded the available molecular marker resources and provided a basis for examining their association with traits of interest (Eckert *et al.* 2013). The markers genotyped in these breeding populations also improved the density of the genetic linkage map for loblolly pine (Eckert *et al.* 2009, 2010; Martínez-García *et al.* 2013). The first significant insight into the genome came from the analysis of 10 bacterial artificial chromosome (BAC) sequences (Kovach *et al.* 2010).

Gymnosperms are represented by just four divisions: Pinophyta (conifers), Cycadophyta (cycads), Gnetophyta (gnetophytes), and Ginkgophyta (*Ginkgo*). Their genome sizes range considerably, but are generally large, between 12 and 32 Gbp. The pine family (Pinaceae) possesses tremendous genome size variation. Pines (*Pinus*) diverged from spruces (*Picea*), their closest relatives, 85 MYA and possess larger genomes on average, estimated between 22 and 32 Gbp (Guillet-Claude *et al.* 2004; Willyard *et al.* 2007). The size of these genomes has previously served as a barrier to whole-genome sequencing, but recent advances in sequencing technologies and informatics have made assembling these megagenomes tractable. Unlike many large and complex crop genomes, there is no evidence to support a whole-genome duplication event. The large genome size has primarily been attributed to an extensive contribution of interspersed repetitive content (Morse *et al.* 2009; Kovach *et al.* 2010; Wegrzyn *et al.* 2013). Assembly of the Norway spruce genome has shown that LTR retrotransposons in particular are frequently nested within the long introns of some gene families (Nystedt *et al.* 2013). In addition, there is evidence for gene duplication, pseudogenes, and paralogs, although the extent of these is not clear (Kovach *et al.* 2010; Pavy *et al.* 2012).

To provide a foundation to study the biology of conifers, we annotated the loblolly pine genome, the first and largest pine genome assembled to date. The whole-genome shotgun sequencing and assembly (Zimin *et al.* 2014) produced two reference sequences. Version 1.0, the direct output of the MaSuRCA assembler (Zimin *et al.* 2013), was based on

paired-end reads from a haploid megagametophyte and the matching long insert linking read pairs from diploid needle tissue. Version 1.01, which applied scaffolding from independent genome and transcriptome assemblies, spans 20.1 Gbp of sequence and is distributed in just over 14.4 million scaffolds covering 23.2 Gbp with an N50 of 66.9 kb (based on a genome size of 22 Gbp). Our annotation of the loblolly pine genome provides insight into the organization of the genome, its size, content, and structure.

Materials and Methods

Sequence alignments

Aligning DNA, messenger RNA (mRNA), or protein sequence to the loblolly pine genome presents challenges, as the genome is too large for many common bioinformatic programs. In our approach, we sorted the genomic data by descending scaffold length and partitioned the scaffolds into 100 bins such that the genomic sequence for each bin contained roughly the same number of bases. This allowed us to parallelize the computations and examine how fragmentation of the genomic data affected our ability to align sequence data to the genome. We generated initial mappings to the genome using blat (Kent 2002) with each bin as a target and then used blat utility programs to merge data from the 100 bins into a single file and filter that data according to quality metrics. In-house scripts were used to parse the blat results and create input files for exonerate (Slater and Birney 2005), which generated the final, more refined alignments to the genome.

A set of 83,285 *de novo*-assembled loblolly pine transcripts (BioProject PRJNA174450) served as the primary transcriptome reference. These were derived from multiple assemblies of 1.3 billion RNA-Seq reads, selected for uniqueness and putative protein-coding quality, and represented samplings from mixed sources of vegetative and reproductive organs, seedlings, embryos, haploid megagametophytes, and needles under environmental stress (Supporting Information, File S1). The transcriptome reference in addition to 45,085 sequences generated from >300,000 reclustered loblolly pine ESTs (Eckert *et al.* 2013) were aligned to the genome. Sanger-sequenced transcripts from four other pines available from the TreeGenes database (Wegrzyn *et al.* 2012) provided additional alignments: *Pinus banksiana* (13,040 transcripts), *Pinus contorta* (13,570 transcripts), and *Pinus pinaster* (15,648 transcripts). Transcriptome assemblies generated via 454 pyrosequencing and assembled with Newbler (Roche GS *De novo* Assembler) for *Pinus palustris* (16,832 transcripts) and *Pinus lambertiana* (40,619 transcripts) (Lorenz *et al.* 2012) were also aligned. Sequence alignments were examined at four different cutoffs for the loblolly sequence sets and two cutoffs for the other conifer resources. Stringent thresholds of 98% identity/98%

coverage served as the starting point for loblolly pine while other conifer species were given more permissive (95% identity/95% coverage) cutoffs. The thresholds were lowered for all sequence sets to 95% identity/50% coverage to further examine the effects of genome fragmentation.

To discover orthologous proteins and align them to the genome, we began with 653,613 proteins spanning 24 species from version 2.5 of the PLAZA data set (Van Bel *et al.* 2012). PLAZA provides a curated and comprehensive comparative genomics resource for the Viridiplantae, including annotated proteins. This set was further curated to exclude proteins that were not full length, those shorter than 21 amino acids, and those that had genomic coordinates that did not agree with the reported coding sequence (CDS) or did not translate into the reported protein. To this set, 25,347 angiosperm proteins reported by the Amborella Genome Project (<http://www.amborella.org/>) were added. From annotated full-length mRNAs available in GenBank, a set of 10,793 proteins from *Picea sitchensis* were included. From the *Picea abies* v1.0 genome project (Nystedt *et al.* 2013), 22,070 full-length proteins were included where the reported CDS agreed with the translated protein (File S2 and Table S1). From the loblolly pine transcriptome, all 83,285 transcripts were translated for alignment. For the PLAZA protein alignments, the target version 1.01 genome was hard-masked for repeats; for all other alignments, the v1.01 genome was not repeat-masked. We accepted an alignment when at least 70% of the query sequence was included in the alignment and the exonerate similarity score (ESS) ≥ 70 .

Gene annotation

Annotations for the assembly were generated using the automated genome annotation pipeline MAKER-P, which aligns and filters EST and protein homology evidence, produces *ab initio* gene predictions, infers 5' and 3' UTRs, and integrates these data to produce final downstream gene models with quality control statistics (Campbell *et al.* 2014). Inputs for MAKER-P include the *Pinus taeda* genome assembly (v1.0), *Pinus* and *Picea* ESTs, conifer transcriptome assemblies, a species-specific repeat library (PIER) (Wegrzyn *et al.* 2013), protein databases containing annotated proteins for *P. sitchensis* and *P. abies*, and version 2.5 of the PLAZA protein database (Van Bel *et al.* 2012). MAKER-P produced *ab initio* gene predictions via SNAP (Korf 2004) and Augustus (Stanke and Waack 2003). A subset of annotations (500 Mb of sequence) were manually reviewed to develop appropriate filters for the final gene models. Given the large genome size and potential for spurious annotations, conservative thresholds for these filters were chosen. Filters included the initial removal of single-exon annotations because of apparent pseudogene bias, annotations not containing a recognizable protein domain as interpreted using InterProScan (Quevillon *et al.* 2005), or annotations that do not partially overlap the conifer transcriptome

resources available. Among the selected, nonoverlapping gene models, a subset of high confidence gene models was further analyzed based on the annotation edit distance (AED) score of < 0.20 with canonical start sites and splice sites. All gene models identified in v1.0 were also mapped to the latest assembly (v1.01). Functional annotations of the gene models were generated through *blastp* alignments against the National Center for Biotechnology Information (NCBI) nr and plant protein databases for significant (E -values $< 1e-05$) and weak (E -value < 0.001) hits.

Alignments of the high-confidence MAKER-P sequences against the genome allowed for identification of large introns. Introns of lengths >20 , >50 , and >100 kbp and with $<25\%$ gap regions were selected for further analysis. Clusters from the Markov cluster algorithm (MCL) analysis that represented gene families with *P. taeda* members and contained primary introns (first CDS) >20 kbp were aligned and manually reviewed. The intronic sequences were investigated for the presence of intron-mediated expression signals (IMES). IMES were predicted via sequence motifs using the methodology outlined in Parra *et al.* (2007).

Orthologous proteins

The analysis of orthologous genes included a subset of the species that were previously selected from PLAZA. A total of 10, including: *Arabidopsis thaliana* (27,403), *Glycine max* (46,324), *Oryza sativa* (41,363), *Physcomitrella patens* (28,090), *Populus trichocarpa* (40,141), *Ricinus communis* (31,009), *Selaginella moellendorffii* (18,384), *Theobroma cacao* (28,858), *Vitis vinifera* (26,238), and *Zea mays* (39,172) were used. Three external protein sequence sets were also included: *Amborella trichopoda* (25,347), *P. abies* (22,070), and *P. sitchensis* (10,521). The primary source of the *P. taeda* sequence was the complete set of 50,172 gene models generated from the MAKER-P pipeline. All 14 sequence sets (including the 10 from PLAZA) were clustered to 90% identity within species and combined to generate 399,358 sequences.

The MCL analysis (Enright *et al.* 2002), as implemented in the TRIBE-MCL pipeline (Dongen and Abreu-Goodger 2012), was used to cluster the 399,358 protein sequences from 14 species into orthologous groups. The methodology was selected due to its robust implementation that avoids merging clusters that share only a few edges. This leads to accurate identifications of gene families even in the presence of lower-quality BLAST hits or promiscuous domains (Frech and Chen 2010). The analysis was performed by running pairwise NCBI *blastp* v2.2.27+ (Altschul *et al.* 1990) (E -value cutoff of $1e-05$) against the full set of proteins described above. In this pipeline, the negative \log_{10} of the resulting *blastp* E -values produces a network graph that serves as input to define the orthologous groups. The user-supplied inflation value is used in the second stage to simulate random walks in the previously calculated graph. A large inflation value defines more clusters with lower amount of members (fine-grained granularity); a small inflation value

defines not as many clusters, but the clusters have more members (coarse granularity). A moderate inflation value of 4.0 was selected to define the orthologous groups here. Following their generation, Pfam domains (Punta *et al.* 2012) were assigned from the PLAZA annotations of the individual sequences. InterProScan 4.8 (Hunter *et al.* 2012) was applied to those sequences obtained outside of PLAZA (*A. trichopoda*, *P. sitchensis*, *P. abies*, and *P. taeda*). Pfam and Gene Ontology (GO) assignments with E -values $< 1e-05$ were retained. To effectively compare GO annotations, the terms were normalized to level four of the classification tree. When all predicted domains for a given family were classified as retroelements, the family was removed. After functional assessment and filtering, custom scripts and Venn diagrams (<http://bioinformatics.psb.ugent.be/webtools/Venn/>) were applied to visualize gene family membership among species.

Gene family gain-and-loss phylogenetics

The DOLLOP v3.695 program from the Phylip package (Felsenstein 1989) was used to reconstruct a parsimonious tree explaining the gain and loss of gene families under the DOLLOP parsimony model. The DOLLOP algorithm estimates phylogenies for discrete character data with two states (either a 0 or 1), which assumes only one gain but as many losses as necessary to explain the evolutionary pattern of states. The filtered 8519 gene families (containing 112,899 sequences representing 13 species, the small number of sequences from *P. sitchensis* excluded) were used to create a gene family gain-and-loss matrix. Gene families that represented all species were dropped from the input to DOLLOP, as their phylogenetic classification would be obfuscated by a disparate number of starting proteins per species in the analysis. Branch lengths were calculated by counting the number of gains or losses for a given node. To produce the final phylogenetic reconstruction, a manual curation step was introduced to bring the *P. patens* and *Selaginella moellendorffii* branches into agreement with known phylogenies. DOLLOP was rerun on this updated tree to reconstruct the final gene family configurations of the ancestral species. Only *P. patens*, *S. moellendorffii*, and their common ancestor were updated during this step. The fidelity of the reconstructed trees was evaluated against a known phylogeny available at Phytozome (Goodstein *et al.* 2012).

Tandem repeat identification

Tandem Repeat Finder (TRF) v4.0.7b (Benson 1999) was run with the following parameters: matching weight of 2, mismatch weight of 7, indel penalty of 7, match probability of 80, indel probability of 10, minimum score of 50, and a maximum period size (repeating unit) of 2000. Both the genome and transcriptome were examined and investigated for tandem content. To accurately assess the overall coverage and distribution of tandem repeats, we filtered overlaps by discriminating against multimeric repeats, following previously described approaches (Melters *et al.* 2013), and

excluded those found within interspersed repeats, such as the long terminal ends of LTR transposable elements. Mononucleotides (period size of 1) were not scrutinized due to the high likelihood of error and/or repeat collapse in the assembly process. To maintain reproducibility, common nomenclature terms—such as “microsatellites” or simple sequence repeats (SSRs) describing 1- to 8-bp periods, “minisatellites” describing 9- to 100-bp periods, and “satellites” describing >100 -bp periods—were used for classification. For comparative analysis, these methods were applied to the reference genomes of *A. thaliana* v1.6.7, *V. vinifera* v1.4.5, *S. moellendorffii* v1.0.0, *C. sativus* v1.2.2, and *P. trichocarpa* v2.1.0, each available through Phytozome (Goodstein *et al.* 2012). The draft genome sequences of *P. glauca* v1.0.0 (Birol *et al.* 2013), *P. abies* (Nystedt *et al.* 2013), and *A. trichopoda* v1.0.0 were included. Both the filtered TRF output and consensus sequences derived from clustering the filtered TRF output (UCLUST utility at 70% identity) were used as queries in similarity searches. USEARCH (E -value < 0.01) was used to search the PlantSat database (Macas *et al.* 2002). Potential centromeric sequences were assessed by finding the monomeric tandem array that covered the largest amount of the genome. Interstitial and true telomeric sequences were isolated from the filtered TRF output by searching for (TTTAGGG) n motifs ($n > 3$ and length > 1 kbp). The thresholds applied were based on conservative estimates from telomere restriction fragment lengths described for *P. taeda* (Flanary and Kletetschka 2005).

Homology-based repeat identification

RepeatMasker 3.3.0 (RepeatMasker 2013) was used to identify previously characterized repeats. RepeatMasker was run using standard settings on the entire genome, with PIER 2.0 as a repeat library (Wegrzyn *et al.* 2013). A masked version of the genome was generated at this stage. Redundancy was eliminated through custom Python scripts by matching each reference base pair with the highest scoring alignment. For full-length estimates, we required that the genomic sequence and the reference PIER elements aligned with at least 80% identity and 70% coverage. Repeat content in introns was independently characterized using the same methodology. High-copy elements were identified by sorting families by full-length copy number. High-coverage elements were determined by sorting families by base-pair coverage, including both full-length and partial hits. MITE Hunter (release 11/2011) (Han and Wessler 2010) was used to search for miniature inverted-repeat transposable elements (MITEs) within intronic regions.

De novo repeat identification

The workflow for characterization and annotation of novel repeats largely mirrored that described in Wegrzyn *et al.* (2013). REPET 2.0 (Flutre *et al.* 2011) was used to identify sequences to form the repeat library for CENSOR 4.2.27 (Kohany *et al.* 2006). REPET's *de novo* repeat discovery

Table 1 Mapping EST/transcriptome resources against *P. taeda* version 1.01 genome

Project	Total sequence	Identity	Coverage	Unique hits	Non-unique hits	Total % mapped
<i>P. taeda</i> (reclustered ESTs)	45,085	98	98	26,700	712	60.8
<i>P. taeda</i> (reclustered ESTs)	45,085	98	95	29,676	1,845	69.91
<i>P. taeda</i> (reclustered ESTs)	45,085	95	95	31,324	2,074	74.01
<i>P. taeda</i> (reclustered ESTs)	45,085	95	50	29,744	5,486	78.14
<i>P. taeda</i> (<i>de novo</i>)	83,285	98	98	29,262	1,731	35.21
<i>P. taeda</i> (<i>de novo</i>)	83,285	98	95	42,822	5,130	57.58
<i>P. taeda</i> (<i>de novo</i>)	83,285	95	95	43,972	5,409	59.29
<i>P. taeda</i> (<i>de novo</i>)	83,285	95	50	44,469	28,116	87.15
<i>P. palustris</i> (454)	16,832	95	95	11,242	719	71.06
<i>P. palustris</i> (454)	16,832	95	50	11,181	1,949	78.06
<i>P. lambertiana</i> (454 + RNASeq)	40,619	95	95	13,134	317	33.11
<i>P. lambertiana</i> (454 + RNASeq)	40,619	95	50	23,376	3,792	66.88
<i>P. banksiana</i> (TreeGenes clusters)	13,040	95	95	9,703	513	78.34
<i>P. banksiana</i> (TreeGenes clusters)	13,040	95	50	9,470	1,473	83.92
<i>P. contorta</i> (TreeGenes clusters)	13,570	95	95	9,575	396	73.48
<i>P. contorta</i> (TreeGenes clusters)	13,570	95	50	9,534	1,083	78.24
<i>P. pinaster</i> (TreeGenes clusters)	15,648	95	95	9,738	943	68.26
<i>P. pinaster</i> (TreeGenes clusters)	15,648	95	50	10,221	2,491	81.24

performs an all-versus-all alignment of the input sequence, an unscalable, computationally intensive operation. As such, the 63 longest scaffolds in the assembly were used as input, representing ~1% of the genome (bin 1). For use in REPET's classification steps, we provided REPET with the PIER database, in addition to a set of seven conifer repeat libraries described in Nystedt *et al.* (2013). A set of 405,109 publicly available full and partial *P. taeda* and *Pinus elliottii* transcripts were provided to REPET for host gene identification.

