Genomic and functional approaches reveal a case of adaptive introgression from *Populus balsamifera* (balsam poplar) in *P. trichocarpa* (black cottonwood).

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ABSTRACT

Natural hybrid zones in forest trees provide systems to study the transfer of adaptive genetic variation by introgression. Previous landscape genomic studies in *Populus trichocarpa*, a keystone tree species, indicated genomic footprints of admixture with its sister species *P. balsamifera* and identified candidate genes for local adaptation. Here, we explored patterns of introgression and signals of local adaptation in *P. trichocarpa* and *P. balsamifera*, employing genome resequencing data from three chromosomes in pure species and admixed individuals from wild populations. Local ancestry analysis in admixed *P. trichocarpa* revealed a telomeric region in chromosome 15 with *P. balsamifera* ancestry, containing several candidate genes for local adaptation. Genomic analyses revealed signals of selection in certain genes in this region (e.g. *PRR5, COMT1*), and functional analyses based on gene expression variation and correlations with adaptive phenotypes suggest distinct functions of the introgressed alleles. In contrast, a block of genes in chromosome 12 paralogous to the introgressed region showed no signs of introgression or signatures of selection. We hypothesize that the introgressed region in chromosome 15 has introduced modular, or cassette-like variation into *P. trichocarpa.* These linked adaptive mutations are associated with a block of genes in chromosome 15 that appear to have undergone neo- or sub-functionalization relative to paralogs in a duplicated region on chromosome 12 that show no signatures of adaptive variation. The association between *P. balsamifera* introgressed alleles with the expression of adaptive traits in *P. trichocarpa* supports the hypothesis that this is a case of adaptive introgression in an ecologically important foundation species.

INTRODUCTION

Introgression between recently diverged species with incomplete reproductive barriers is a widespread process that can provide novel genetic recombinants and promote adaptation to new environments (Arnold 2006). Although stochastic processes such as genetic drift are main drivers underlying the geographic distribution of genetic regions introduced by introgressive hybridization, natural selection also plays an important role when adaptive genes are exchanged across species boundaries (Barton & Gale 1993; The Heliconius Genome Consortium 2012; Hamilton *et al.* 2013; Abbott *et al.* 2013). For instance, hybridization can contribute to adaptive genetic variation if recombination leads to the introgression of genomic regions with modular, or cassette-like variation, i.e. multiple linked mutations across blocks of genes, associated with adaptive traits (Abbott *et al.* 2013).

Forest tree species are attractive targets to study adaptive introgression largely because they exhibit extensive natural hybrid zones (Lexer *et al.* 2004), but also because of their large ranges across geographical and climatic clines, as well as substantial trait variation (Savolainen *et al.* 2007; Soolanayakanahally *et al.* 2009; Keller *et al.* 2011; McKown *et al.* 2013). Research on the contribution of interspecific hybridization and introgression to local adaptation is rapidly expanding in long-lived tree species [e.g spruce (de Lafontaine *et al.* 2015; Hamilton *et al.* 2014), *Eucalyptus* (Larcombe *et al.* 2015), and oak (Abadie *et al.* 2012)]. However, studies documenting fine-scale introgression patterns within and around target genes, and identifying adaptive introgression at the gene level have mainly focused on taxa with short generation spans in both plants and animals [(Whitney *et al.* 2015; Martin *et al.* 2006; Wang *et al.* 2014; The Heliconius Genome Consortium 2012; Norris *et al.* 2015) but see (Martinsen *et al.* 2001; Lind-

Riehl *et al.* 2014; Racimo *et al.* 2015)], and have not been carried out in tree species. The characterization of population-wide genomic diversity in keystone or foundation forest tree species will enable the study of species complexes involving ecologically divergent yet hybridizing taxa (Lexer *et al.* 2004; Buerkle & Lexer 2008), to explicitly test for adaptive introgression at a fine genomic scale. Such genomic scans could be used to identify genomic regions that are more prone to introgression than others, potentially underlying adaptive processes. Clarifying the magnitude and impact of introgressed genes contributing to functionally relevant variation in trees has great potential for forest ecology, management, and restoration efforts in the face of climate change (Lexer *et al.* 2004; Whitham *et al.* 2006; Hamilton & Miller, 2015).

Buerkle and Lexer (2008) proposed using admixture mapping, a gene mapping method for traits that differ in frequency across populations, to reveal genomic regions associated with adaptation. Recent applications of this approach to trees has provided a first glimpse of the genetic architecture of ecologically important traits (Caseys *et al.* 2015; Lindtke *et al.* 2013), but much higher marker densities and more highly recombinant mapping populations are required to obtain precise map locations of candidate genes. Based on the large-scale characterization of genomic diversity in wild populations of *Populus*, trees of this genus have emerged as an important model for population genomic studies of adaptation (Weigel & Nordborg 2015). Here, we used such data from *P. trichocarpa*, *P. balsamifera* and their hybrids, including whole genome single nucleotide polymorphism (SNP) data for hundreds of individuals (Evans *et al.* 2014; Slavov *et al.* 2012; Geraldes *et al.* 2014), to detect introgressed regions at a fine scale using three target chromosomes. We also implemented functional and phenotypic tests to determine if introgressed regions are associated with adaptation, using extensive data on

phenotypic and transcriptome diversity in many of the same individuals grown in a common garden (McKown *et al.* 2103; McKown *et al*. 2014; Corea *et al*. in preparation).

Populus trichocarpa and *P. balsamifera* are sibling poplar species of the section *Tacamahaca* that diverged in allopatry rather recently (~76 Ka) during Pleistocene glaciations (Levsen *et al.* 2012); [see (Ismail *et al.* 2012) for an alternative - older - estimate]. They are major components of the forest ecosystems of northern North America and are economically important forest trees, being wood pulp sources and potential feedstock for cellulosic ethanol production (Jansson & Douglas 2007; Porth & El-Kassaby 2015). Despite their recent divergence and morphological similarity, with some minor differences in flower and fruit morphology, the species are ecologically divergent and adapted to strongly contrasting environments. *P. trichocarpa* is distributed throughout the western US and Canada, from northern California to southern Alaska, and is adapted to relatively humid, moist, and mild conditions west of the Rocky Mountains. *P. balsamifera*, on the other hand, is largely a boreal species distributed from Alaska to Newfoundland, with high frost tolerance and is adapted to environments where there can be huge annual temperature differences (-62˚C to 44˚C) and generally less annual precipitation (Richardson *et al.* 2014).

