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The *Pinus taeda* BAC Browser

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The *Pinus taeda* BAC Browser (http://www.conifergdb.org/db/genome3352v1/) is an open-access bioinformatics resource designed for fast data dissemination, seamless data integration, and effective data mining of current and future BAC sequencing data for loblolly pine. BAC sequences are retrieved from GenBank and run through in-house pipelines that conduct repeat identification/masking, cDNA-to-genome alignment, SNP detection, *ab initio* gene prediction, and initial annotation. All 4 million clean ESTs are mapped to the BACs using stringent criteria. By integrating open-source tools including RepeatMasker, Maker, and GMAP with in-house tools like SeqViewer and Genome Browser, the BAC Browser provides biologists with powerful data search, filtration, and visualization functions to facilitate data analysis. Each BAC is referenced based on its GenBank accession number, sequence name, length, and sequencing status. Through AlignView, all gene models and associated cDNA alignments can be compared at either bird's-eye view or single-nucleotide-resolution levels, and users can navigate individual BACs smoothly by specifying genomic positions and/or gene ID. Through SeqView, users can extract any fragment of BAC sequence for download and conduct nucleotide positioning, 6-frame translations, and motif detection. SnpView tallies all high-quality SNPs recovered from cDNA-to-genome alignments and links directly to SNP nucleotide alignments. Users can search through GO, KEGG, EC, and InterProScan annotations of all gene models and examine the relevant gene sequences, cDNA alignments, and other sequence features. Furthermore, users can upload their own sequences to BLAST against the BAC sequences. We are in the process of improving this web portal by incorporating other tools like WebGMAP and displaying more sequences features like repeats.