Previously characterized elements were removed using the PIER and spruce repeat databases and the *blastn-blastx* structural filters proposed in Wicker *et al.* (2007) and implemented in Wegrzyn *et al.* (2013). Previously classified elements were identified by *blastn* alignments passing the 80-80-80 threshold (80% identity covering 80% of each sequence for at least 80 bp). Unclassified elements were analyzed using *blastx* against a database of ORFs, recovered from the PIER/spruce nucleotide database with USEARCH's "findorfs" utility at default parameters (Edgar 2010). Elements that were classified only to the superfamily level and unclassified repeats were separately clustered with UCLUST (Edgar 2010) at 80% identity. Consensus sequences for each cluster were derived from multiple alignments built with MUSCLE (Edgar 2010) and PILER (Edgar and Myers 2005). Finally, separate clusters were chained into families in which each cluster's consensus sequence aligned with at least 80% identity with at least one other sequence in the family. Further classification of LTR retroelement families was performed using the in-house tool, GCclassif (Figure S1 and File S4).

Results and Discussion

Sequence alignments

Aligning the 83,285 *de novo*-assembled transcripts to the genome allowed us to infer information about gene regions,

including introns and repeats (Table 1). At a stringency of 98% query coverage and 98% identity, 30,993 transcripts mapped to the genome, most of which (29,262) mapped with a unique hit; 1731 transcripts mapped to two or more genomic regions. Relaxing the cutoff criteria to 95% identity and 95% query coverage resulted in increases in the number of transcripts with unique (43,972) and non-unique hits (5409). At 95% identity and 50% query coverage, the number of transcripts with unique hits to the genome rose to 44,469, and transcripts aligning to more than one locus to 28,116. Possible reasons for a transcript aligning to two or more genomic locations include gene duplications, pseudogenes, assembly errors, and actively transcribed retroelements in the transcriptome assembly.

To elucidate how genome fragmentation affected our ability to map sequence to the genome, the v1.01 genome scaffolds were sorted by descending length and divided into 100 bins, with each bin containing ~1% of the genomic sequence. Peaks in the gap region content were found in bin 59 (36.0% "N" bases) and in bin 82 (47.8% "N" bases), reflecting gaps due to linking libraries (Figure S2A). While gap-region content is greatly reduced in bins 86–100, these same bins show a sharp decrease in scaffold size and hence a sharp increase in the number of scaffolds per bin (Figure S2B). As expected, the ability to align transcripts to the genome decreased as the scaffold length shortened, with 56.4% of these transcript mappings occurring in the first 25 bins, and just 8.5% in the last 25 bins (Figure S2C).

Using the same techniques, we produced transcriptome-to-genome alignments beyond those generated with the *de novo* transcriptome using existing EST and transcriptome data for loblolly pine and other closely related species (Table 1). A total of 74.1% of the loblolly pine reclustered ESTs mapped at 95% query coverage, 95% sequence identity. Sequencing technology did not affect the percentage of sequence sets aligning to the genome as much as the

Table 2 Mapping protein sequence against *P. taeda* version 1.01 genome

Full-length proteins from:	Total sequence	Unique hits	Non-unique hits	Total % mapped	Data source
<i>P. abies</i>	22,070	11,580	3,638	68.95	Nystedt <i>et al.</i> (2013)
<i>P. sitchensis</i>	10,793	6,516	1,574	74.95	GenBank
<i>P. taeda</i>	83,285	45,656	24,427	84.15	Current assembly
PLAZA (24 species)	653,613	90,149	19,492	16.77	Van Bel <i>et al.</i> (2012)

phylogenetic relationships among the species. *P. palustris* is most closely related to loblolly pine and obtains mapping rates similar to the reclustered ESTs at 71.1% with 95% query coverage and 95% identity. *P. lambertiana* is most distant, and this is reflected in the minimal mapping success of the transcripts (Table 1).

The common lineage of the angiosperms and the gymnosperms split >300 MYA (Jiao *et al.* 2011), impeding searches for nucleic acid sequence homology between angiosperms and loblolly pine. However, we expect a subset of proteins to remain relatively conserved over multiple geological periods. The results of mapping and aligning three protein data sets to the loblolly pine v1.01 genome are shown in Table 2, where we determined the initial protein-to-scaffold mapping with blat and created a refined alignment with exonerate. The subset of the PLAZA data set used includes over half a million proteins from 24 non-gymnosperm plant species, 16.8% of which aligned to the loblolly pine genome. Aligning proteins from members of the genus *Picea* (last common ancestor 85 MYA) to the loblolly pine genome proved more fruitful. Seventy-five percent of >10,000 full-length Sitka spruce proteins [the majority predicted from high-quality full-length Sanger-sequenced complementary DNA data (Ralph *et al.* 2008)] aligned to the genome. Sixty-nine percent of 22,070 *P. abies* proteins from the Congenie project aligned to the loblolly pine genome. A total of 84% of the loblolly pine proteins gleaned from the transcriptome assembly aligned.

Fewer than 30% of each PLAZA species protein set aligned to the genome at our initial cutoff (query coverage $\geq 70\%$ and ESS ≥ 70). For 18 species in the PLAZA data set, as well as *A. trichopoda*, *P. sitchensis*, *P. abies*, and translated *P. taeda* transcriptome sequences, we further break down the protein-to-genome alignments that passed the initial cutoff into three categories: ESS ≥ 90 , $90 < \text{ESS} \leq 80$ and $70 \leq \text{ESS} < 80$ (Figure 1). In the ESS ≥ 90 category, 45.2% of Norway spruce proteins, 60.6% of Sitka spruce proteins, and 70.0% of loblolly pine proteins aligned to the genome (File S2). The differences between the two spruce protein sets may be partially attributed to the sequencing technologies employed to generate the original transcriptomes (Sanger vs. next-generation technologies).

Gene annotation

The MAKER-P annotation pipeline considered the transcript alignments in addition to *ab initio* models to predict potential coding regions. The initial predictions generated >90,000 gene models; ~44% were fragmented or otherwise

indicative of pseudogenes. Previous studies of pines have identified pseudogene members in large gene families (Wakasugi *et al.* 1994; Skinner and Timko 1998; Gernandt *et al.* 2001; Garcia-Gil 2008), and pseudogene content may be as much as five times that of functional coding regions (Kovach *et al.* 2010). Conservative filters were therefore necessary to deduce the actual gene space. The multi-exon gene model requirement is likely biased against intronless genes, but it reduces false positives associated with repeats and pseudogenes. Because ~20% of *Arabidopsis* and *O. sativa* genes are intronless (Jain *et al.* 2008), it is likely that our approach ignores as much as 20% of the gene space.

After applying multi-exon and protein domain filters, 50,172 gene models remained. These transcripts ranged from 120 bp to >12 kbp in length and represented >48 Mbp of the genome, with an average coding sequence length of 965 bp (Table S2). Since a recognizable protein domain was a requirement, the majority of gene models are functionally annotated (File S3). Functional annotations of the translated sequences revealed that 49,196 (98%) of the transcripts have homology to existing sequences in NCBI's plant protein and nr database. A slightly smaller number, 48,614 (97%), align to a functionally characterized gene product.

The full-length gene models that are well supported by aligned evidence and with an AED score < 0.20 total 15,653. These high-confidence transcripts cover >30 Mbp of the genome and have an average coding sequence length of 1295 bp with an average of three introns per gene (Table S2). Once again, 98% of these sequences are functionally annotated; ~23% of the high-quality alignments are to *V. vinifera*. Given the fragmentation of the genome and the lack of intronless genes reported, true estimates of gene number may be as high as 60,000, particularly given the 83,285 unique gene models generated from broad *P. taeda* RNA evidence (File S1). Previous estimates of gene number in conifers vary widely. The gene content of white spruce is estimated to be ~32,000 (Rigault *et al.* 2011). While comprehensive evaluation of maritime pine transcriptomic resources from EuroPineDB produced >52,000 UniGenes (Fernandez-Pozo *et al.* 2011).

Introns

Plant introns are typically shorter than those found in mammals (Shepard *et al.* 2009). The gene models derived from MAKER-P yielded maximum intron lengths >50 kbp, with several >100 kbp. A total of 147,425 introns were identified in the 50,172 transcripts. A requirement of <25% gap-region content was used to calculate values on

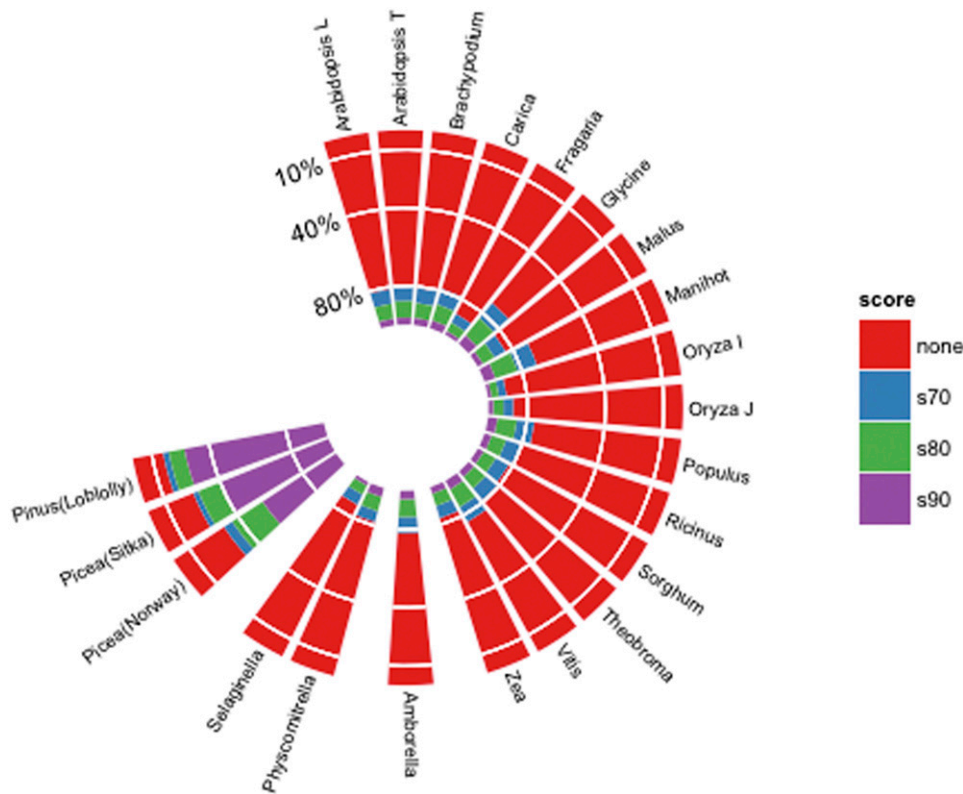


Figure 1 Orthologous proteins derived from PLAZA and mapped to the loblolly pine genome (1.01) at various similarity scores. Also included are proteins based on *Picea sitchensis* sequence from GenBank, *P. abies* proteins from the Congenie Genome project, and proteins from the Amborella Genome project. These data were generated by examining the proteins for which at least 70% of the protein was included in the local alignment. We then generated for each species, four categories based on the ESS: s90 ($100 < ESS < 90$), s80 ($90 < ESS < 80$), s70 ($80 < ESS < 70$) and none ($70 < ESS$).

144,425 introns (Table 3). The average length of these introns was >2.7 kbp, with a maximum length of 318 kbp. Compared with mapping the loblolly pine transcriptome against the genome, we identified only 3350 sequences (13%) with one or more introns. Among these sequences, 10,991 introns were present, an average of 3.28 per sequence. Their maximum reported lengths are ~ 150 kbp. The number of genes in the transcriptome containing introns is much lower than in other eukaryotes, although this is likely skewed by the requirement of full-length genes against a fragmented genome. For this reason, we focused the analysis on our high-confidence set of 15,653 MAKER-derived transcripts, which had 48,720 usable introns with an average length of 2.4 kbp. The longest reported intron in this set is 158 kbp. In total, 1610 introns were between 20 and 49 kbp in length, 143 between 50 and 99 kbp, and 18 >100 kbp in length (File S5). When compared with the protein sequences from 22 other plant species aligned to their genomes, only *A. trichopoda* and *Z. mays* reported similar maximum values (Figure 2A). The median and mean values for *P. taeda* introns are comparable to the other plant species (Figure 2B), although it is likely that our intron lengths are an underestimate due to the fragmentation of the assembly. Estimates from the recent genome assembly of *P. abies* reported intron lengths >20 kbp and a maximum length of 68 kbp (Nystedt *et al.* 2013). Long intron lengths have been estimated for pines for some time and are noted to contribute to their large genome sizes (Ahuja and Neale 2005).

Long intron sizes delay the production of protein products and increase the error rate in intron splicing in animals (Sun and Chasin 2000). In plants, increasing intron length is positively correlated with gene expression (Ren *et al.* 2006). In most eukaryotes, the first (primary) intron is usually the longest (Bradnam and Korf 2008) and is generally in the 5' UTR. The first intron in the CDS region is also generally longer than distal introns (Bradnam and Korf 2008). This is largely true for loblolly pine, as well.

IME refers to specific, well-conserved sequences in introns that enhance expression. IMEs in *Arabidopsis* and *O. sativa* introns near the transcription start site have greater signal than those more distal (Rose *et al.* 2008; Parra *et al.* 2011). We applied the word-based discriminator IMETER, designed to identify these signals in intronic sequences to the first introns in the CDS (as a comprehensive set of introns in the 5' UTR was not available). We identified 400 primary CDS introns between 20 and 49 kbp, 38 between 50 and 99 kbp, and 8 >100 kbp in length, all with a IMETER score > 10 , and several with a score >20 , which suggests strong enhancement of expression. Transcripts in this category include those annotated as transcription factors (WRKY), cysteine peptidases (cathepsins), small-molecule transporters (non-aspanins), transferases, and several that are less characterized (File S5).

Orthologous proteins

A comparison of the 47,207 clustered loblolly pine gene models to the 352,151 proteins curated from 13 plant

Table 3 Summary of intron statistics

Total sequences	Total no. of introns	Introns with minimal gap regions	Longest intron (bp)	Average intron length (bp)	No. of introns		No. of first introns		No. of first introns	
					20-49 kbp	50-99 kbp	20-49 kbp	50-99 kbp	>100 kbp	>100 kbp
50,172	147,425	144,579	318,524	2741	699	1840	343	108	63	18
15,653	49,720	48,720	158,878	2396	143	592	84	18	13	13

species resulted in 20,646 unique gene families (after filtering the domains that exclusively annotate as transposable elements) representing 361,433 (90.5%) sequences with an average of 17 genes per family (File S6). As with most *de novo* clustering methods, these predictions are likely to be an overrepresentation of family size and number, since clusters are formed for all non-orphan predictions by MCL (Bennetzen *et al.* 2004). The families range in size from 5229 members from 14 species to 2 members from one species.

P. taeda genes belong to 7053 gene families (File S7). Distribution of gene families among conifers (*P. abies*, *P. sitchensis*, and *P. taeda*); a basal angiosperm species, *A. trichopoda*; mosses (*S. moellendorffii* and *P. patens*); monocots (*O. sativa* and *Z. mays*); and dicots (*A. thaliana*, *G. max*, *P. trichocarpa*, *T. cacao*, *R. communis*, and *V. vinifera*) are shown in Figure 3. We identified 1554 conifer-specific gene families that contain at least one sequence in the three conifer species (*P. taeda*, *P. abies*, and *P. sitchensis*) (File S8), slightly higher than the 1021 reported by the *P. abies* genome project (Nystedt *et al.* 2013). Some of the largest families annotated include transcription factors (Myb, WRKY, and HLH), oxidoreductases (*i.e.*, cytochrome p450), disease resistance proteins (NB-ARC), and protein kinases. Among the conifer-specific families, 159 were unique to *P. taeda*, 32 of which had 5 or more members (Neale *et al.* 2014).