Recently, Geraldes et al. (2014) showed that introgression from *P. balsamifera* plays a role in shaping the geographically and climatically associated patterns of genetic variation of *P. trichocarpa* across much of its range. This admixture, geographically limited to contact zones located in Alaska, northwestern Canada and the Canadian Rockies (Figure 1) (Viereck & Foote 1970; Geraldes *et al.* 2014), may be driving adaptive processes if introgressed alleles are functionally different and linked to adaptive phenotypic traits. For example, introgression of *P. balsamifera* genes associated with faster growth rates that compensate for short growing seasons

at higher latitudes may allow admixed *P. trichocarpa* individuals to colonize new environments in northern and eastern regions. This could also be the case if introgressed *P. balsamifera* genes are associated with cold or drought tolerance (Soolanayakanahally *et al.* 2009).

Previous studies based on a 34K SNP genotyping array in ~500 *P. trichocarpa* individuals from the Pacific Northwest (Geraldes *et al.* 2013), found 88 genes with F_{ST} outlier SNPs (Geraldes *et al.* 2014) associated with 30 phenotypic traits (McKown *et al.* 2014) putatively underlying adaptive processes. Two unique sets of SNPs in candidate genes, located in chromosome 6 and chromosome 15 respectively, had F_{ST} values that were among the 10 highest - genome wide - and were strongly correlated with geoclimate variables (Geraldes *et al.* 2014). In addition, these SNPs were in high linkage disequilibrium (LD) with other candidate SNPs in the same chromosome, and/or had multiple trait associations based on a genome-wide association analysis (GWAS) (McKown *et al.* 2014). In this study, we tested if introgression from *P. balsamifera* was a source of any signals of local adaptation found in *P. trichocarpa* populations. In chromosome 6, adjacent genes *FAR1* (Potri.006G020600) and *FHY3* (Potri.006G020700), encoding transcription factors related to the far red light response, had SNPs with the highest F_{ST} genome wide, which are in high LD (Geraldes *et al.* 2014). In chromosome 15, a genomic region of ~600-kb showed strong patterns of structure and association with latitude, environmental variables (Geraldes *et al.* 2014) and phenology, biomass and ecophysiology traits (McKown *et al.* 2014). This 'gene block' had candidate SNPs in high pairwise LD, including those from a gene encoding a phenylpropanoid enzyme (*COMT1,* Potri.015G003100) and from transcription factors putatively involved in light and developmentally regulated gene expression (*TTG1*, Potri.015G002600; *PRR5,* Potri.015G002300; *ANAC062*, Potri.015G004100) (McKown *et al.* 2014). Interestingly, a paralog region of this genomic block found in chromosome 12, that was

produced by a whole genome duplication event in the Salicoid lineage (Tuskan *et al.* 2006), did not show signals of population structure or association with phenotypic traits, suggesting that these gene paralogs have followed different evolutionary trajectories.

Based on these results, we focused the current study on data obtained from population-wide genome resequencing of chromosomes 15 and 6 in *P. trichocarpa* and *P. balsamifera,* and of chromosome 12, which had a paralog block of the chromosome 15 candidate genes showing no signatures of selection. We (i) identified hot spots of introgression (i.e. regions that exhibited excess introgression relative to chromosomal averages) and tested if candidate regions for adaptation in *P. trichocarpa* have alleles introgressed from *P. balsamifera*, (ii) implemented genomic and gene ontology enrichment tests in introgressed regions to detect signals of selection and overrepresented biological terms respectively, (iii) analyzed gene expression levels to test if introgressed alleles could function differently from *P. trichocarpa* alleles, and (iv) compared phenotypes of admixed vs. pure *P. trichocarpa* individuals to explore the potential functional effects of introgressed alleles.

MATERIALS AND METHODS

Samples

Populus trichocarpa accessions used in this study were collected by the British Columbia Ministry of Forests, Lands and Natural Resource Operations (MFLNRO) (Xie *et al.* 2009), and outplanted in a common garden at the University of British Columbia (McKown *et al.* 2013). These individuals comprised 28 “drainages” (i.e., topographic units separated by watershed barriers) spanning 14° in latitude (45.6°–59.6°) from throughout the species range. For *P. balsamifera*, we used accessions from 46 provenances throughout the species range obtained

from the Agriculture and Agri-Food Canada AgCanBaP collection (Soolanayakanahally *et al.* 2009). For local ancestry analysis in RASPberry (Wegmann *et al.* 2011), 50 reference individuals and 68 admixed individuals (36 *P. trichocarpa* individuals with *P. balsamifera* admixture, and 32 *P. balsamifera* individuals with *P. trichocarpa* admixture) were selected from the sympatric zone between *P. trichocarpa* and *P. balsamifera* as well as from allopatric populations (Figure 1). These 118 individuals were selected from a collection of 435 *P. trichocarpa* and 448 *P. balsamifera* genotypes, using a previous genome wide admixture analysis (see Supporting Information: Materials and Methods; Geraldes *et. al.,* In preparation). Additional sample information and data generated in this and previous studies can be found in Table S1; Supporting Information.

Sequencing, read mapping and variant calling

Three different sample sets were used to call SNPs (Table S1; Supporting Information). For gene sequence analysis, SNPs were called for three genes (*COMT1, PRR5,* and *TTG1*) among 302 *P. trichocarpa* genotypes and for one gene (*COMT1*) among 243 *P. balsamifera* genotypes. For local ancestry analysis SNPs were called in three chromosomes (6, 12, 15) for 118 individuals (see above and Supporting Information: Materials and Methods). For phenotypic and gene expression analysis, 161 *P. trichocarpa* individuals were classified in genotypic categories using SNPs in a telomeric region of chromosome 15. We sequenced each of the genotypes at an expected coverage ranging from 15X to 30X using the Illumina HiSeq2000 platform. Short reads from the sequencing libraries were independently aligned to the *P. trichocarpa* version 3 (v3.0) genome using BWA (version 0.6.1-r104) with default parameters. We corrected mate pair metadata and marked duplicate molecules using the FixMateInformation and MarkDuplicates methods in the Picard package (http://picard.sourceforge.net). Reads present

in areas surrounding InDels were re-aligned using the IndelRealigner method from GATK (version v1.5-25-gf46f7d0). Next, we called SNPs and small indels independently using the UnifiedGenotyper method from GATK. SNPs were then filtered to exclude variants within 3bp of any identified variants, having a mapping quality less than 5, and a variant quality less than 30. Each SNP was annotated using SNPeff (Cingolani *et al.* 2012) with version 3 of *P. trichocarpa* genome. All raw sequencing data and alignment information have been deposited on SRA (Accession: PRJNA298917 ID: 298917).

Inference of local ancestry

We estimated the probabilities for each of the possible ancestral configurations (*P. balsamifera*, *P. trichocarpa* or mixed ancestry) in every SNP across three chromosomes (6, 12 and 15), in 50 reference individuals and 68 admixed individuals using RASPberry, a software that implements a reliable Hidden Markov model (HMM) for admixture (Price *et al.* 2009).

For RASPberry analyses, SNPs with missing data in the parental genotypes were removed using Plink 1.07 (Purcell *et al.* 2007), the parental genotypes (50) were then phased with fastphase (Scheet & Stephens 2006) by creating the input files with FCGENE (Roshyara & Scholz 2014), and ancestries for each admixed individual were estimated in ADMIXTURE (Alexander *et al.* 2009). To select the parameters in RASPberry that best fit our data, we ran a number of parameter combinations - including time since admixture and recombination rate – using the 971k SNPs genome-wide data set (see Supporting Information: Materials and Methods), and selected the model with the highest log likelihood value (Table S2; Supporting Information). Using the 971k SNPs data set for this preliminary analysis allowed us to both estimate individual ancestries based on a genome-wide approach, and to run different parameter combinations relatively fast. For local ancestry analyses based on the whole sequence of

chromosome 6, 12 and 15, only SNP ancestries with probabilities >95% in one of the three categories were considered. The proportion of *P. balsamifera* ancestry in *P. trichocarpa* admixed individuals was calculated, for each SNP, by counting sites with *P. balsamifera* ancestry as two, and sites with mixed ancestry as one. We detected regions with unusually high levels of introgression in admixed *P. trichocarpa* individuals using a sliding window approach, and a significance cut-off of three standard deviations (SD) from the weighted mean across the three chromosomes based on SNP density per window. We used 100-kb, 500-kb and 1-Mb windows with steps of 20-kb, 100-kb and 200-kb respectively. The same procedure was implemented to estimate levels of *P. trichocarpa* ancestry in *P. balsamifera* admixed individuals.

Characterization of introgressed regions and test of selection in pure species and admixed individuals

First, we performed Gene Ontology enrichment analysis by comparing the list of introgressed genes with the list of all poplar genes (41,335) and the best annotated orthologs in *Arabidopsis thaliana* (based on Popgenie annotation; http://popgenie.org/), using the DAVID online database (Huang *et al.* 2008). Second, we estimated Tajima's D values across chromosome 6, 12 and 15 for the 50 pure species individuals, using 50-kb windows in VCFtools v0.1.12b (Danecek *et al.* 2011). For introgressed regions with positive Tajima's D values, we performed neighbor-joining analysis with 1000 bootstrap replicates using MEGA (Tamura *et al.* 2007). Third, we calculated levels of nucleotide diversity (π) for the pure species individuals across the three chromosomes using 50-kb windows in VCFtools v0.1.12b. Fourth, we estimated the average proportion of amino acid substitutions driven by directional selection (alpha) in pure species individuals for all introgressed regions including a section with the lowest nucleotide diversity (π) level, using Smith and Eyre-Walker's alpha (Smith & Eyre-Walker 2002), and

generated confidence intervals by randomly selecting genes with replacement (bootstrapping) 1000 times in R v. 3.2.1 (R Development Core Team, http://www.r-project.org). Fifth, we estimated pairwise linkage disequilibrium (LD) as r^2 in the pure species and a set of admixed individuals (see Supporting Information: Materials and Methods), and detected haplotype blocks in the pure species using Haploview version 4.2 (Barrett *et al.* 2005) and the same phased genotypes used in RASPberry analysis. The decay of LD with physical distance was estimated following Remington et al. (2001) with expected values, $E(r^2)$, computed using the formula from Hill & Weir (1998) in an R script (http://www.r-project.org/).

Haplotype distribution of candidate genes for local adaptation

For three candidate genes in chromosome 15 (*PRR5*, Potri.015G002300; *TTG1*, Potri.015G002600; *COMT1*, Potri.015G003100) that showed signatures of selection in previous studies (Table S3; Supporting Information) (McKown *et al.* 2014; Geraldes *et al.* 2014), we estimated the F_{ST} value per SNP using Arlequin 3.5.1.2 (Excoffier *et al.* 2005), in 302 accessions from 28 drainages across much of the *P. trichocarpa*'s range. These F_{ST} values were compared to *P. trichocarpa*'s whole genome average F_{ST} (mean=0.05; 99th percentile = 0.18) following Geraldes *et al.* (2014). Based on the coding regions of each gene, we inferred haplotypes using PHASE 2.1 (Stephens *et al.* 2001) and mapped the haplotype distributions. For the *COMT1* gene, we also estimated allele frequencies across 46 *P. balsamifera* provenances (484 individuals). Finally, we analyzed a protein alignment of *COMT2*, a paralog of *COMT1* encoded on chromosome 12, from *P. balsamifera* and *P. trichocarpa* genotypes, and a protein alignment of different homologous sequences retrieved from Phytozome (http://www.phytozome.net).

Gene expression and phenotypic analysis in admixed *P. trichocarpa* individuals

For phenotypic analyses, we used data from McKown *et al.* (2013). Gene expression data were obtained from a population-wide RNAseq dataset based on a subset of the *P. trichocarpa* accessions from trees outplanted in the common garden at the University of British Columbia as described above (Xie *et al.* 2009; McKown *et al.* 2013). RNA was isolated from 385 developing xylem samples from 197 of the accessions, and from 389 samples of expanding leaves of defined developmental stage from a subset of 191 of the accessions. For both phenotypic and gene expression data, we focused on one introgressed region in chromosome 15 and on individuals from northern and central parts of the *P. trichocarpa* range. By excluding genotypes from southern locations, we aimed to remove the latitudinal variation inherent in some phenotypic traits of *P. trichocarpa* (McKown *et al.* 2013), and targeted locations close to the contact zone. We used published phenotypic data from 146 *P. trichocarpa* genotypes (McKown *et al.* 2013) and RNAseq data, as FPKM (Fragments Per Kilobase of transcript per Million mapped reads), from a subset (33) of those *P. trichocarpa* genotypes (Supporting Information: Materials and Methods, Table S1). Each of the 146 *P. trichocarpa* individuals were classified into one of three genotypic categories: homozygotes for *P. balsamifera* haplotypes (bb), heterozygotes (bt) and homozygotes for *P. trichocarpa* haplotypes (tt), based on phased genomic sequences of one introgressed region in chromosome 15 (Figure S1; Supporting Information). Nine phenotypic traits and expression levels of 134 genes were then compared among the three genotypic categories (bb, bt and tt) using ANOVAs with adjusted P-values with Bonferroni correction, and Tukey tests for multiple comparisons. For one candidate gene, *PRR5*, we used a gene co-expression network analysis for the xylem RNASeq dataset to identify the top 25 co-expressed genes, and compared the average mean-centered expression levels of these genes between the

three genotypic categories (bb, bt and tt) using an ANOVA. Finally, we validated the RNAseq data using quantitative reverse transcription PCR (qRT-PCR) in *COMT1*, a selected candidate gene (Table S4; Supporting Information).