Sixty-six unique molecular function terms apply to the 8795 (42.45%) gene families annotated in 14 species. A total of 24 molecular function terms describe 241 of the 1554 conifer-specific gene families (Figure 4). When comparing the GO distribution of all 14 species against the conifer-specific families, four of the top five GO assignments are the same (protein binding, nucleic acid binding, ion binding, and hydrolase activity), with conifers having an additional large contribution from small-molecule binding (31 families). The 11,686 gene families with no contributions from conifers are described by 43 molecular function terms (Figure 4). The largest categories in this group include: hydrolase activity, nucleic acid binding, peroxidase activity, and lyase activity. Of the 7053 gene families with a *P. taeda* member, 6094 (86.4%) have at least one protein domain assignment and 5249 (74.42%) have molecular function GO term assignments. Since these families have members in most of the plant species analyzed, they are likely conserved across eukaryotes, thus reflecting their higher annotation rate. The largest categories containing *P. taeda* include protein binding, transferase activity, and nucleic acid binding, similar to recent findings for *P. glauca* and *Picea mariana* (Pavy *et al.* 2012). Examination of these large gene families across species also provides a preview of intron expansion, examples of which are seen in several gene families, including those involved in lipid metabolism, ATP binding, and hydrolase activity (Figure S3 and File S9).

Gene family gain-and-loss phylogenetics

Using DOLLOP, we constructed a single maximum parsimony tree from all TRIBE-MCL clusters containing five or

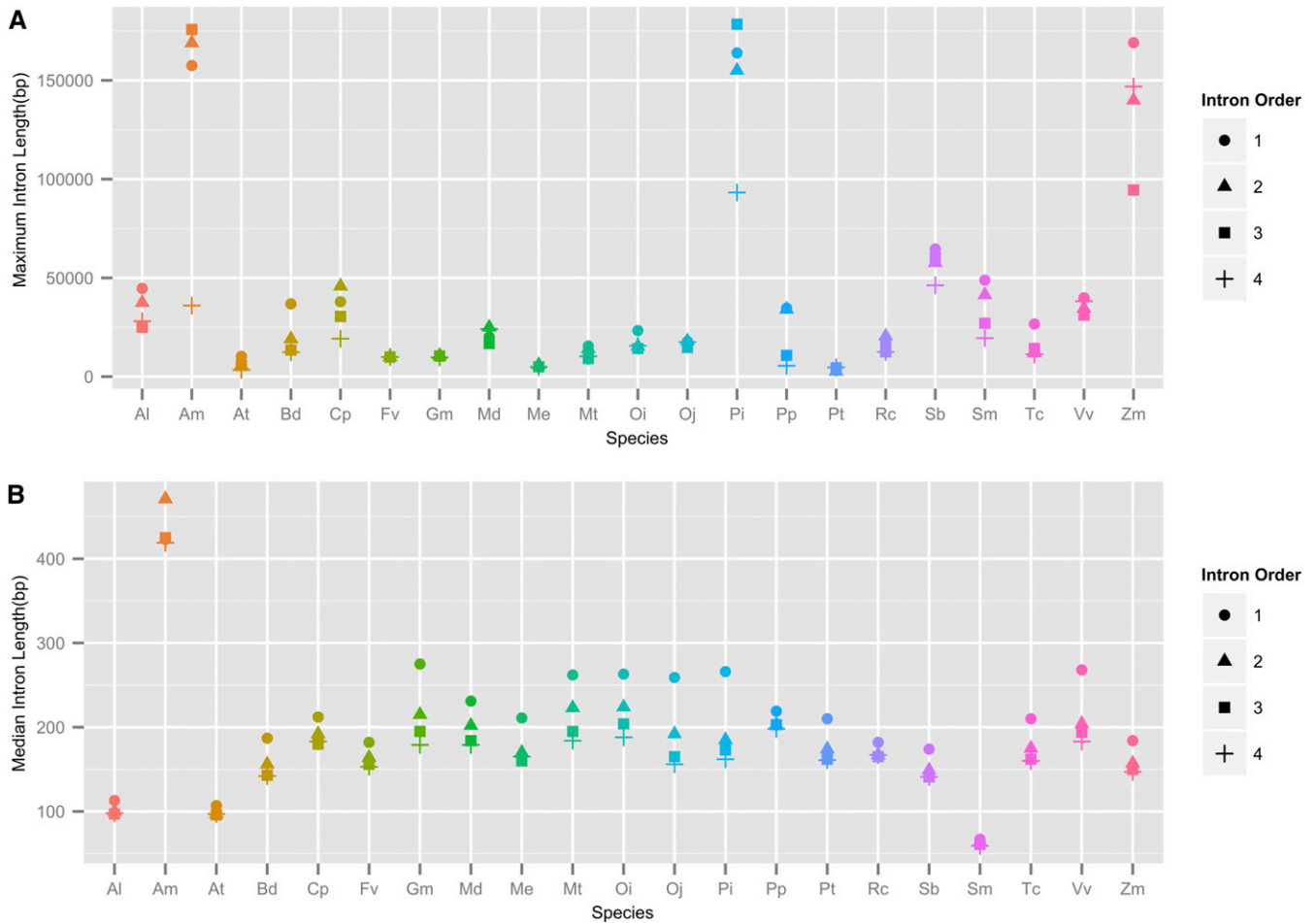


Figure 2 Intron lengths were compared for 23 species, which include 21 species curated by the PLAZA project, *A. trichopoda*, and *P. taeda*. (A) Comparison of maximum intron lengths for the first four intron positions in the CDS. Species codes are the following: Al (*Arabidopsis lyrata*), Am (*A. trichopoda*), At (*A. thaliana*), Bd (*B. distachyon*), Cp (*Carica papaya*), Fv (*Fragaria vesca*), Gm (*G. max*), Md (*Malus domestica*), Me (*Manihot esculenta*), Mt (*Medicago truncatula*), Oi (*O. sativa* ssp. *indica*), Oj (*O. sativa* ssp. *japonica*), Pi (*P. taeda*), Pp (*P. patens*), Pt (*P. trichocarpa*), Rc (*R. communis*), Sb (*S. bicolor*), Sm (*S. moellendorffii*), Tc (*T. cacao*), Vv (*V. vinifera*), and Zm (*Z. mays*).

more genes. This represented 10,877 gene families with a mean size of 31 genes and a total of 336,571 splice forms. Smaller gene families contributed noise to phylogenetic reconstruction that may be due to overclassification of the smaller family sizes. The final phylogenetic matrix contained 13 of the 14 species in the original MCL analysis with 8519 gene families of size ≥ 5 . *P. sitchensis* was removed from the analysis because of the partial sequence representation.

The resulting tree presents our best estimate of gene family evolution for the 13 focal species (Figure 5 and Table S3). Note that the gymnosperm–angiosperm split (Pavy *et al.* 2012; Nystedt *et al.* 2013) is reproduced and represents the longest internal edge in the reconstruction. The gymnosperm common ancestor is separated from the rest of the tree by a large number of gains and losses. Similarly, there are also many lineage-specific gains and losses from the ancestral gymnosperm to the two extant gymnosperms. Notably, there are more gene families not present in

gymnosperms than present in angiosperms. We observe this as many more losses than gains on the gymnosperm side of the gymnosperm–angiosperm split.

Tandem repeat identification

Tandem repeats are the chief component of telomeres and centromeres in higher order plants and other organisms. They are also ubiquitous across heterochromatic, pericentromeric, and subtelomeric regions (Richard *et al.* 2008; Navajas-Perez and Paterson 2009; Cavagnaro *et al.* 2010; Leitch and Leitch 2012). Tandem repeats affect variation through remodeling of the structures that they constitute; they modify epigenetic responses on heterochromatin and alter expression of genes through formation of secondary structures, such as those found in ribosomal DNA (Jeffreys *et al.* 1998; Richard *et al.* 2008; Gemayel *et al.* 2010). Present at ~ 5.6 million loci (Table S4), tandem repeats seem unusually abundant in loblolly pine. However, these loci

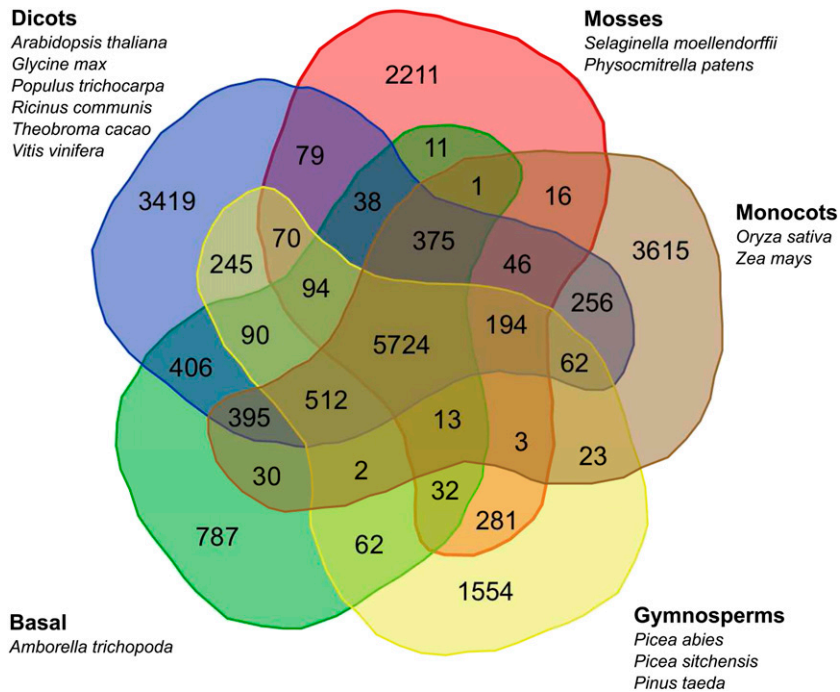


Figure 3 Results of the TRIBE-MCL analysis that distinguishes orthologous protein groups. The Venn diagram depicts a comparison of protein family counts of five plant classifications: gymnosperms (*P. abies*, *P. sitchensis*, and *P. taeda*), monocots (*O. sativa* and *Z. mays*), mosses (*P. patens* and *S. moellendorffii*), dicots (*A. thaliana*, *G. max*, *P. trichocarpa*, *R. communis*, *T. cacao*, and *V. vinifera*), and a basal angiosperm (*A. trichopoda*).

represent only ~2.86% of the genome, consistent with previous studies of loblolly pine (Hao *et al.* 2011; Magbanua *et al.* 2011; Wegrzyn *et al.* 2013) and spruce (2.71% in *P. glauca* and 2.40% in *P. abies*). Conifers are in the middle of the spectrum of tandem content among nine plant species evaluated, with estimates ranging from 1.53% in *C. sativus* to 4.29% in *A. trichopoda* (File S10).

Clustering at 70% identity cuts the number of unique tandem repeat loci to less than a quarter its original size (from 5,696,347 to 1,411,119 sequences), with the largest cluster having 4999 members. This suggests an abundance of highly diverged yet somewhat related repeats, as has been described by others (Kovach *et al.* 2010; Wegrzyn *et al.* 2013). When accounting for overlap with interspersed repeat content, loblolly pine's total tandem repeat coverage falls to 0.78% of the genome (Table S4 and Table S5). Only 33.8% of tandem content is found outside of interspersed repeats, including the LTR retrotransposons that make up the majority of conifer genomes (Nystedt *et al.* 2013; Wegrzyn *et al.* 2013). Further blurring the line between these two classes of repeats, retrotransposons have been shown to preferentially insert into pericentromeric heterochromatin of rice and SSR-rich regions of barley (Ramsay *et al.* 1999; Kumekawa *et al.* 2001)

Considering microsatellites, the *P. taeda* genome has the densest and highest coverage of microsatellites of any conifer to date (0.12%, 467,040 loci), although not by a wide margin (Figure 6A and Table S4). Heptanucleotides are statistically more represented in loblolly pine than in the other two conifers (chi square test, $\chi^2 = 7.367$, d.f. = 2, $P = 0.0251$) (Figure 6A). AT-rich di- and trinucleotides are common in dicot plants (Navajas-Perez and Paterson 2009; Cavagnaro *et al.* 2010). Among conifers, (AG/TC)*n*

is the most common dinucleotide in loblolly pine, while (AT/TA)*n* and (TG/AC)*n* are favored in *P. abies* and *P. glauca*, respectively. The most common trinucleotides are (AAG)*n* in loblolly pine, (ATT)*n* in *P. abies*, and (ATG)*n* in *P. glauca* (File S11). These findings support the notions that microsatellites are unstable and that microsatellite secondary structures are likely more conserved than their specific sequences (Jeffreys *et al.* 1998; Richard *et al.* 2008; Navajas-Perez and Paterson 2009; Gemayel *et al.* 2010; Melters *et al.* 2013). The CDS of loblolly pine is depleted in microsatellites compared to the full genome, but is denser in hexanucleotides and almost equal in trinucleotides (Figure 6B). Multiples of three (e.g., trinucleotides, hexanucleotides) are normally conserved in coding regions due to selection against frameshift mutations (Cavagnaro *et al.* 2010; Gemayel *et al.* 2010).

Minisatellites (period length of 9–100) are also slightly more represented in loblolly pine at ~4.7 million loci representing 1.76% of the genome, compared to 1.72% in *P. glauca* and 1.53% in *P. abies* (Table S4 and Table S5). Satellites (period length of 100+) follow a similar pattern (*P. taeda*, 0.98%; *P. abies*, 0.77%; and *P. glauca*, 0.96%) (Table S4). Minisatellites seem to make up the overwhelming majority of the tandem repeat content. Different assemblies and/or sequencing technologies alter the quantity of tandem repeat content by as much as twofold, as can be seen by comparing the microsatellite density between the loblolly BAC assemblies, fosmid assemblies, and the full genome (Figure 6B) (Wegrzyn *et al.* 2013). Tandem repeats are troublesome for the assembly of large genomes, which are often partial toward dinucleotide and 9- to 30-bp periods (Figure S4) (Navajas-Perez and Paterson 2009). In fact, the top three period sizes in coverage of the genome are 27, 21,

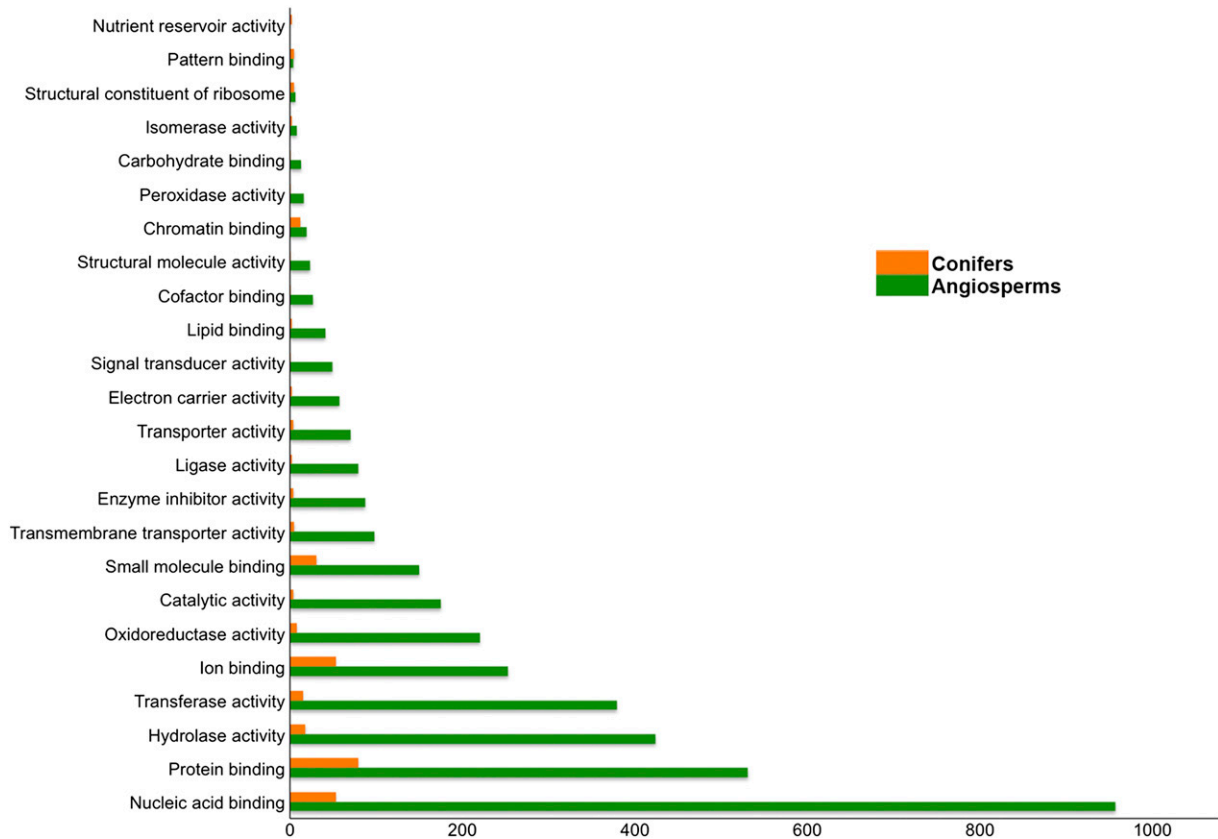


Figure 4 Gene Ontology distribution normalized for molecular function. The orthologous groups defined are exclusive to the angiosperms and conifers, respectively. The angiosperm set includes *A. trichopoda*, *A. thaliana*, *G. max*, *P. trichocarpa*, *P. patens*, *S. moellendorffii*, *R. communis*, *O. sativa*, *T. cacao*, *V. vinifera*, and *Z. mays*. The conifer set includes *P. abies*, *P. sitchensis*, and *P. taeda*.

and 20 bp, in that order. Minisatellites, especially those ~20 bp in length, contribute as much or more to the genome than microsatellites. This trend extends to other conifers (Table S5) as well as to angiosperms, including *C. sativus*, *A. thaliana*, and *P. trichocarpa*. In total, two consensus sequences and five monomer sequences, representing approximately five different species from PlantSat, share homology with loblolly pine satellites and minisatellites. The average coverage, however, is low (~45%), with the most abundant hits to centromeric sequences of *Pinus densiflora* and *Z. mays* (Table S6).