RESULTS

Local ancestry analysis revealed three introgressed regions

Using 186,376 SNPs across chromosome 6, 12 and 15, we detected three regions with *P. balsamifera* ancestry in admixed *P. trichocarpa* individuals (36): two in chromosome 15 and one in chromosome 6. These regions were above a significance cutoff of three Standard Deviations (SD) from the mean *P. balsamifera* ancestry (0.096, SD 0.066, weighted by SNP density), using 50-kb, 100-kb and 1-Mb window analysis. This was consistent with genome wide estimates based on a 971k SNP data set, where the mean *P. balsamifera* ancestry was 0.13 (SD 0.036). Across the remaining regions of *P. trichocarpa* chromosomes 6 and 15, and across the entire *P. trichocarpa* chromosome 12, levels of *P. balsamifera* ancestry were for the most part low, and did not surpass the significance cutoff. For downstream analyses, we used the results based on 100-kb windows (Figure 2), since this window size provided the best compromise between large numbers of windows with missing data (50-kb windows) and low resolution (1-Mb windows) (Figure S2; Supporting Information).

In chromosome 15, a large introgressed segment (880-kb) was located in a telomeric region (peak B in Figure 2), and included candidate genes *PRR5, TTG1* and *COMT1* as well as another 131 genes (Table 1; Table S3 and S5; Supporting Information). A second 580-kb introgressed region in chromosome 15 was located 13.34 Mb from the start of the chromosome and included 84 genes (peak C in Figure 2). In chromosome 6, a 580-kb introgressed region

comprised 67 genes and was located at 3.36 Mb from the start of the chromosome (peak A in Figure 2), downstream of candidate genes for adaptation (Table 1; Table S3 and S5; Supporting Information). Local ancestry analysis of *P. balsamifera* admixed individuals did not reveal introgression from *P. trichocarpa* (Figure S3; Supporting Information).

Selection in pure *P. balsamifera* and *P. trichocarpa*

The three introgressed regions revealed different patterns of Tajima's D and alpha estimates in the parental genotypes. A section of introgressed region B (telomeric introgressed region of chromosome 15) that included candidate gene *PRR5* revealed positive values of Tajima's D in *P. balsamifera* but not in *P. trichocarpa*, with estimates greater than the neutral expectation (Figure 3). In *P. balsamifera* the first two 50-kb windows of this region showed Tajima's D estimates above the 1% of the distribution (0 to 49-kb = 2.58; 50 to 99-kb = 3.18), and the following window showed Tajima's D estimates above the 5% of the distribution (100 to 149-kb = 2.14) (Table S6; Supporting Information). A neighbour-joining (NJ) tree based on the first 880-kb of chromosome 15 revealed two haplotype clusters in *P. balsamifera*, both of which occur in populations from the northwestern and central parts of the species range (Figure S4; Supporting Information).

Region C in chromosome 15 also showed positive values of Tajima's D higher than the 1% of the distribution, in both *P. trichocarpa* and *P. balsamifera,* but only in one 50-kb window (13.45 Mb to 13.50 Mb) (Figure 3), comprising three genes. Tajima's D values in introgressed region C in chromosome 6 did not deviate from neutral expectations in either *P. trichocarpa* or *P. balsamifera* (Figure S5; Supporting Information).

Region B in chromosome 15 exhibited extended LD decay in both admixed and pure *P. balsamifera* individuals. In admixed individuals, average LD in this region did not decay below

2kb until past 10 kb, as it did in the second introgressed region (region C) and across the remainder of chromosome 15 (r^2 decay to 0.2 at 2 kb and 5 kb respectively) (See Supporting Information and Figure S6). In pure *P. trichocarpa* and *P. balsamifera* LD decay also was extended in region B, with average LD not dropping below 2kb for 5 kb and 4 kb, respectively. LD decay in introgressed regions A and C in chromosomes 6 and 15, respectively, was similar to that in the chromosome-wide average (2 kb; Figure S6; Supporting Information). In pure *P. balsamifera*, a haplotype block at the start of chromosome 15 extended for 130 kb and was followed by a shorter block of 26 kb that included candidate genes *PRR5* and *TTG1* (Figure 4A). In pure *P. trichocarpa*, the haplotype block at the start of chromosome 15 extended for only 36 kb, and other blocks downstream were not longer than 8-kb (Figure 4B).

In addition to positive values of Tajima's D and relatively long haplotype blocks in pure *P. balsamifera* individuals, the first ~200 kb of chromosome 15 from region B (i.e. *P. balsamifera* introgressed region B in *P. trichocarpa* individuals) showed the highest levels of nucleotide diversity compared to levels across the three chromosomes examined (Figure S7; Supporting Information). Levels of nucleotide diversity (π) in the first 160 kb, comprising 25 genes including *PRR5*, were in the top 5% of the distribution in *P. balsamifera*. However the contiguous downstream region had the lowest *P. balsamifera* π values (lower than the bottom 5% of the distribution). Alpha estimates of this 110-kb region (from 183 kb to 280 kb in chromosome 15), comprising 14 genes including *COMT1* and *ANAC062*, revealed signals of positive selection in 46% and 41% of all amino acid substitutions in *P. trichocarpa* and *P. balsamifera* respectively (Table 2). The alpha estimate for the entire telomeric introgressed region in chromosome 15 (region B) was not significantly different from zero, and neither was that for the introgressed region in chromosome 6 (region A). For the second introgressed region

in chromosome 15 (region C), synonymous and non-synonymous substitutions were not detected (Ds and Dn = 0) and alpha was undefined (Table 2).

Haplotype distribution of candidate introgressed genes on *P. trichocarpa*

In *COMT1* from *P. trichocarpa*, we identified 171 SNPs with a MAF (minor allele frequency) > 0.01, eight of which were in the coding region. The highest F_{ST} value in the coding region was for a synonymous SNP located in the first exon of the gene (amino acid position A84, F_{ST} = 0.3), and the second largest F_{ST} value was found in a nonsynonymous SNP (nsSNP, P287Q, F_{ST} =0.23) (Figure 5A), both of which were higher than the 99th percentile of the genome wide distribution (0.18) based on a previous analysis (Geraldes *et al.* 2014).

The P287Q polymorphism is located in the O-methyltransferase domain of the COMT1 enzyme, and the P287 variant was strictly conserved in all homologs including *COMT2*, a paralog of *COMT1* encoded on *Populus* chromosome 12, and in *COMT* homologs from other species (Figure S8; Supporting Information). In *P. trichocarpa,* this site was polymorphic with the alternative Q287 variant occurring at a relatively low frequency (8.6%), and restricted to northern and interior populations (Figure 5B). In *P. balsamifera,* the Q287 allele was almost fixed (95%) and the alternative P287 variant only occurred in admixed individuals with *P. trichocarpa* and *P. deltoides* (Geraldes *et. al.,* In preparation) (Figure 5C). These results support our finding of signals for positive selection in *COMT1* and flanking genes (110-kb region from 170-kb to 280-kb in chromosome 15), and suggest that the rare Q287 *COMT1* variant selected for in *P. balsamifera,* but not found in any other homologous *COMT* genes, introgressed to *P. trichocarpa* in regions close to the contact zone with *P. balsamifera.*

In *TTG1* we found 20 SNPs with a MAF >0.01, five of which were in the coding region. The highest F_{ST} values in the coding region were for two sSNPs (L238-G/T, L323-A/C F_{ST}= 0.25), with T238/C323 alleles restricted to the north and interior (Figure S9-A, B; Supporting Information). In *PRR5* we found 75 SNPs with a MAF >0.01, 12 of which were in the coding region and five of which were nsSNPs. The highest F_{ST} value in the coding region was found in nsSNP R396W (F_{ST} =0.24), where R396 was the most common allele and W396 was restricted to the north and interior with an allele frequency of 9.1% (Figure S9-C, D; Supporting Information).

Evidence for adaptive introgression based on GO, gene expression and phenotypic analysis

GO term enrichment analysis of the three introgressed regions (region A in chromosome 6; region B and C in chromosome 15) revealed 11 GO terms and three protein groups overrepresented in region A in chromosome 6 (14 genes) and region B in chromosome 15 (25 genes) (Table S6; Supporting Information). From the total 39 genes associated with these biological processes, four genes - including *PRR5* - were found in a genomic region showing an excess of intermediate-frequency alleles in *P. balsamifera,* and two genes, namely *NAC147* and *ANAC062*, were located in a region with signals of positive selection in both *P. balsamifera* and *P. trichocarpa* (Table 1). The signals of selection and overrepresentation of genes that may play roles in adaptive traits (e.g. RNA processing, response to far red light, ATPase activity) further supports the potential of the telomeric region of chromosome 15 in adaptive introgression. In turn, genes in the second introgressed region (C) of chromosome 15 were not overrepresented in any of the 75,000 functional terms tested.

Based on gene expression analysis in the 880-kb introgressed region B, we identified seven genes - including *TTG1* and *COMT1* - out of 134 in which the level of expression was

significantly different in admixed individuals with *P. balsamifera* haplotypes (bb and bt), compared to *P. trichocarpa* genotypes (tt) in both xylem and leaf samples (Table S7; Supporting Information). *TTG1* and *COMT1* were among the most highly expressed genes and for both the highest expression was found in those homozygous for *P. balsamifera* haplotypes (bb), followed by heterozygotes (bt), with those homozygous for *P. trichocarpa* haplotypes (tt) showing the lowest expression (Figure 6). This variation in expression, especially pronounced for *COMT1* and validated using qRT-PCR (Table S4, Figure S10; Supporting Information), suggests that introgressed alleles are functionally distinct at the level of gene expression.

In *PRR5* we found that the mean-centered FPKM from the top 25 co-expressed genes was significantly lower in *P. trichocarpa* individuals homozygous for *P. balsamifera PRR5* alleles (bb, W396W), compared to either individuals that were heterozygotes (bt, W396R), or homozygotes for *P. trichocarpa PRR5* alleles (tt, R396R) (Figure S11; Supporting Information). Thus, the introgressed W396-*PRR5* variant from *P balsamifera* may encode a functionally distinct protein with respect to its ability to regulate transcription of direct or indirect target genes in *P. trichocarpa*.

Analyses of the phenotypic variation, based on a suite of nine ecophysiology, phenology and biomass traits, some measured in multiple years (Table S8; Supporting Information), also revealed significant differences between admixed individuals with *P. balsamifera* haplotypes (bb and bt) and *P. trichocarpa* genotypes (tt). Admixed individuals with *P. balsamifera* haplotypes (bb and bt) in the first 880-kb of chromosome 15 (region B, Figure 2) exhibited higher leaf chlorophyll content across two years (2009 and 2011, Figure 6A, B), and higher leaf nitrogen content in 2009 (Figure 6C). Leaf nitrogen content was not significantly different among

genotypes in 2010, probably due to a smaller sample size; in this year some trees set bud before measurements took place (McKown, personal communication).

DISCUSSION

Our study revealed an approximately 880-kb genomic region in chromosome 15 with strong evidence for introgression from *P. balsamifera* into *P. trichocarpa* populations at higher frequencies than the genomic background, and provides evidence that this is an example of adaptive introgression. In contrast, a paralog block of duplicated genes on chromosome 12 showed no signs of introgression or signatures of selection, suggesting alternative evolutionary trajectories of these duplicated genes in *Populus*. Our analyses suggest that specific introgressed *P. balsamifera* alleles on chromosome 15 are under selection, are functionally distinct, and are correlated with the expression of adaptive traits in *P. trichocarpa* individuals that harbor them. Admixed individuals with these introgressed *P. balsamifera* haplotypes are restricted to northern and central areas of the geographical range of *P. trichocarpa,* and have been assigned to distinct climate clusters (Porth *et al.* 2015). Based on historical climate data, northern and north-central regions have significantly lower mean annual temperature (MAT: 4.2 ˚C), number of frost-free days (NFFD: 175 d), and mean annual precipitation (MAP: 744 mm) than coastal and southern regions (MAT: 9.5˚C, NFFD: 287 d, MAP 2805 mm) (Porth *et al.* 2015), suggesting potential niche differentiation between populations with and without the introgressed region.

A telomeric region on chromosome 15 is a hot spot for introgression

Local ancestry analysis revealed three introgressed regions, one of which was located in a telomeric region of chromosome 15 (region B), showed high LD levels and signals of selection in both pure species, and included several candidate genes for local adaption identified by

previous association studies (McKown *et al.* 2014) and F_{ST} outlier tests (Geraldes *et al.* 2014) (Table S3; Supporting Information). To explain these results we propose two scenarios: recent hybridization and adaptive introgression, which are not mutually exclusive.