The telomeric sequence (TTTAGGG)*n*, first identified in *A. thaliana* (Richards and Ausubel 1988), has the most loci (23,926) of any tandem repeat motif and the most overall sequence coverage (at ~2.1 Mbp, or ~0.01% of the genome). Its instances range from 1.04 to 9.5 kbp in length and from 2 to 317 in numbers of copies of the monomer per locus. Variants like those from tomato [TT(T/A)AGGG]*n* (Ganal *et al.* 1991) and multimers with those variants were not assessed, so our estimate of the amount of telomeric sequence is likely low. These estimates include the true telomeres, which are on the longer side of the spectrum in length, and copies, along with ITRs. The longest locus is 15 kbp. Telomeres appear especially long in pine (e.g., 57 kbp in *Pinus longaeva*) (Flanary and Kletetschka 2005), and

in our assembly could be positively affected from the megagametophyte source, as has been shown in *Pinus sylvestris* (Aronen and Ryyanen 2012). These ITRs are remnants of chromosomal rearrangements that occupy large sections of gymnosperm chromosomes (Leitch and Leitch 2012). A potential centromere monomer, TGGAAACCCCAAA TTTTGGGCGCCGGG (27 bp), is moderately high in frequency across the scaffolds and represents the second highest fraction of the genome covered, with 5183 loci covering ~1.8 Mbp (~0.009% of the genome). Its period size is substantially shorter than the ~180-bp average from other plants (Melters *et al.* 2013). About 0.3% of the scaffolds contain this potential centromeric sequence, and these scaffolds average 779 bp in length. A close variant, TGGAAACCCCAAA TTTTGGGCGCCGCA (21 bp), also high in coverage and frequency, shares homology (*E*-value = 3e-9; 100% identity) with the repetitive sequence of an 881-bp probe (GenBank accession: AB051860) developed to hybridize to centromeric and pericentromeric regions of *P. densiflora* (Hizume *et al.* 2001). Perhaps this second variant forms a type of “library” that facilitates centromere evolution by forming a higher-order repeat structure with the first variant. Whether the centromere is evolving in pines cannot be deduced by assembling short reads, as they fail to accurately capture such structures (Melters *et al.*

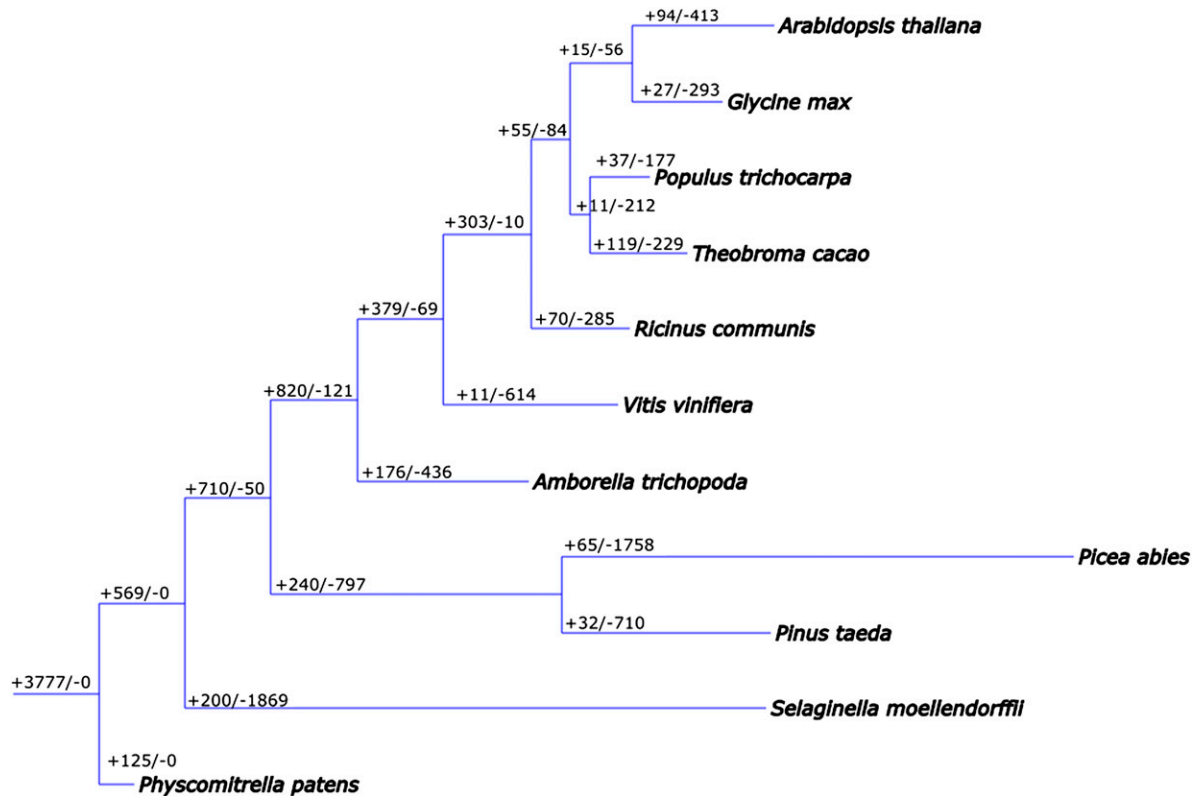


Figure 5 Parsimonious tree predicted by DOLLOP with protein families derived from the MCL analysis of size ≥ 5 . The gains and losses of 13 species (*A. thaliana*, *A. trichopoda*, *G. max*, *O. sativa*, *P. patens*, *P. trichocarpa*, *P. abies*, *P. taeda*, *R. communis*, *S. moellendorffii*, *T. cacao*, *V. vinifera*, and *Z. mays*) are indicated on tree nodes and branches.

2013). It is also important to note that the actual coverage of centromeric sequence is likely much higher than reported, as these two variants likely do not represent the entirety of the centromere. Homologs were not found in *P. abies* or *P. glauca*, consistent with it being specific to the subgenus *Pinus* (Hizume *et al.* 2001). The presence of the *Z. mays* centromeric sequence along with the *Pinus* centromeric sequence conceivably supports the hypothesis that although certain satellites are conserved across species, their localization is not (Leitch and Leitch 2012).

Homology-based repeat identification

RepeatMasker, with PIER as a repeat library, identified 14 Gbp (58.58%) of the genome as retroelements, 240 Mbp (1.04%) as DNA transposons, and 1.2 Gbp (5.06%) as derived from uncategorized repeats (Table 4). Considering only full-length repeats, there are 179,367 (5.61%) retroelements, 11,026 (0.13%) DNA transposons, and 56,024 (0.48%) uncategorized repeats. Most studies in angiosperms have found a surplus of class I compared to class II content (Kumar and Bennetzen 1999; Civián *et al.* 2011), and loblolly pine continues this trend with or without filtering for full-length elements. The ratio of uncategorized repeats to all repeats is $\sim 1:12$ for the genome, as seen in a previous BAC and fosmid study (Wegrzyn *et al.* 2013). Introns contained 34.52% LTRs, 54.28% retrotransposons, and 3.52%

DNA transposons (Figure S5 and File S12). First introns < 20 kbp have the lowest amount of repetitive content at 50.26%, while distal introns > 100 kbp have the highest amount at 73.75%. We expected higher repetitive content in longer introns, since intron expansion can be partially attributed to proliferation of repeats.

LTR retroelements make up 9.7 Gbp (41.68%) of the genome sequence, of which 2.5 Gbp (10.98%) are Gypsy elements and 2.1 Gbp (9.14%) are Copia elements (Table S7). Gypsy and Copia LTR superfamilies are found across the plant phylogeny and are often a significant portion of the repetitive content (Kejnovsky *et al.* 2012). Partial and full-length alignments have a 1.2:1 ratio of Gypsy to Copia elements; full-length elements show a slightly more skewed ratio of 1.3:1, lower than the previous estimate of 1.9:1 in *P. taeda* (Wegrzyn *et al.* 2013). Estimates in other conifers are, on average, 2:1 with the exception of *Abies sibirica*, which was reported 3.2:1 (Nystedt *et al.* 2013). Estimates in angiosperms represent a wide range: 1.8:1 in *V. vinifera*, 1:3 in *P. trichocarpa*, 2.8:1 in *A. thaliana*, and 1:1.2 in *C. sativus* (Wegrzyn *et al.* 2013). The large number of LTRs that cannot be sorted into superfamilies may be due to the presence of long autonomous retrotransposon derivatives (LARDs) and terminal-repeat retrotransposons in miniature (TRIMs) among LTR content. GCclassif was able to detect protein domains on many LTRs, but fewer than half were

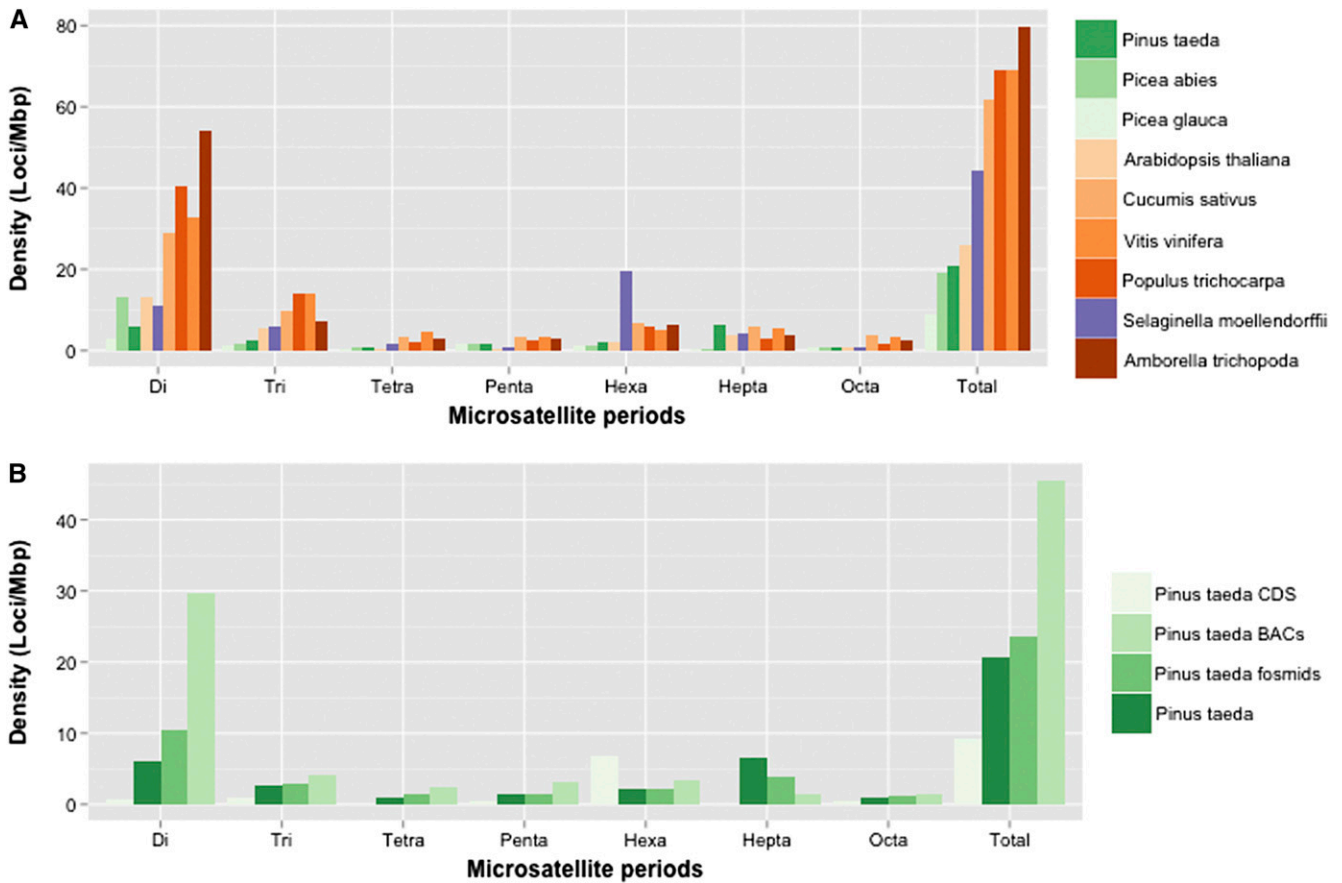


Figure 6 (A) Microsatellite density for three conifer genomes (green), one clubmoss genome (purple), and five angiosperm genomes (orange), (loci per megabase). (B) Microsatellite density (loci per megabase) of the coding sequence of the loblolly pine genome compared to the v1.0 genome and two other loblolly genomic data sets (BACs and fosmids).

classifiable based on the ordering of their domains. These LTRs may be nonfunctional, requiring actively transposing elements to supply the genes needed for proliferation, similar to LARDs and TRIMs (Witte *et al.* 2001; Kalendar *et al.* 2004).

Non-LTR retroelement content is usually found at lower frequencies in conifers (Friesen *et al.* 2001). Long interspersed nuclear elements (LINEs) cover 546 Mbp (2.35%) of the genome (Table S7), higher than the 0.71% previously recorded (Wegrzyn *et al.* 2013) and higher than in *P. sylvestris* (0.52%) and *P. abies* (0.96%) (Nystedt *et al.* 2013). Some angiosperms show comparable coverage of LINEs: 2.96% in *Brachypodium distachyon* (Jia *et al.* 2013), 2.82% in *Brassica rapa* (Wang *et al.* 2011), and 3.4% in *C. sativus* (Huang *et al.* 2009). LINEs are thought to have played roles in telomerase and gene evolution (Schmidt 1999). Short interspersed nuclear elements (SINEs) cover 268 kbp (0.001%), a miniscule portion of the genome, as previously reported (Wegrzyn *et al.* 2013). SINE content is similarly negligible in *P. sylvestris* and *P. abies* (Nystedt *et al.* 2013). Low ratios of non-LTR to LTR retroelements are also seen in most angiosperms (Jia *et al.* 2013).

DNA transposons make a negligible contribution to interspersed element content. Terminal inverted repeats (TIRs)

cover 186 Mbp (0.80%) of the genome, and helitrons cover 22 Mbp (0.10%) of the genome (Table S7). Repeats within introns are involved in exon shuffling (Bennetzen 2005) and epigenetic silencing (Liu *et al.* 2004). As expected, introns are richer in DNA transposons, at 3.52%, compared to 1.04% across the genome, and 93% of intronic DNA transposon content is composed of TIRs, compared to 77% across the genome (File S12). MITEs have been identified in loblolly pine BACs (Magbanua *et al.* 2011) and are preferentially located near genes in rice (Zhang and Hong 2000). However, the methodologies that we applied extracted only two MITE sequences across 25 Mb of intron sequence. Class II content is lower in most conifers, including *P. sylvestris*, *P. abies* (Nystedt *et al.* 2013), and *Taxus maireri* (Hao *et al.* 2011). This has generally been the case in angiosperms as well (Civáň *et al.* 2011), although there are exceptions (Feschotte and Pritham 2007).