Region B in chromosome 15 was the largest among the three introgressed regions and had LD levels higher than the genomic background, which may indicate recent admixture with insufficient time for recombination to have reduced LD within the introgressed region. The micro-evolutionary processes at work in the hybrid zone may not – or not yet – have impacted adjacent or allopatric populations of the hybridizing species (Harrison & Larson 2014), also explaining the low frequencies of introgressed alleles in candidate genes (e.g. 8.6% *COMT1*-Q287, 9.1% *PRR5*-W396) in *P. trichocarpa,* and the relatively high levels of divergence still present in parental linages (Figure S4; Supporting Information). However in pure *P. balsamifera,* the presence of haplotype blocks in the telomeric region of chromosome 15 (first 150-kb), the excess of intermediate-frequency alleles and the segregation of two distinct haplotypes, all of which could be signatures of balancing selection (Vitti *et al.* 2013), lead us to an alternative scenario: two types of haplotype blocks selected for in pure *P. balsamifera* introgressed as a modular, or cassette-like block of genes into *P. trichocarpa*, and these now underlie adaptive processes in the *P. trichocarpa* admixed individuals as well as in the *P. balsamifera* donor species.

In line with the latter adaptive introgression scenario, the telomeric region of chromosome 15: (i) is enriched for genes that may play crucial roles for survival and adaptation, such as those related to response to far red light, RNA processing and ATPase activity, (ii) contains a section (from 200 kb to 280 kb) showing signals of positive selection in both pure *P.*

balsamifera and *P. trichocarpa*, and (iii) includes introgressed alleles affecting *P. trichocarpa* phenotypes according to functional as well as phenotypic analyses.

Evidence that introgressed *P. balsamifera* alleles are functionally different from *P. trichocarpa* variants

The introgressed region B in chromosome 15 is enriched for 11 GO terms and three protein groups with overrepresentation of genes that may play crucial roles for survival and adaptation, such as those related to response to far red light, RNA processing and ATPase activity. Four of the genes associated with these biological processes, including *PRR5*, were found in a section of the introgressed region that showed signals of excess intermediate-frequency alleles in *P. balsamifera*, and two other genes (*NAC147* and *ANAC062*) were located in a region with signals of positive selection in both *P. balsamifera* and *P. trichocarpa*. A third candidate gene that showed signals of purifying selection in both pure *P. trichocarpa* and *P. balsamifera* genotypes is *COMT1*, which encodes a key phenylpropanoid enzyme. The functions of candidate genes *PRR5* and *COMT1*, and evidence for functional differentiation of introgressed alleles of *PRR5* and *COMT1*, are discussed below.

Candidate gene PRR5. The *Populus PSEUDORESPONSE REGULATOR5* (*PRR5*) in the introgressed region encodes a transcriptional regulator that is an important component of the circadian clock mechanism, based on studies in Arabidopsis (Nakamichi *et al.* 2010; Wang *et al.* 2010). In *Populus*, *PRR5* is upregulated at the onset of short days and it may play a crucial role in the timing of the onset of bud dormancy in *P. trichocarpa* (Ruttink *et al.* 2007; Ko *et al.* 2011). Furthermore, a transcriptomic analysis of an Arabidopsis *prr9*, *prr7, prr5* triple mutant suggested that these pseudo-response regulators negatively affect the expression of genes encoding enzymes associated with chlorophyll biosynthetic pathways (Fukushima *et al.* 2009).

Introgressed *PRR5 P. balsamifera* variants have a nsSNP W396 substitution located between the pseudoreceiver domain and the CCT motif, in a highly conserved 44-amino acid region shown to be essential for PRR5 transcription repressor activity in Arabidopsis (Nakamichi *et al.* 2010). This position in *P. trichocarpa* alleles, as in other *PRR* genes from other species including Arabidopsis, is usually occupied by an amino acid with a positively charged R-group (R or H). It is possible that the *P. balsamifera* W396 *PRR5* allele, with a nonpolar amino acid at that site, represses target genes in a different manner compared to common *P. trichocarpa* alleles, which instead have a polar amino acid at that site (R396). In *P. trichocarpa*, we found that the levels of expression of the top 25 genes co-expressed with *PRR5* are significantly lower in *P. trichocarpa* individuals homozygotes for *P. balsamifera PRR5* alleles (WW) compared to either individuals that were heterozygotes (WR) or homozygotes for *P. trichocarpa PRR5* alleles (RR) (Figure S11; Supporting Information). This finding suggests that the introgressed W396 protein variant is functionally distinct, since it appears to differ in its transcriptional regulatory activity in the clock-regulated gene network. Future functional studies will test the hypothesis that the PRR5 protein variants have different biochemical and/or physiological functions.

Analysis of phenotype partitioning in admixed *P. trichocarpa* individuals revealed that those with *P. balsamifera* haplotypes on the telomeric region of chromosome 15, including the *PRR5* W396 allele, showed higher chlorophyll content and higher leaf nitrogen content compared to those without *P. balsamifera* alleles (Figure 6). Previous studies in *Picea abies* (Norway spruce) (Oleksyn *et al.* 1998) and *P. balsamifera* (Soolanayakanahally *et al.* 2009) showed that higher chlorophyll and leaf nitrogen content are associated with higher photosynthetic rates, and in *P. balsamifera* these traits were also correlated with faster growth and higher carbon acquisition. In *P. trichocarpa* (McKown *et al.* 2013) and *P. balsamifera*

(Soolanayakanahally *et al.* 2009) photosynthetic rates are also positively correlated with latitude; where faster growth and higher carbon acquisition may counteract shorter growth seasons at higher latitudes. Our analysis of the genetic effects of introgressed balsam alleles on *P. trichocarpa* phenotype (higher chlorophyll and leaf nitrogen content) suggests that admixed individuals may grow and acquire carbon faster than pure *P. trichocarpa* individuals from the same provenances. Future glasshouse studies will test this hypothesis in an effort to elucidate the importance of this phenotype in *P. trichocarpa* northern populations.

Candidate gene COMT1. A second candidate gene that showed signals of purifying selection in both pure *P. trichocarpa* and *P. balsamifera* genotypes is *COMT1* (*CAFFEIC ACID 3-O-METHYLTRANSFERASE 1*), which encodes a key phenylpropanoid enzyme required for the biosynthesis of sinapyl alcohol and metabolites derived from sinapyl alcohol, and that could be involved in lignification and/or pathogen defense (Barakat *et al.* 2011). In *COMT1*, we also found evidence for functionally distinct *P. balsamifera COMT1* alleles based on gene expression differences in both leaf and xylem (Figure 6). *COMT1* expression in *P. trichocarpa* admixed individuals homozygous for *P. balsamifera* introgressed alleles (bb) is high, in tt individuals low, and in bt individuals intermediate, suggesting that *P. balsamifera* alleles are functionally different from *P. trichocarpa* alleles and have the potential to affect the phenotype of admixed individuals. In *COMT1* we found one SNP in the promoter region in tight linkage with a nsSNP (P287Q) that differentiates *P. balsamifera* from *P. trichocarpa COMT1* alleles (Figure S12; Supporting Information), and that could potentially be a cis-regulatory element causing the difference in expression.