De novo repeat identification

Considering a smaller subset of the entire genome sequence allowed us to compare *de novo* and similarity-based repeat annotation methods. In the 63 longest scaffolds, REPET discovered 15,837 putative repeats (Table S8), forming just

Table 4 Summary of interspersed repeats from homology-based identification

Class	Order	Superfamily	Full-length			All repeats		
			No. of elements	Length (bp)	% genome	No. of elements	Length (bp)	% genome
I	LTR	Gypsy	49,183	264,644,712	1.14	5,127,514	2,544,140,822	10.98
I	LTR	Copia	36,952	207,086,169	0.89	4,385,545	2,119,375,506	9.14
Total LTR	LTR		179,367	962,249,326	4.15	17,432,917	9,660,836,674	41.68
I	DIRS (Dictyostelium transposable element)		4,935	26,820,856	0.12	596,008	335,540,558	1.45
I	Penelope		4,966	13,456,930	0.06	422,276	188,350,501	0.81
I	LINE		15,353	53,411,263	0.23	906,403	545,648,705	2.35
I	SINE		137	68,023	0.00	670	182,264	0.00
Total RT (Retrotransposon)			262,028	1,299,761,701	5.61	25,166,637	13,577,984,814	58.58
II	TIR		7,932	20,499,522	0.09	420,769	185,871,618	0.80
II	Helitron		1,105	3,500,491	0.02	47,003	22,396,711	0.10
Total DNA			11,026	31,035,610	0.13	519,708	240,545,369	1.04
Uncategorized			56,024	110,604,852	0.48	3,164,894	1,172,394,606	5.06
Total interspersed			336,037	1,458,952,566	6.29	29,249,206	15,145,555,948	65.34
Tandem repeats				210,810,342	0.91		210,810,342	0.91
Total				1,669,762,908	7.20		15,356,366,290	66.25

under 7000 novel repeat families. Full-length repeats cover 64 Mbp (28.2%) of the sequence set, and full-length and partial *de novo* sequences combined account for 180 Mbp (79.3%). This ratio is markedly different from the fraction of full-length repeats in the full genome determined by similarity alone. Full-length sequences identified as previously classified, or which could be classified to the superfamily level, cover 11.3 Mbp (4.98%) of the bin 1 sequence according to *de novo* analysis. Of these, 6.6 Mbp overlap with RepeatMasker's similarity-based annotation of the bin. Full-length novel repeats cover 52.9 Mbp (23.26%) of the bin 1 sequence in the *de novo* analysis. Similarity analysis overlapped 7.4 Mbp of these repeats. As expected, REPET's *de novo* contribution was left largely undiscovered by RepeatMasker's similarity-based annotation method. In total, we see an overlap of 14 Mbp between our similarity and *de novo* annotation methods, and a total combined full-length repeat coverage of 69.7 Mbp.

Highly represented repeat families

High-coverage elements varied between similarity and *de novo* approaches. PtAppalachian, PtRLC_3, PtRLG_13, and PtRLX_3423 are shared among the top high-coverage elements (Table S9). Many of the high-coverage elements found are not highly represented in Wegrzyn *et al.* (2013), which used a similar approach. This corroborates a high rate of divergence and a high incidence of incomplete retrotransposon content. PtRLG_Conagree, the highest-coverage repeat, annotated 0.75% of the genome, covering 174 Mbp (Table S9). TPE1, a previously characterized Copia element, has the second-highest coverage with 114 Mbp (0.49%). Other highly represented elements include PtRLG_Ouachita, PtRLG_Talladega, PtRLX_Piedmont, PtRLG_Appalachian, and PtRLG_Angelina, which were previously characterized as part of a set of high coverage *de novo* repeat families

(Wegrzyn *et al.* 2013). PtIFG7, a Gypsy element, covers 90 Mbp (0.39%) (Table S9). As previously noted in Kovach *et al.* (2010), no single family dominates the repetitive content, with the highest-coverage element, PtRLG_Conagree, accounting for <1% of the genome (Table S9). Gymny, thought to occupy 135 Mb in the genome with full-length elements (Morse *et al.* 2009), comprises only 3.3 Mbp; IFG7, thought to occupy up to 5.8% of the genome (Magbanua *et al.* 2011), occupies only 0.39% of the genome. The top 100 highest-coverage elements account for <20% of the genome (Figure 7A). Among high-coverage intronic repeats, PtRLX_106 and PtRLG_Appalachian were identified in both bin 1 and in the genome. Side-by-side comparisons of high-copy and high-coverage families show a much lower contribution per family in the introns, compared to the genome (Table S8 and Table S9).

The highly divergent nature of most of the transposable elements seems to conflict with the uniformity seen in those that are highly represented. A total of 4397 full-length PtAppalachian sequences and 2835 PtRLG_13 sequences were >80% similar to their reference sequences, and 1559 and 237 sequences align at >90% identity and 90% coverage, respectively. These alignments suggest that many of the highly represented elements may be actively transposing, despite the diverged nature of many transposable element families.

Repetitive content summary

In total, 15.3 Gbp (65.34%) of genomic sequence was labeled as interspersed content via homology (Table 4), while *de novo* estimates place total interspersed content at 79.3% (similarity and *de novo* combined in bin 1 yield 81.81%). This is consistent with the *de novo* figures reported by Wegrzyn *et al.* (2013) at 86% and by Kovach *et al.* (2010) at 80%, but is higher than in *P. sylvestris* at 52% (Nystedt

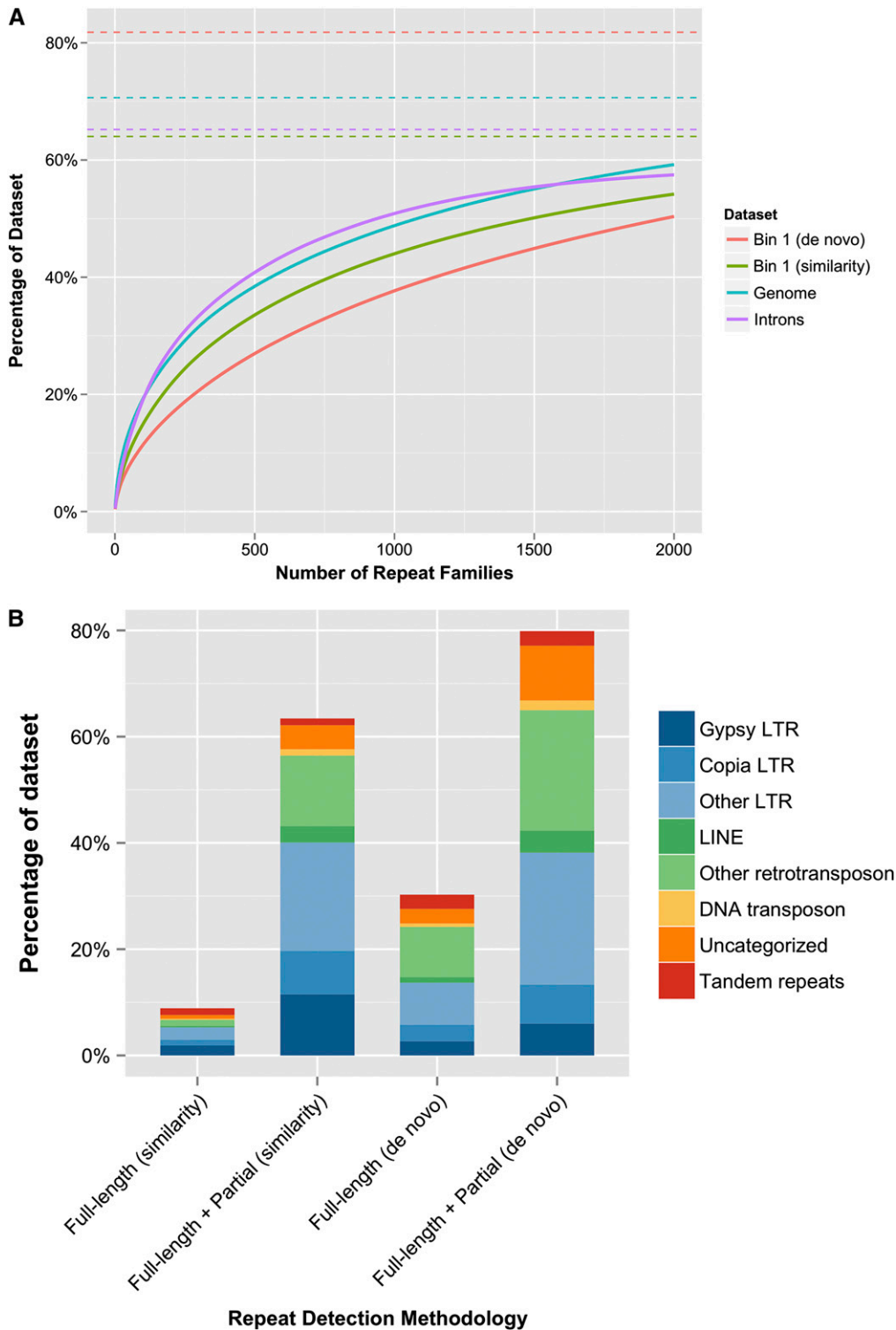


Figure 7 (A) Repeat family coverage. Repeat families on the x-axis are ordered by coverage in descending order. Solid lines illustrate cumulative coverage as more families are considered. Dashed lines represent the total repetitive content for that data set. (B) Comparison of bin 1 repetitive content for both partial and full-length annotations. “Full-length + Partial” refers to all full-length and partial hits, and “Percentage of dataset” is a function of the total length annotated by each classification.

et al. 2013), *P. glauca* at 40–60% (Hamberger *et al.* 2009; Liu *et al.* 2011; Nystedt *et al.* 2013), *P. abies* at 70% (Nystedt *et al.* 2013), *Sorghum bicolor* at 63% (Paterson *et al.* 2009), and *Secale cereale* at 69.3% (Bartos *et al.* 2008). Masking all repeat content results in the complete masking of 9 million scaffolds, covering 3.2 Gbp of sequence. Full-length elements cover only 7.20% of the genome, much lower than

the 25.98% previously estimated in BAC and fosmid sequences (Wegrzyn *et al.* 2013).

Strict filters, as described in Wegrzyn *et al.* (2013), ensured the quality of the discovered *de novo* sequence, and the repeat library used in similarity analysis, PIER, was derived from *de novo* content in loblolly pine BACs and fosmids discovered with the same methodology. It is surprising, then,

that similarity analysis characterized 66% of the genome sequence as repetitive, while *de novo* analysis characterized 79.3% of bin 1 as repetitive, suggesting a plethora of further high-quality novel repeat content. One possibility is that the large number of new repeat sequences discovered *de novo* may be due to TRIMs and LARDs, the latter for which transposition events yield high sequence variability even among mRNA transcripts (Kalendar *et al.* 2004). LARDs are a subset of LTRs and class I retrotransposons and could easily inflate the figures for these two categories while reducing the number and coverage of known superfamilies. High variability in retrotransposition is common among angiosperms and gymnosperms—not surprising, as reverse transcription is known to be highly error-prone (Gabriel *et al.* 1996). A single burst of retrotransposition can potentially result in hundreds of repeats, all independently diverging (El Baidouri and Panaud 2013). One such event may have occurred long ago in loblolly pine, resulting in the many ancient, diverged, single-copy repeat families being identified. Finally, we note that repetitive elements are a common obstacle in genome assembly; scaffold resolution may have decreased the amount of detectable repetitive content as repeats located on a terminal end of a sequence may be collapsed upon assembly. With this level of repetitive content, the likelihood of terminal repeat collapse is markedly higher than in smaller and less repetitive genomes.

Conclusion

We have presented a comprehensive annotation of the largest genome and first pine. The size of the genome and the absence of well-characterized sequence for close relatives presented significant challenges for annotation. The inclusion of a comprehensive transcriptome resource generated from deep sequencing of loblolly pine tissue types not previously examined was key to identifying the gene space. This resource, along with other conifer resources, provided a platform to train gene-prediction algorithms. The larger gene space enabled us to better quantify and examine the those that are unique to conifers, and potentially to gymnosperms. The long scaffolds available in our sequence assembly facilitated the identification of long introns, providing a resource to study their role in gene regulation and their relationship to the high levels of repetitive content in the genome. To characterize sequence repeats, we applied a combined similarity and *de novo* approach to improve upon our existing repeat library and to better define the components of the largest portion of the genome. This annotation will not only be the foundation for future studies within the conifer community, but also a resource for a much larger audience interested in comparative genomics and the unique evolutionary role of gymnosperms.

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Note added in proof: See Zimin *et al.* 2014 (pp. 875–890) in this issue for a related work.

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Supporting Information

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Unique Features of the Loblolly Pine (*Pinus taeda* L.) Megagenome Revealed Through Sequence Annotation

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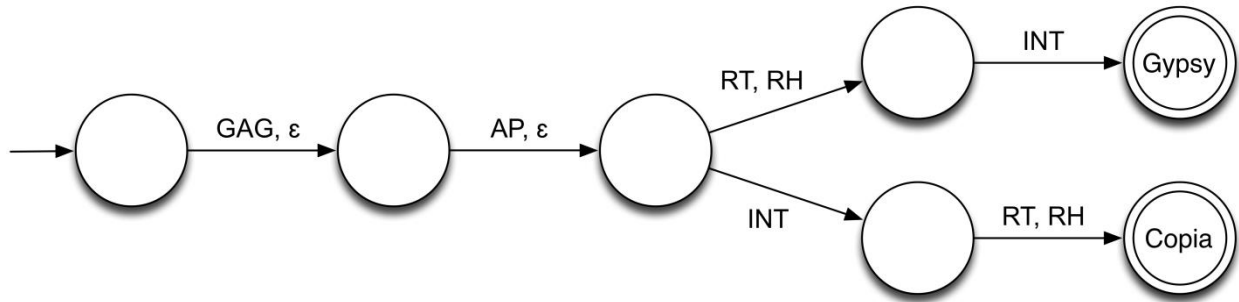


Figure S1 Flowchart for GCclassif. Circles represent states in GCclassif in which the arrows containing the proper input represent transitions to the next state. AP is aspartic protease, RT is reverse transcriptase, RH is RNase H, and INT is integrase. Epsilons allow states to be skipped.

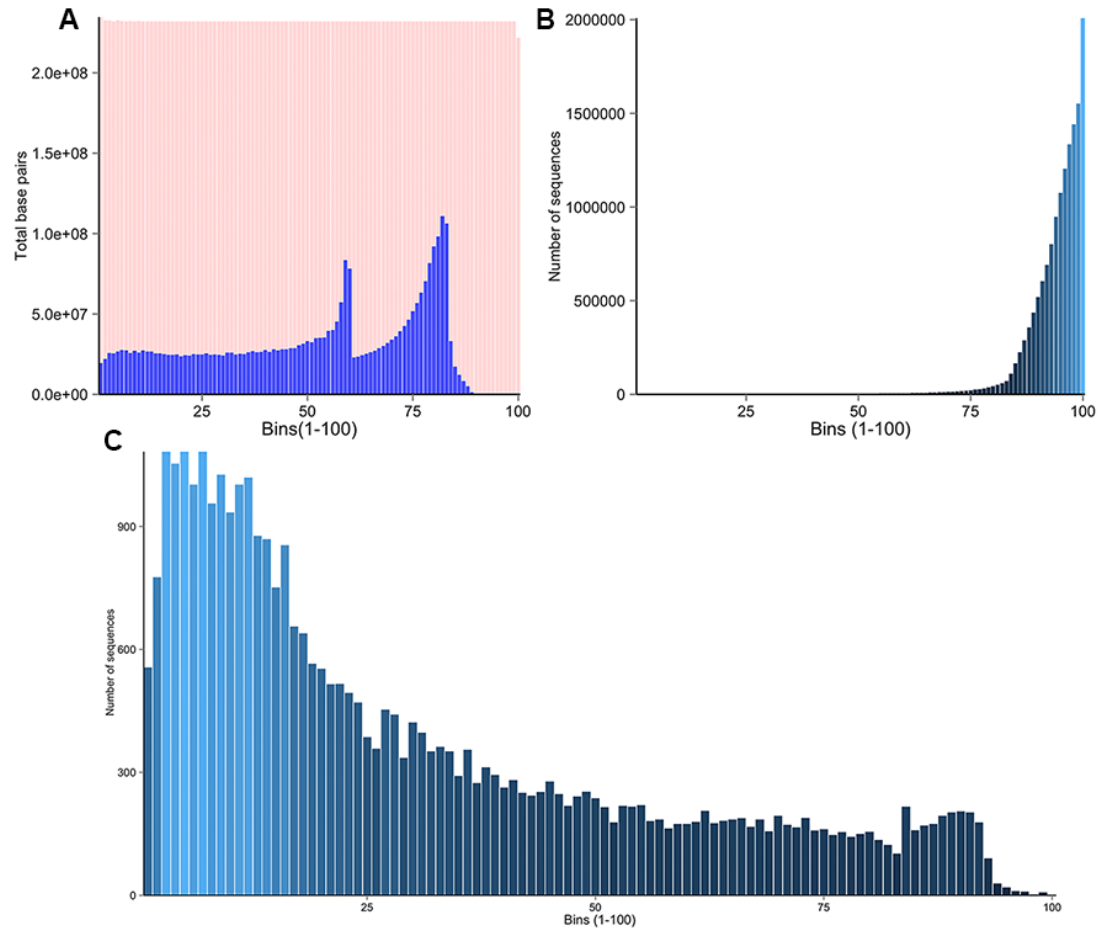


Figure S2 The genome sorted by descending scaffold size and placed in 100 bins. (A) The total number of bases in each bin is in pink while the proportion of gap regions is shown in purple. (B) Number of scaffolds per bin. (C) The *de-novo* transcriptome data aligned to the genome where each bar indicates the number of transcripts that were aligned to sequence in each bin and where the transcript was required to align to a unique location in the genome with 98% query coverage and 98% identity.