The introgressed *COMT1* Q287 allele is restricted to northern *P. trichocarpa* populations in close proximity to contact zones (Figure 5), but is nearly fixed and under selection in *P.*

balsamifera (Figure 5). The unusual *P. balsamifera COMT1* Q287 variant - P287 was strictly conserved in all COMT homologs; Figure S8; Supporting Information - may affect the enzyme activity, with a substitution of a nonpolar amino acid (proline-P) for a polar amino acid (glutamine-Q), in a site in close proximity to conserved catalytic histidine (H) and glutamic acid (E) residues (Zubieta *et al.* 2002) (Figure S13; Supporting Information). This could result in a competitive disadvantage to individuals with introgressed Q287 alleles at lower latitudes, where both temperature and precipitation are higher. It is also possible that Q287-*COMT1* variants have lower enzyme efficacy and that an increase in gene expression is needed to overcome this change in enzyme activity. These results suggest that functional differences between *P. balsamifera* and *P. trichocarpa COMT1* alleles may contribute to differences in fitness in specific environments.

Overall, our results suggest that *PRR5* and *COMT1* are good candidate genes to explain the signals of selection found in the telomeric introgressed region B of chromosome 15, consistent with the introduction of modular, or cassette-like variation into *P. trichocarpa*, where multiple linked introgressed alleles such as *PRR5* R396W and *COMT* P287Q are associated with adaptive traits (Abbott *et al.* 2013). However, since this region comprises 134 genes, a plausible alternative scenario is that *PRR5, COMT1* and other candidate genes are hitchhiking and the actual targets (or target) of selection remain to be uncovered. Future work will be required to distinguish between these possibilities.

Introgression and functional divergence in paralogous genes

While genes within block B on the chromosome 15 telomeric region are under selection, are associated with adaptation, and have apparently adaptively introgressed into northern and central *P. trichocarpa* populations (this study; Geraldes *et al.* 2014; McKown *et al.* 2014), a highly syntenic block of paralogous duplicated genes on chromosome 12, derived from the

whole genome duplication event in the Salicoid lineage (Tuskan *et al.* 2006), showed neither evidence for introgression nor signatures of selection. This is consistent with the lack of signatures of adaptation for the chromosome 12 paralogs in previous studies (Geraldes *et al.* 2014; McKown *et al.* 2014). Interestingly, chromosome 12 paralogs - such as *TTG2* and *COMT2* - and candidate genes in chromosome 15 - such as *TTG1* and *COMT1* - have different expression patterns (Sjödin *et al.* 2009; Hefer *et al.* 2015). For example, while the expression pattern of the *COMT2* paralog on chromosome 12 clearly implicates this gene in developmental lignification (Barakat *et al.* 2011), the chromosome 15 paralog *COMT1* is not highly expressed in developing xylem, but is strongly induced by herbivory (Barakat *et al.* 2011). These data suggest potential sub- and/or neo-functionalization of paralogs on chromosomes 15 and 12, which may have facilitated the co-opting of certain chromosome 15 paralogs for new roles in adaptation. A plausible scenario is that further microevolution of chromosome 15 paralogs such as *COMT1*, *PRR5*, and *TTG1* contributed to local adaptation in *P. balsamifera*, and that such alleles subsequently introgressed into *P. trichocarpa* populations, adapting them to transitional environments at the northern and north-central extremes of this species' range.

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Data Accessibility

All raw whole genome sequencing data and alignment information has been deposited on SRA (Accession: PRJNA276056; ID: 276056) available at this link: http://www.ncbi.nlm.nih.gov/sra/?term=PRJNA276056. All RNA-seq data has been deposited in the NCBI under Bioproject ID 300564, available at this link: http://www.ncbi.nlm.nih.gov/bioproject/300564.The input files and data used in all the analyses have been archive in dryad: doi:10.5061/dryad.0817m (see Supporting Information: Materials and Methods).

Author Contributions

AS-G, CJD and CL designed the study, with input from QCBC. AS-G performed the research and analyzed data with assistance from CC (RASPberry analysis) and OC (gene co-expression network analysis). CH performed SNP calling and RNA-seq bioinformatics analyses. CJD, QCBQ, and CL provided funding. All authors contributed to writing the manuscript and approved the final version.

Tables

Table 1. List of three introgressed regions (A, B, C – see Figure 2) from *P. balsamifera* in *P. trichocarpa* in chromosome (Chr) 6 and 15. Genes in region B with signals of selection, and associated with enriched GO terms (11) and protein groups (3) are shown.

Chr	Region	Genomic coordinates		# of Genes	Genes under selection and associated with enriched GO terms
		start	end		
6	A	3360000	3940000	67	
15	B	0	880000	134	Potri.015G000200 § Potri.015G001200 § Potri.015G002200 § Potri.015G002300 § Potri.015G002900 ¶ Potri.015G004100 ¶
15	C	13340000	13920000	84	

§ Genes showing relatively high levels of Tajima's D.
¶ Genes showing signals of positive selection (alpha).

Table 2. Alpha estimates for three introgressed *P. balsamifera* regions in *P. trichocarpa*, one in chromosome (Chr) 06 (region A) and two in chromosome 15 (B and C).

Chr	Region	Species	# of Genes	alpha	CI
6	A	*P. balsamifera*	67	0.16	-0.6286
		P. trichocarpa	67	0.16	-0.6271
15	B	*P. balsamifera*	128	-0.47	-1.3095
		P. trichocarpa	128	-0.38	-1.29
15	B†	*P. balsamifera*	14	0.41	0.1285 - 2.5087*
		P. trichocarpa	14	0.46	0.1625 - 2.2363*
15	C	*P. balsamifera*	83	NA	NA
		P. trichocarpa	83	NA	NA

CI: Bootstrap confidence intervals.
† Genomic region with lowest levels of nucleotide diversity (p) in P. balsamifera (< the bottom 5% of the distribution).
* alpha estimate significantly different from zero.
NA: No polymorphism data; alpha is undefined.