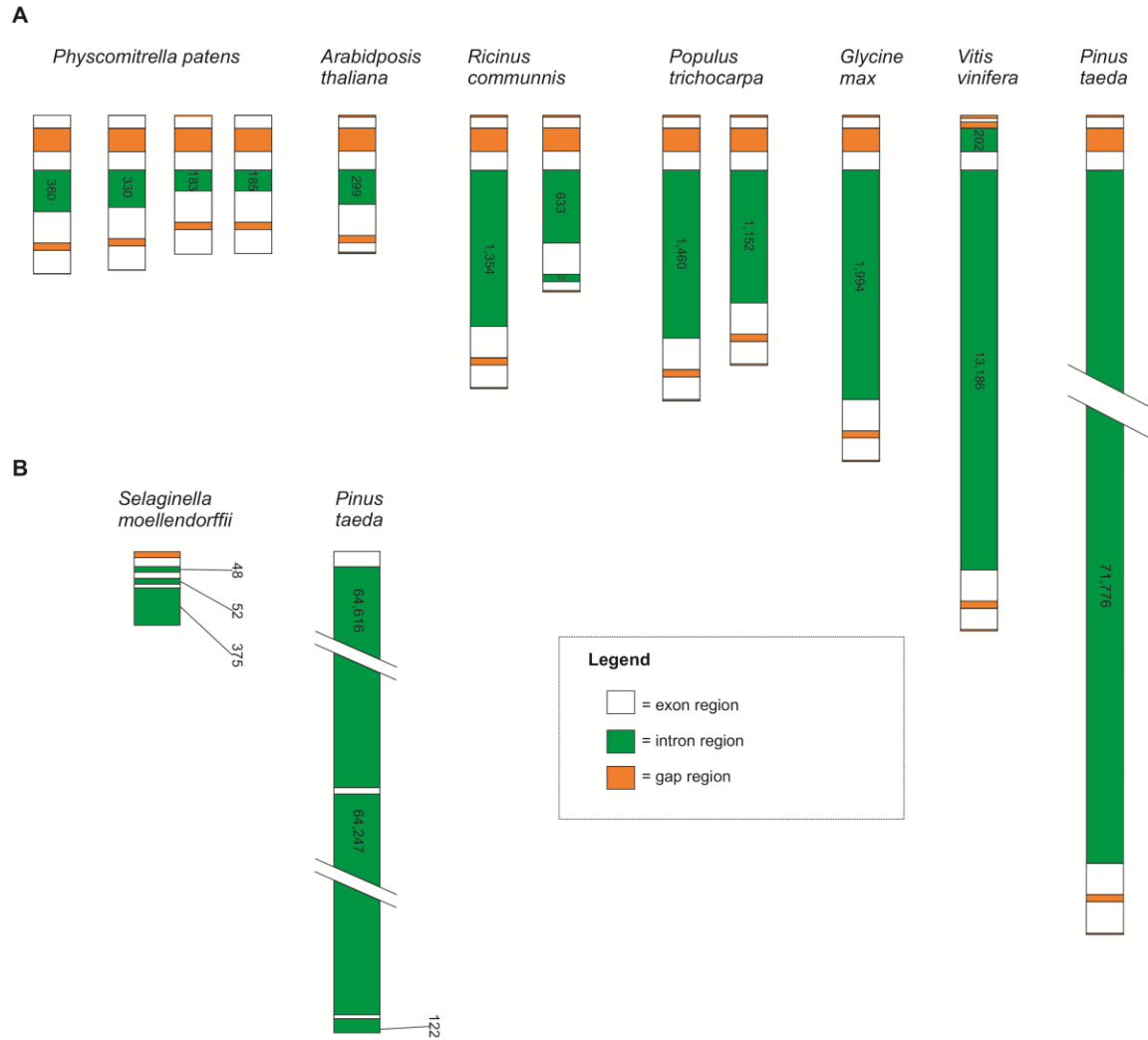


Figure S3 Multiple Sequence Alignment between genes predicted to be within a gene family where the units are measured in base pairs. Introns (green), coding regions (white), and alignment gaps (orange) are depicted for both families. (A) Cernaidase: *Physcomitrella patens*, *Arabidopsis thaliana*, *Ricinus communis*, *Populus trichocarpa*, *Glycine max*, *Vitis vinifera*, and *Pinus taeda* (B) Hydrolase: *Selaginella moellendorffii* and *Pinus taeda*

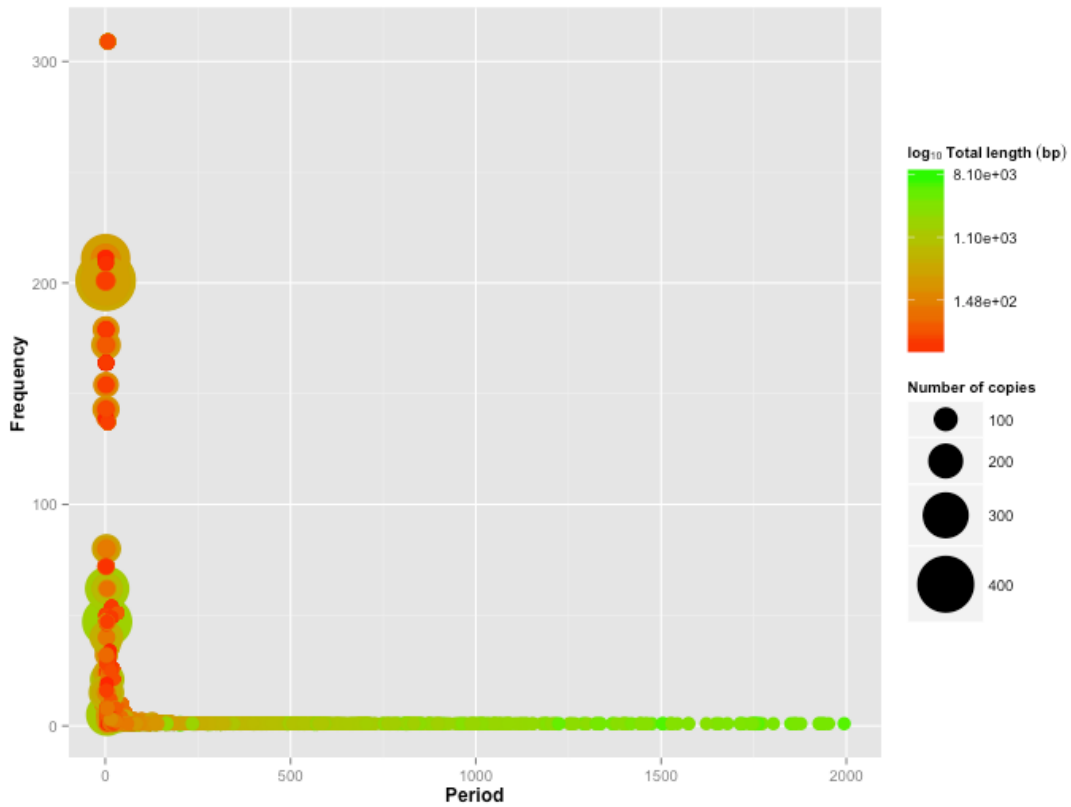


Figure S4 Tandem repeat content of the genomic sequence in bin 1 of the genome. Each locus (tandem array) is plotted by its period (x-axis) and the frequency of that particular period (y-axis). The size of each locus corresponds to the number of copies of the tandem repeat. The color corresponds to the total length (in bp) of that locus, with red being the largest and green being the smallest.

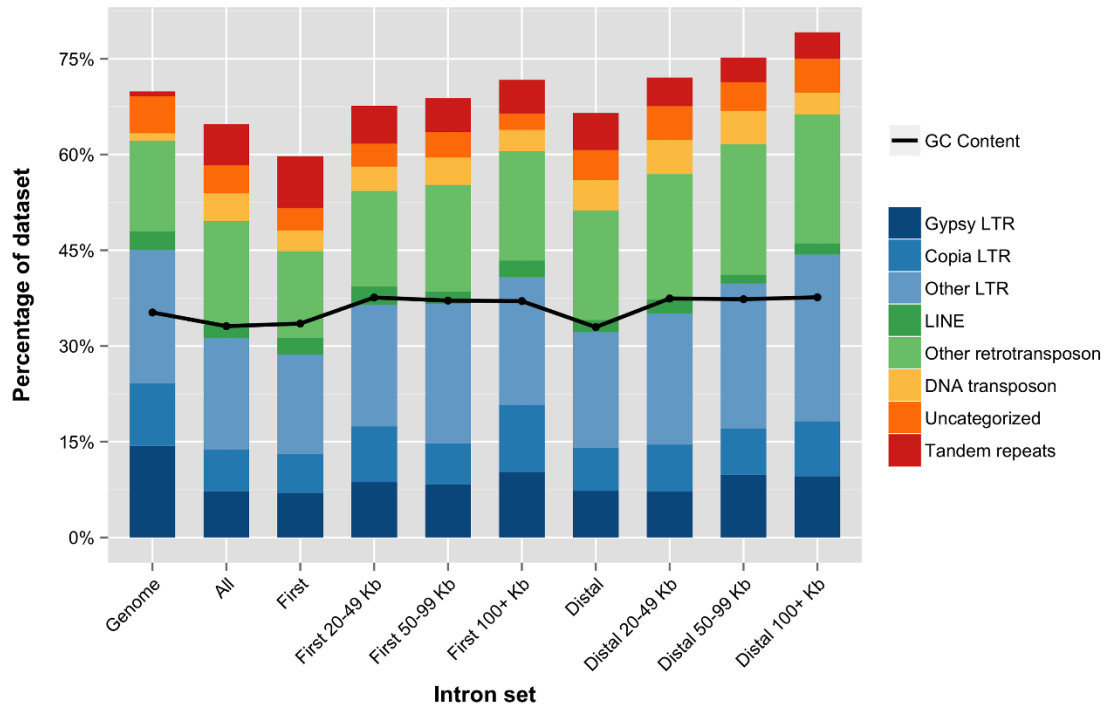


Figure S5 Intronic repeats. Introns were separated into primary and distal categories, in addition to length categories (20-49 Kbp, 50-99 Kbp, and greater than 100 Kbp). The intronic sequence was analyzed via homology-based methods against the PIER database.

Table S1 Orthologous proteins from the PLAZA project aligned to the *Pinus taeda* versions 1.01 genome

Species	Protein count	Query protein count	Aligned uniquely	Percent aligned uniquely	Aligned non-uniquely
<i>Arabidopsis lyrata</i>	32,657	30,892	4720	15.3	1029
<i>Arabidopsis thaliana</i>	27,407	27,160	4482	16.5	1018
<i>Brachypodium distachyon</i>	26,632	26,200	4099	15.6	880
<i>Carica papaya</i>	26,954	23,199	4098	17.7	793
<i>Chlamydomonas reinhardtii</i>	16,784	13,001	384	3.0	107
<i>Fragaria vesca</i>	34,748	34,702	3412	9.8	752
<i>Glycine max</i>	46,324	37,388	8336	22.3	1788
<i>Malus domestica</i>	63,515	46,856	6257	13.4	1356
<i>Manihot esculenta</i>	30,748	25,474	5937	23.3	1231
<i>Medicago truncatula</i>	45,197	44,699	3803	8.5	888
<i>Micromonas</i> sp. RCC299	9,985	8,934	389	4.4	101
<i>Oryza sativa</i> ssp. <i>indica</i>	48,788	48,629	3787	7.8	846
<i>Oryza sativa</i> ssp. <i>japonica</i>	41,363	41,186	4300	10.4	915
<i>Ostreococcus lucimarinus</i>	7,769	6,322	382	6.0	105
<i>Ostreococcus tauri</i>	7,994	6,762	231	3.4	64
<i>Physcomitrella patens</i>	28,090	22,807	3302	14.5	812
<i>Populus trichocarpa</i>	40,141	36,393	7185	19.7	1530
<i>Ricinus communis</i>	31,009	28,113	4475	15.9	910
<i>Selaginella moellendorffii</i>	18,384	13,661	1436	10.5	329
<i>Sorghum bicolor</i>	33,117	26,513	3880	14.6	842
<i>Theobroma cacao</i>	28,858	28,136	4457	15.8	877
<i>Vitis vinifera</i>	26,238	25,663	5096	19.9	1069
<i>Volvox carteri</i>	15,520	13,118	478	3.6	147
<i>Zea mays</i>	39,172	37,805	5223	13.8	1103
PLAZA proteins (24 species)	727,394	653,613	90,149	12.7	19,492

For 24 species in the PLAZA data set, a subset of proteins that passed additional quality checks (denoted ‘Query proteins’ comprised the set of proteins we attempted to align to the loblolly pine genome by first mapping with blat and then a performing a final alignment exonerate. The minimum query coverage is 70% and the minimum similarity is an exonerate-calculated similarity score of 70. Proteins that aligned once or more than once at this criteria were counted as ‘Aligned uniquely’ or ‘Aligned non-uniquely’ respectively.

Table S2 Summary of MAKER Gene Annotations

Total sequence	Average length (bp) (CDS)	Median length (bp) (CDS)	Shortest Sequence (bp)	Longest sequence (bp)	Total sequence (bp)	GC (%)	Total introns	Avg. introns/gene
50,172	965	727	120	12,657	48,440,991	42.56	147,425	2
15,653	1,290	1,067	150	12,657	20,190,331	43.56	49,720	3

Table S3 Gain/Loss Protein Matrix Table

	Arabidopsis thaliana	Amborella trichopoda	Glycine max	Picea abies	Picea sitchensis	Pinus taeda	Physcomitrella patens	Populus trichocarpa	Ricinus communis	Selaginella moellendorffii	Theobroma cacao	Vitis vinifera
Arabidopsis thaliana	0	314	-53	3003	3991	1988	1857	-339	-334	3084	-369	347
Amborella trichopoda	-314	0	-367	2689	3677	1674	1543	-653	-648	2770	-683	33
Glycine max	53	367	0	3056	4044	2041	1910	-286	-281	3137	-316	400
Picea abies	-3003	-2689	-3056	0	988	-1015	-1146	-3342	-3337	81	-3372	-2656
Picea sitchensis	-3991	-3677	-4044	-988	0	-2003	-2134	-4330	-4325	-907	-4360	-3644
Pinus taeda	-1988	-1674	-2041	1015	2003	0	-131	-2327	-2322	1096	-2357	-1641
Physcomitrella patens	-1857	-1543	-1910	1146	2134	131	0	-2196	-2191	1227	-2226	-1510
Populus trichocarpa	339	653	286	3342	4330	2327	2196	0	5	3423	-30	686
Ricinus communis	334	648	281	3337	4325	2322	2191	-5	0	3418	-35	681
Selaginella moellendorffii	-3084	-2770	-3137	-81	907	-1096	-1227	-3423	-3418	0	-3453	-2737
Theobroma cacao	369	683	316	3372	4360	2357	2226	30	35	3453	0	716
Vitis vinifera	-347	-33	-400	2656	3644	1641	1510	-686	-681	2737	-716	0

Table S4 Summary of tandem repeat content in *Pinus taeda*

Microsatellites (2-8 bp)	Total number of loci	Total number of copies	Variants	Total length (bp)	% of sequence sets
Dinucleotide	136469	3142395.5	10	6107780	0.03%
Trinucleotide	59777	1085375.9	61	3210065	0.01%
Tetranucleotide	22748	296377.3	205	1160245	0.01%
Pentanucleotide	32605	789203	609	3901223	0.02%
Hexanucleotide	47314	495142.9	2159	2956985	0.01%
Heptanucleotide	145992	1294995.8	2448	8931410	0.04%
Octanucleotide	22135	135945.3	3903	1066823	0.00%
Total	467040	7239435.7	9395	27334531	0.12%
Minisatellites (9-100 bp)					
9-30	3205612	10632848.2	1446648	205169621	0.91%
31-50	853241	2256180.7	635066	84379493	0.37%
51-70	377512	1023726.7	338958	59129899	0.26%
71-100	247280	570682.8	235021	47737215	0.21%
Total	4683645	14483438.4	2655693	396416228	1.76%
Satellites (>100 bp)					
101-200	351264	780770.7	345179	106605726	0.47%
201-300	79942	171933.9	79699	42421186	0.19%
301-400	28494	61647.7	28406	20617800	0.09%
>400	35428	78714.6	35329	51362778	0.23%
Total	495128	1093066.9	488613	221007490	0.98%
Grand Total	5645813	22815941	3153701	644758249	2.86%

Table S5 A comparison of the most common tandem period in *Picea abies*, *Picea glauca* and *Pinus taeda*.

	<i>Pinus taeda</i> v1.01			<i>Picea glauca</i> v1.0			<i>Picea abies</i> v1.0		
	Micro ^a	Mini ^b	Sat ^c	Micro	Mini	Sat	Micro	Mini	Sat
Most frequent period size	7	21	123	2	21	102	2	50	101
Cumulative length (Mbp)	8.93	20.09	8.66	2.26	8.70	4.89	10.38	29.00	5.25
Num. of loci	145,992	361,356	27,422	62,592	179,716	23,256	255,380	285,648	24,895
Most frequent period (%)	0.04%	0.09%	0.04%	0.01%	0.04%	0.02%	0.05%	0.15%	0.03%
Total cumulative length (Mbp)	27.33	396.42	221.01	7.48	357.90	198.83	18.63	299.25	151.81
Total %	0.12%	1.76%	0.98%	0.04%	1.72%	0.96%	0.10%	1.53%	0.77%
Total overall content		2.86%			2.71%			2.40%	

^aMicrosatellites; ^bMinisatellites; ^cSatellites

Table S6 Summary of hits to the PlantSat database

	Family	Genbank Accessions	Number of hits	Localization	Best hit Identity (%)	Best hit length (bp)	Best hit coverage (%)	Best hit e-value
Consensus Sequences	Citrus_limon_90	M38369	3	B/+/-/-/-/-	98.2	56	62.2	3.1e-20
	Zea_mays_MBSc216	AF139910	2	N/A	89.5	38	17.6	7.5e-05
Monomer Sequences	Pinus_PCSR	AB051860	67	B/+/-/-/-/-	100.0	27	100.0	2.6e-06
	Zea_mays_MBSc216	AF139910	2	B/+/-/-/-/-	89.5	38	17.6	7.50E-05
	Cucurbita_160	X82944	5	N/A	100	23	13.6	0.0027
	Citrus_limon_90	M38369	3	B/+/-/-/-/-	98.2	56	62.2	3.10E-20
	Lens_Lc30	AJ401232	1	B/-/+/-/+/-	96	25	44.64	0.0032

Table S7 Repeat summary

Class	Full-length		Genome			Bin 1 (similarity)			Bin 1 (de novo)		
	Order	Superfamily	No. hits	Length (bp)	% Genome	No. hits	Length (bp)	% Bin 1	No. hits	Length (bp)	% Bin 1
I	LTR	Gypsy	49,183	264,644,712	1.14%	754	4,458,891	1.90%	999	6,037,536	2.66%
I	LTR	Copia	36,952	207,086,169	0.89%	746	4,677,850	1.99%	1187	7,052,312	3.10%
I	LTR	Total LTR	179,367	962,249,326	4.15%	4,100	25,437,955	10.84%	5,231	31,092,722	13.68%
I	DIRS		4,935	26,820,856	0.12%	196	1,429,987	0.61%	440	2,914,879	1.28%
I	Penelope		4,966	13,456,930	0.06%	208	1,065,465	0.45%	325	1,508,976	0.66%
I	LINE		15,353	53,411,263	0.23%	479	2,198,208	0.94%	544	2,467,615	1.09%
I	SINE		137	68,023	0.00%	1	603	0.00%	3	1,981	0.00%
I	Total RT		262,028	1,299,761,701	5.61%	8,244	44,210,140	18.84%	10,691	55,053,548	24.22%
II	TIR		7,932	20,499,522	0.09%	167	695,097	0.30%	262	975,835	0.43%
II	Helitron		1,105	3,500,491	0.02%	57	224,957	0.10%	61	238,921	0.11%
II	Total DNA		11,026	31,035,610	0.13%	248	1,009,025	0.43%	530	1,428,855	0.63%
Uncategorized			56,024	110,604,852	0.48%	2,088	5,194,122	2.21%	2,978	6,399,249	2.81%
Total interspersed			336,037	1,458,952,566	6.29%	10,894	51,324,564	21.87%	14,822	64,201,063	28.24%
Simple repeats				210,810,342	0.91%		2,332,498	0.99%		6,183,302	2.72%
Total				1,669,762,908	7.20%		53,657,062	22.87%		70,384,365	30.96%

Class	Full and Partial		Genome			Bin 1 (similarity)			Bin 1 (de novo)		
	Order	Superfamily	No. hits	Length (bp)	% Genome	No. hits	Length (bp)	% Bin 1	No. hits	Length (bp)	% Bin 1
I	LTR	Gypsy	5,127,514	2,544,140,822	10.98%	16,784	18,521,637	7.89%	8,672	13,666,373	6.01%
I	LTR	Copia	4,385,545	2,119,375,506	9.14%	17,032	17,772,754	7.57%	11,093	16,667,678	7.33%
I	LTR	Total LTR	17,432,917	9,660,836,674	41.68%	81,177	89,930,243	38.33%	69,115	86,762,081	38.16%
I	DIRS		596,008	335,540,558	1.45%	3,464	4,176,321	1.78%	4,950	6,703,253	2.95%
I	Penelope		422,276	188,350,501	0.81%	3,277	2,898,029	1.24%	5,505	4,750,750	2.09%
I	LINE		906,403	545,648,705	2.35%	5,604	7,182,211	3.06%	8,489	9,442,087	4.15%
I	SINE		670	182,264	0.00%	1	603	0.00%	19	10,326	0.00%
I	Total RT		25,166,637	13,577,984,814	58.58%	125,116	138,159,710	58.88%	134,429	147,803,493	65.02%
II	TIR		420,769	185,871,618	0.80%	2,928	2,348,313	1.00%	3,464	2,867,146	1.26%
II	Helitron		47,003	22,396,711	0.10%	625	638,648	0.27%	909	820,607	0.36%
II	Total DNA		519,708	240,545,369	1.04%	3,747	3,214,509	1.37%	4,793	4,029,664	1.77%

Uncategorized	3,164,894	1,172,394,606	5.06%	13,489	12,946,531	5.52%	29,904	23,547,945	10.36%
Total interspersed	29,249,206	15,145,555,948	65.34%	144,640	156,597,131	66.74%	175,093	179,808,257	79.09%
Simple repeats		210,810,342	0.91%		2,332,498	0.99%		6,183,302	2.72%
Total		15,356,366,290	66.25%		158,929,629	67.73%		185,991,559	81.81%

Table S8 High Copy Full-Length Elements

Bin 1 (Similarity)		Bin 1 (De novo)		Full Genome		Introns	
Family	No. full-length	Family	No. full-length	Family	No. full-length	Family	No. full-length
PtRLG_13	49	PtRXX_107	174	PtAppalachian	4,347	PtRLX_2461	1925
PtAppalachian	41	PtRLC_3	70	PtRLG_13	2,835	PtRXX_4292	1506
PtRLX_3765	29	PtRLX_3765	65	PtRLX_1912	2,638	PtRLX_3423	1452
PtRLX_1912	29	PtAppalachian	62	PtRLC_283	1,882	PtRLX_3902	1249
PtRLC_782	26	IFG7_I	57	PtRLX_291	1,810	PtRLC_601	1247
PtRLX_3423	24	PtRXX_2933	55	PtRLX_11	1,630	PtRLX_2504	928
PtRXX_2933	24	PtRLX_3423	43	PtRLC_334	1,535	PtRLX_3298	910
PtRLX_291	23	PtPineywoods	39	PtRLC_782	1,407	PtRLX_106	891
PtPineywoods	19	PtRLG_13	38	PtPineywoods	1,386	PtRLX_2798	847
PtRLX_3902	19	PtRLX_2461	33	PtRLG_432	1,361	PtRLX_140	844
PtRLX_2461	18	PtNoCat_2490	31	PtRLX_106	1,285	PtRLG_476	826
PtRLC_283	17	PtRLX_291	30	PtRLC_488	1,187	PtDTX_135	816
PtRLG_854	17	PtRLX_3871	30	PtRLG_673	1,103	PtDTX_145	786
PtRXX_3669	17	PtRLC_494	29	PtRLG_854	1,097	PtRLX_2789	785
PtRLX_14	16	PtRLX_3435	29	PtRLC_514	1,090	PtRLC_860	723
PtRLX_11	16	PtRYX_183	27	PtRLG_504	1,071	PtRLG_933	717
PtRIX_403	16	PtNoCat_2560	24	PtRLG_10	1,040	PtRLC_822	714
PtNoCat_2560	15	PtRLX_3902	24	PtRXX_121	1,036	PtRYX_173	713
PtRLG_504	15	PtRXX_3669	24	PtRXX_109	1,030	PtRXX_2933	684
PtRYX_183	15	PtRXX_4898	24	PtRLG_537	1,004	PtRLX_2876	676
PtRLX_106	15	PtRLX_3892	23	PtRLC_577	964	PtRLC_616	672
PtRXX_109	15	PtRLX_2487	22	PtRIX_403	957	PtDTX_114	670
PtRLC_334	14	PtRLX_14	21	PtRLG_18	950	PtRLG_688	653
PtRLC_482	14	PtDXX_123	20	PtRLX_1335	929	PtRLX_3104	634
PtRLG_673	13	PtRLX_11	20	PtRLX_3008	887	PtRLX_3184	627
PtRLG_432	13	PtRLC_617	19	TPE1	875	PtRLG_445	627
PtRIX_31	13	PtRLC_665	19	PtRLC_390	864	PtRLC_617	625
PtRXX_121	13	PtRLX_119	19	PtRLX_119	863	PtRLC_824	621
PtRPX_11	12	PtRLX_90	19	PtRIX_13	859	PtDTX_24	595
PtRLC_577	12	PtRIX_403	18	PtRLX_3765	858	PtRLX_3719	593
PtRLC_617	12	PtRLC_482	18	PtRLG_551	848	PtRLC_621	589
PtRLG_551	12	PtRLC_857	18	PtRLG_708	840	PtDTX_72	585
PtRLX_3435	12	PtRXX_4980	18	PtRLX_2005	824	PtRXX_1672	582
PtRIX_13	12	PtRYX_88	18	PtRLG_440	823	PtRLX_90	575
TPE1	12	Contig5_LTR	17	PtRLC_346	804	PtPotentialGene_173	564
PtRLX_3871	11	PtRLC_528	17	PtRPX_11	786	PtRLC_692	558

PtRXX_4898	11	PtRLG_18	17	PtRLX_28	772	PtDTX_121	556
PtRLG_885	11	PtRLG_854	17	PtRLX_14	762	PtRLG_673	553
PtRPX_174	11	PtRLG_885	17	PtRLX_194	703	PtRLC_346	542
PtRLC_709	11	PtRXX_3144	17	PtRLG_1	701	PtRXX_27	536

Table S9 High Coverage Elements

Bin 1 (Similarity)		Bin 1 (De novo)		Full Genome		Introns	
Family	% of bin 1	Family	% of bin 1	Family	% of genome	Family	% of introns
PtRLX_3423	0.56%	PtRLX_3765	0.20%	PtRLG_Conagree	0.77%	PtRLX_3423	0.30%
PtRLC_3	0.46%	PtAppalachian	0.15%	TPE1	0.50%	PtRLX_90	0.30%
PtNoCat_2560	0.27%	IFG7_I	0.14%	PtRLC_3	0.47%	PtRLX_106	0.29%
PtRLC_617	0.25%	PtRLC_3	0.14%	PtRLX_3423	0.46%	PtRLC_3	0.27%
PtAngelina	0.24%	PtRLX_3423	0.13%	PtOuachita	0.42%	PtRLX_2461	0.25%
PtRLX_3765	0.24%	PtRXX_2933	0.11%	PtRLG_IFG7	0.40%	PtRLG_673	0.23%
PtRLX_106	0.23%	PtNoCat_2560	0.10%	PtRLG_708	0.39%	PtRLC_824	0.22%
PtRLG_708	0.20%	PtRLX_2487	0.09%	PtRLC_515	0.39%	PtAppalachian	0.21%
PtAppalachian	0.19%	PtRLX_3435	0.09%	PtNoCat_2560	0.32%	PtRXX_4292	0.21%
PtRLG_6	0.19%	PtRYX_183	0.08%	PtTalladega	0.30%	PtRLX_2798	0.19%
PtRLG_13	0.19%	PtRLG_13	0.08%	PtRXX_4403	0.29%	PtRLG_476	0.19%
PtTalladega	0.17%	PtRLC_617	0.08%	PtPiedmont	0.29%	PtRLC_352	0.18%
PtRLX_2487	0.17%	PtPineywoods	0.08%	PtRLC_488	0.27%	PtRLC_346	0.17%
PtRLX_205	0.17%	PtRXX_4898	0.08%	PtAppalachian	0.24%	PtRLC_621	0.16%
PtPiedmont	0.17%	PtRLC_494	0.07%	PtAngelina	0.23%	PtRLC_860	0.16%
PtBastrop	0.16%	PtRLX_2461	0.07%	PtRLX_33	0.23%	PtRLC_444	0.16%
PtRLX_3058	0.16%	PtRXX_3669	0.07%	PtRLG_2	0.23%	PtRLX_3184	0.16%
PtRLX_14	0.16%	PtRLX_3058	0.07%	PtRLX_106	0.22%	PtRLX_3298	0.15%
PtRLC_390	0.15%	PtRLX_3902	0.06%	PtRLX_2487	0.21%	PtRLG_6	0.14%
PtOuachita	0.15%	PtRLX_14	0.06%	PtRLC_493	0.21%	PtRLX_140	0.14%
PtRLC_516	0.15%	PtRLX_3008	0.06%	PtRLC_390	0.20%	PtDTX_145	0.13%
PtPineywoods	0.14%	PtRPX_174	0.05%	PtBastrop	0.19%	PtRLX_205	0.13%
PtRLC_782	0.14%	PtRLC_630	0.05%	PtRLG_6	0.19%	PtRLX_3902	0.13%
PtRLC_334	0.13%	PtRYX_74	0.05%	PtRLC_516	0.17%	PtNoCat_2560	0.12%
PtRLC_492	0.13%	PtRLX_11	0.05%	PtRLC_340	0.17%	PtDTX_24	0.12%
PtRLX_3708	0.13%	PtRXX_3144	0.05%	PtRLG_Ozark	0.17%	PtDTX_11	0.12%
PtRLX_1912	0.13%	PtRIX_403	0.05%	PtRLC_492	0.17%	PtRLC_639	0.12%
PtRLG_656	0.12%	PtRYX_180	0.05%	PtNoCat_374	0.17%	PtRLC_782	0.11%
PtRLC_488	0.12%	PtRLX_3892	0.05%	PtRLX_205	0.16%	PtRLC_616	0.11%
PtRLX_3008	0.12%	PtRYX_88	0.05%	PtRLX_174	0.16%	PtRLC_349	0.11%
PtRLX_3435	0.11%	PtRXX_107	0.05%	PtRLG_580	0.15%	PtRLC_494	0.11%
PtRLX_109	0.11%	PtRLX_2714	0.05%	PtPineywoods	0.15%	PtRXX_1267	0.11%
PtRYX_180	0.11%	PtRPX_155	0.04%	PtRLC_392	0.15%	PtDTX_135	0.11%
PtRYX_74	0.11%	PtRLG_957	0.04%	PtRLC_617	0.15%	PtRLG_551	0.11%
PtRXX_2933	0.11%	PtBastrop	0.04%	PtRLG_521	0.15%	PtRLC_334	0.11%
PtRLG_479	0.10%	PtRLC_514	0.04%	PtRLX_14	0.14%	PtRLX_2038	0.11%
TPE1	0.10%	PtRLX_291	0.04%	PtRLX_3765	0.14%	PtRLX_306	0.10%

PtRLX_33	0.10%	PtRLG_916	0.04%	PtRLG_585	0.14%	PtRLX_334	0.10%
PtRIX_403	0.10%	PtRLG_643	0.04%	PtRLG_13	0.14%	PtRLG_13	0.10%
PtRPX_174	0.10%	PtRLX_3871	0.04%	PtRLC_334	0.14%	PtRLX_2504	0.10%

File S1

Methodology of the loblolly transcriptome

Total RNA was prepared from 27 loblolly pine collections including vegetative and reproductive organs, seedlings, needles, seeds and isolated megagametophytes from a variety of individuals. Polyadenylated RNA was enriched from total RNA and strand-specific libraries prepared by dUTP exchange in a manner similar to Zhong *et al.* (2011), using Illumina TruSeq mRNA indexed adaptors (Mockaitis lab, Indiana University). Indexed libraries were pooled and sequenced as 102 nt x 2 paired reads on a HiSeq2000 instrument using TruSeq SBS v3 reagents (Scheffler lab, Genomics and Bioinformatics Research Unit, USDA ARS, Stoneville MS). A total of 1.34 billion reads (671 million pairs) were used for sample-specific and grouped assemblies. RNA assemblies, their quality analyses and selection for use will be described in detail (Fuentes-Soriano, Loopstra, Wu, Gilbert and Mockaitis, in preparation). Briefly, reads were trimmed to 89 nts based on equivalent base representation and quality scores >Q20 using a custom Perl script. Trinity (Grabherr *et al.* 2011) versions 2012.10.05 and 2013.02.25, as well as Velvet-Oases (0.2.08) were used to generate parallel assemblies of read sets that were then classified for protein coding completeness, length and uniqueness of sequence using software of the EvidentialGene suite (Gilbert, 2012). 87,241 of 1.4 M transcripts were determined to be the longest of aligned unique sequences that contained complete CDS, and as such were classified as primary. Any potential contaminant transcripts derived from sampling were retained. Of the set 83,285 mapped to the loblolly pine genome assembly with no coverage or mismatch filters and these were used as evidence for annotating putative gene loci described here. The selected transcripts and trimmed reads files are available as TSA and SRA entries within NCBI BioProject PRJNA174450.

References

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- Grabherr, M. G., B. J. Haas, M. Yassour, J. Z. Levin, D. A. Thompson *et al.*, 2011 Full-length transcriptome assembly from RNA-Seq data without a reference genome. *Nature Biotechnol.* **29**: 644-U130.
- Schulz, M. H., D. R. Zerbino, M. Vingron and E. Birney, 2012 Oases: robust de novo RNA-seq assembly across the dynamic range of expression levels. *Bioinformatics* **28**: 1086-1092.
- Zhong, S., J.-G. Joung, Y. Zheng, Y.-r. Chen, B. Liu *et al.*, 2011 High-Throughput Illumina Strand-Specific RNA Sequencing Library Preparation. *Cold Spring Harb. Protoc.* **2011**: pdb.prot5652.

File S2

Accession numbers and additional details for alignment data sets

Available for download as an Excel file at <http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.113.159996/-/DC1>.

File S3

An explanation of PIER and GCclassif

The Pine Interspersed Element Resource (PIER) v2.0 includes 5,280 elements belonging to six families (plnrep, grasrep, mcotrep, dcotrep, oryrep, and athrep) from Repbase Update 17.07 (Jurka *et al.* 2005), five additional elements previously characterized in the literature, and 9,415 elements characterized in loblolly pine BAC and fosmid sequences (Wegrzyn *et al.* 2013). We developed an open-source classification tool, GCclassif, which analyzes the *pol* region characteristic of LTR retroelements to classify LTR retrotransposons into either Gypsy or Copia superfamilies based on the ordering of the protein domains (Figure S1). First, ORFs of an unclassified LTR are identified using the *findorfs* utility in USEARCH with default parameters. HMMER 3.0 (Eddy 2011) follows with *hmmsearch* using selected Pfam profiles as a library against the generated ORFs. Finally, HMMER hits are sorted and chained based so that all combinations of the alignments are considered. After all possible protein family orderings have been constructed, the highest-scoring (log-odds) chain is selected as the correct classification. If there is insufficient evidence, the element remains unclassified. Source code can be found at <http://github.com/bylin/nealelab-scripts/blob/master/GCclassif.py>.

With the subsequently developed GCclassif tool, 498 LTR retroelements were reclassified into the Gypsy superfamily and 416 LTR retroelements were reclassified into the Copia superfamily. 2,430 additional sequences were classified as LTR retrotransposons at the order level, but further classification was made difficult by their lack of detectable internal domains or structures and lack of alignments to known orders or superfamilies. Although portions of protein domains can be detected in 1,782 of these sequences, insufficient evidence kept them from being reclassified into Gypsy or Copia superfamilies. The new classifications were incorporated into PIER prior to analysis of genomic repetitive content.

Files S4-S8

Available for download as Excel files at <http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.113.159996/-/DC1>

File S4 Annotations for MAKER-derived gene models

File S5 Transcript notations including introns > 20Kbp

File S6 Gene Families Greater than or equal to 2

File S7 Genes with Annotations

File S8 Conifer-Specific families

Multiple Sequence Alignments related to Figure S2

GeneFamily 3795

>PP00070G01110

MAGEVFTPSVTQGFWGPITASTEWCEMNYQVTSLVAEFYNTISNIPGIIAFLGVVYSIS
 QKFERRFSVLHLSTIALGIGSILFHATLKYAQQQSDETPMVWAMLLYIYVLYSPDWHYRS
 TMPTVFLYGTIFAILHSQFRFVAGFQIHVYVFLALLCLPRMYKYYMYTKDPLARKLAHLY
 VLCLALGAICWLADRHLCSWICKLVNPOQGHALWHILEGFNSYFGNTFLQYCRAQQLNWN
 PRIDYLLGVVPYVKVQKGDTERKEQ

>PP00188G00180

MAGEALTSSTAQGFWGPITASTEWCEKNEYVTPVLAEFYNTISNIPGIVLAFIGVVYSIS
 QKFERRFSALHLSTIALGMSILFHATLRYAQQQCDETPMVWAMLLYIYVLYSPDWHYRS
 TMPTVFLYGTIFAILHSQFRFVAGFQVHYVFLALLCLPRMYKYYMYTKDPLVRKLAHRY
 VLCLALGAICWLADRHLCSWICKLVNPOQGHGLWHVLMGFNSYFGNTFLQYCRAQQLNWN
 PRIEYSLGVLPPYKVERSDNDRKEE

>PP00055G00680

-MAGEPSSGWLQGYWGPITASTEWCEKNEYVTPMVAEFYNTISNVPGIIAIIIGLYYAS
 QKFERRFSVLHLSTIALCIGSSLFHATLKYAQQQSDETPMVWVWMLLYIYVLYSPDWHYRS
 TMPTVFLYGTIFAVLHSQFRFVGFQLHLVLLAVLCLPRMYKYYIHTKDPVVRKLAHKY
 ILFLVLGGMCWLADRHLCSWICKLVNPOQGHALWHVLMGFNSYIGTTFLLYCRAEQQLNWN
 PKVEYVGLLPPYVKVQKSESERKEQ

>PP00452G00100

-MAEKISPGSHQGYWGPITASTEWCEKNEYVTPMVAEFYNTISNVPGIIALIGLYYAS
 QKFERRFSVLHLSTIALSIGSSLFHATLKYAQQQSDETPMVWVWMLLYIYVLYSPDWHYRS
 TMPTVFLYGTIFAILHSQFRFVGFQLHFVLLALLCLPRMYKYYIHTTDPVVRKLAHKY
 VLFVLMGAICWLVDRLCNQVSKLRINPQGHALWHVFMGYISYLGNTFLQYCRAEQQLNWN
 PKVEHVLGVLPPYVKVQKSDRDRKEQ

>Pita_1A_I9_VO_Locus_71152_Transcript_1_4_Confidence_0.500_Length_1856

-----MASQRVDSFWGPVTSTTDWCEKNEYAVSAYIVEFFNTISNIPCIIAFIGLINSR
 QRFEKRFSLHLSNMALAGSMIFHATLQHAQQQSDETPMVWEMLLYIYVLYSPDWHYTY
 TMPTFLFLYGAFAFTHFRFDLGFKIHYIISAGLCLPRMYKYYIHTTEPAKRLAHLHY
 ILTLILGGMCWLLDRTFCDTVSTWYINPQGHALWHIFMGFNAYFANAFLQFCRAQQREWR
 PEIRHVLGL-PYVKIKFKVSE----

>VV05G06510

-----MISNI-----KFLNTVSNVPGIVLGLFGLINALR
 QGFEKRFSLHISNIILAIGSILHSSLRQLQQQSDETPMVWEMLLYIYLHSPDWHYQS
 TMPTFLFLYGAFAFVHSQVHFVGFQVHILVILCLLCIPRMYKYYIHTQDMSAKRLAKLH
 LGTLFIGSLCWLSHRSLSHKDSHWYFSLQGHALWHVLMGFNSYFANAFMLFCRAQQREWN
 PKVVHFLGL-PYVKIQPKPKI-----

>PT01G31720

-----MAE-AISSFWGPVTS-AEWCEKNEYVSSYIAEFFNTVSIIPGILLALIGLINALR
 QRFEKRFSLHISNMILAIGSMILYHATLQRMQQQGDETPMVWEMLLYFYIYLYSPDWHYRS
 VMPTFLFLYGAFAFHFALVRFEIGFKVHYVILCLLCVPRMYKYYIYTKDASAKRLAKLY
 LATITTTGSLCWLFDRLFCNNISQWYFNPOQGHALWHVLMGFNSYFANTFLMFWRRAQQQLGWN
 PKVAHFMGFFPYVKIQPKPKT-----

>RC29904G00190

-----MAEGGISSFWGPVTSP-EWCEKNEYVSSYIAEFFNTISNVPGILLAFIIGLINALR
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 TMPTFLFFYGAFAFVHSLVRFVGFQVHYAILCLLCVPRMYKYYIYTNVSAKRLAKLY
 VG-----WSFNPOQGHALWHVLMGFNSYFANTFLMFRCRAQQQLGWN
 PKVVDLLGFFPYVKVRKPKT-----

>GM07G39500

-----MAE-SISSFWGPVTSTKECEINYAYSSYIAEFFNTISNIPTILLALIGLINALR
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 TMPIFLVYGFALFVAHVSFHFVGFQVHYIILCLLCVPRMYKYYIYTKDQVSAKRLAKLF
 LGTFVLGSLFGFCDRVFCKEISRWPINPQGHALWHVFMGFNSYFANTFLMFRCRAQQRGWS
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>AT4G22330

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 TMPTFLFLYGAAFAIVHAYLRFGIGFKVHYVILCLLCIPRMYKYIHTEDTAAKRIAKWY
 VATILVGSICWFCDRVFKTISQWPVNPQGHALWHVFMFSNSYCANTFLMFCRAQQRGWN
 PKVKYFLGVLPPYVVKIEPKTKQ----
 >PT11G00510
 -----MAEGGISSFVWGPVTSTTECCEKNYAYSSYIAEFHNTISNIPCVLALVGLINALR
 QRFEKFRSVLHISNMILAIGSMIFHATLQRVQQQSDETPMVWEMLLYMYILYSPDWHYRS
 TMPIFLFLYGAVFAAVHSVRLGIGFKVHYAILCLLCIPRMYKYIYTQDASAKRLAKMY
 VATLLIGTLCWLFDRIFCKEISSWPINPQGHALWHVFMGFNSYLANTFLMFCRARQRGWS
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 >RC29842G00070
 -----MAD-GISSFWGPVTSTTECCEKNYAHSSYIAEFYNTISNIPCILLALIGLINALR
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 TMPTFLFLYGAVFAIVHSVHFGIGFKVHYVILCLLCIPRMYKYIYTQDAAAKWLAKLY
 VATLFIGSLCWLCDRIFCKISNWPINPQGHALWHVFMGFNSYFANTFLMFCRAEQRGWS
 PKVVCFAGILPYVVKIEPKVKQ----

GeneFamily 10970

>Pita_2A_all_VO_Locus_12631_Transcript_1_3_Confidence_0.167_Length_3462
 MPVEKGVCGSIRPAAAMAEVKLTDSQLNTICAPIDRPLMILAAAGSGKTLVICHRIHLHI
 SKGVSPKDILAVTFRTRAGQDLLHRLQCIAAAQCFGGEGSLDVVGIKRVGTFHSCFLSVL
 RAFPNHAGLAPDFVVFTRPKMQLDLENLVEEWHTQRRHEINGQSMQFQDKLARKSKQLQG
 RHQSTAEEKAFFKAGAYRLFQHLRSTQFVKSQEGAADVELNDS-HGDGFSKWVVFHQYHEH
 LLQANGIDFNSFVRYTLDMLKKWPNALASAGLKAQYIFVDEFQDQDVSQFELLKILCKDH
 AHITVVGDDDDQIYSWRGATGLYNIKNFENVFKGGITTKLEQNFSTGAIVASARSLISK
 NQSRMPKTVRTASPTGLMTICECRNDQCEVTAIVDFIISLKKQGVPLQEIAILYRLQRI
 GLEVQHNLQAQIECHIKSGSGSTGNQCLVANGGQVGTGLGDVFDLAVLRLAICESD
 DLASKHLLDLFCPSMSLVIKDCLSYLKLQKGLSLLQAIKSTRSHLVGLLVCDLSSYAPA
 KSIILSES DHLTLEGMHSILKLLAATKNDSKNMGLRDVIFNILQQISYVVRGSRDVPQAL
 KADLDGRKGYNQQLVSSSGKVDTNLSNLSLQYAGIKALLKEAALFDAEIRTSQSNQNSCSI
 KESNSATPQTSYMDLKQHRSRKRL-NLSPDKPGFAGNIDFSLDAKSLDKLRFDRVTL
 KMHDELGENNASIPIRPVQSVSSACDTGVTLSITHQAKGLEWEGVILVRANDGIIPV
 RDSDFVVGPTTPTNPNIIDYGTTRNEDVITREAGNKNLENDISLLGPPILETRGKFSS
 GPNREGIEEERLMYVALTRAKRFVLVTHVMMEGGQMQMTPSCFLADIPPLVRRRTTCYES
 KIPDPGLLLDSVTPSPISTKSVSSANDEAVKGTCDPSGIFYSQNKDTNVKDDMQYSSKI
 LKSTPNMRRKTNLQVNAESELSEMASTGSMDSCHLRKYSSKKTGNVVEISKSDECGSQS
 DDSEFEKPVKGRKRKQKVICSEGEE
 >SM00010G01000
 -----MVELTESQVAAVTAPISCPMLILAAAGSGKTLVLCYRILHLHI
 RNVGPAKEILAVT-----
 -----LELLQELVYEWHLMRSN-----G
 QKCEGSLKQLFRTEAYRMMKQI--GQMQRKHDTAA---LNSAKKGGGMLDWVFLERYHSH
 LQNINAIDFNSFTRRTNDVLESFP-----VDEFQDQDQFQKLLQALSTRH
 HHVTVVGDDDDQIYSWRGAAGIQNLESFSSTFGGATVVKLERNFRSTGAIVAAARSVISR
 NESRMRKSIGTTAPTQKLVAMCECRNVLCEVAASINFISSRAEGVKLSEIAVLYRVHRV
 GVELQHHLQAIGVPCMKMVTGG---SDDSTVSAKGFSS--GEALADILGVLRLILNESD
 DYACKRLMLLFCPDGRSEVLSCVMQLQQAGSSLLQSLKTLRSHVLG-MSKDSLSAPWIQ
 PVVEKLGVLVKEVIKGAQVLMKIMADTKEELQRLGMKDVVMNLLQQIGPYR-----EAR
 TASLQ-----ISSTANLGGG---DFAGIKALLKEAAAFDGDNAFVMAKTA---
 -QTASKSKNASKDMRRLQKRDPGQGTVRSSQSDFKDHT-----QRLRVFLDQVAL
 KLHEYELGEDN-----KTLSSPDC---VTLSTIHQAKGLEWPAIVLARANEVGLPV
 FDTDMV-----SDAQDILEE-----
 -----ITYLMKDSGQQALPSRFLAEIPRGLVKRIVSYDH
 QV-----
 -----TNITATTNTI-----
 -----GRKREERG-----

Files S10-S12

Available for download as Excel files at <http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.113.159996/-/DC1>

File S10 Overview of tandem content in *Arabidopsis thaliana*, *Vitis vinifera*, *Selaginella moellendorffii*, *Cucumis sativus*, *Populus trichocarpa*, *Picea glauca*, *Picea abies* and *Amborella trichopoda*

File S11 Tri/tetra nucleotide motifs and frequency

File S12 Full Repeat Summary for Similarity Search Applied to Intronic Sequence