Figures

Figures

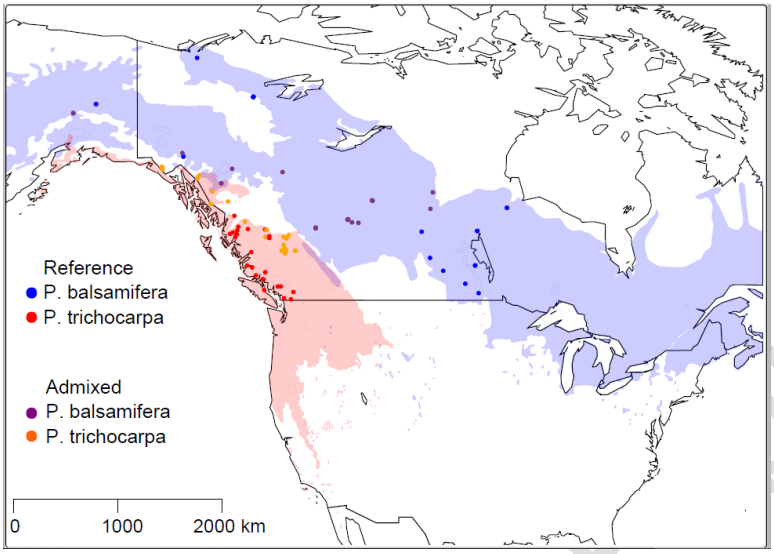

Figure 1. Geographic distribution of admixed and reference individuals used in local ancestry analysis across the contact zones between *P. trichocarpa* and *P. balsamifera*. Ranges of *P. trichocarpa* and *P. balsamifera* are shown in red and blue, respectively (Little 1971).

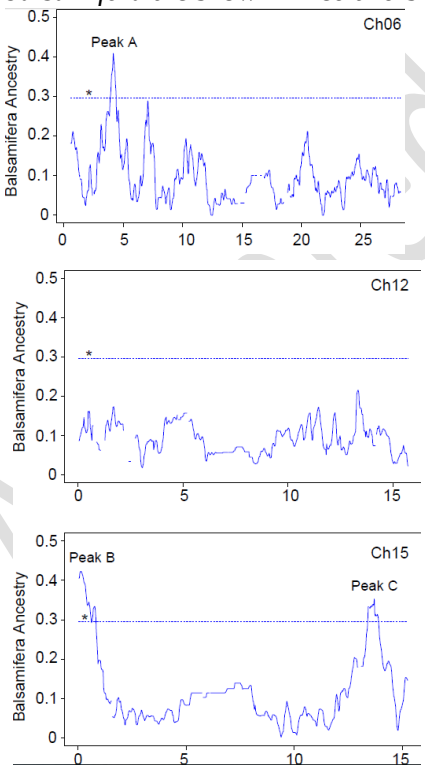

Figure 2. Proportion of *P. balsamifera* ancestry in admixed *P. trichocarpa* individuals across chromosomes 6, 12, and 15 based on sliding window analysis (size: 100-kb, step: 20-kb). Introgressed regions – peaks A, B, C -have *P. balsamifera* ancestry higher than 3 standard deviations from the weighted mean across chromosomes 6, 12 and 15 based on SNP density per window (broken line). Asterisks represent the chromosomal position of candidate genes: *FAR1* (Potri.006G020600) and *FHY3* (Potri.006G020700) in chromosome 6, and *COMT1* (Potri.015G003100), *TTG1* (Potri.015G002600), *PRR5* (Potri.015G002300) *ANAC062* (Potri.015G004100) in chromosome 15. In chromosome 12, the asterisk represents the position of the *COMT1* paralog, *COMT2* (Potri.012G006400).

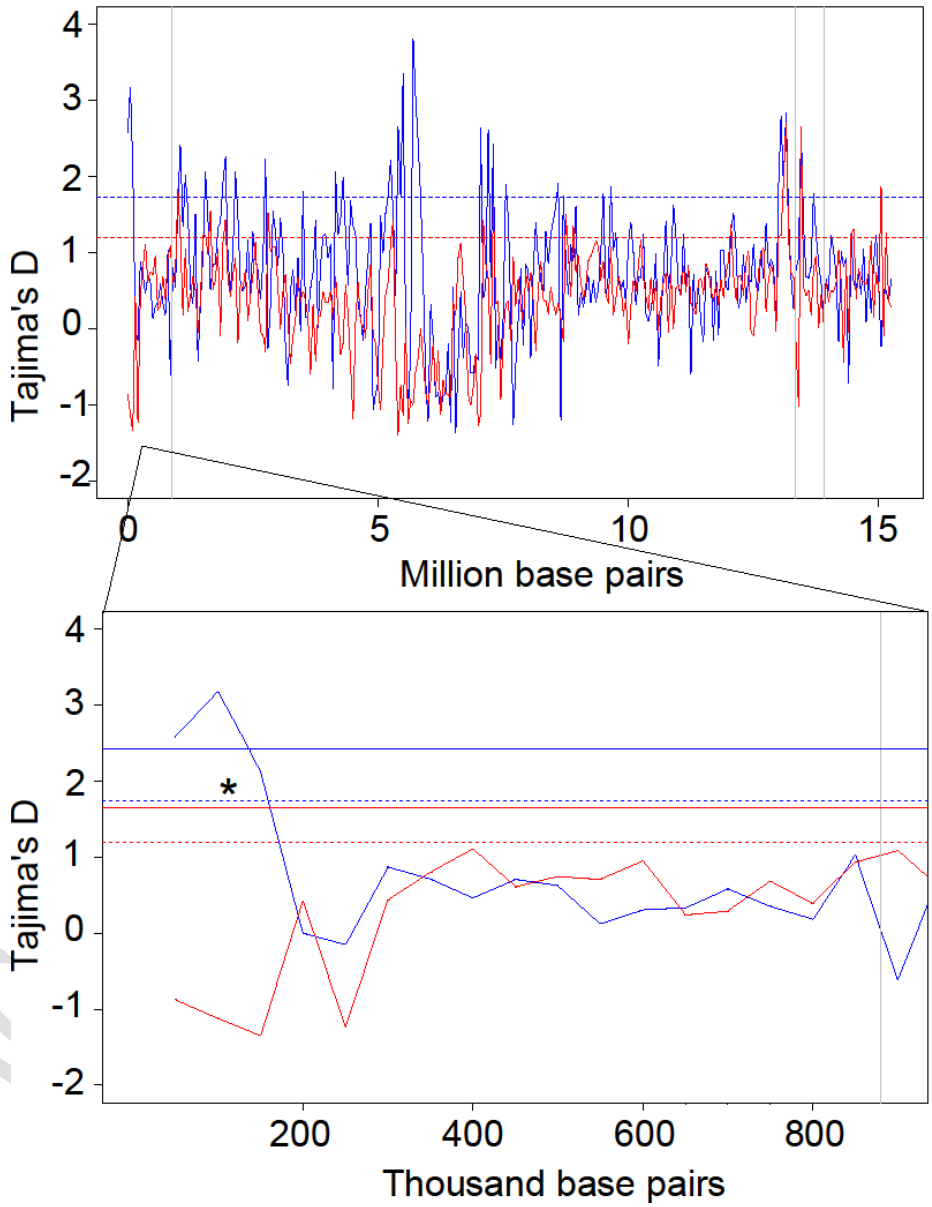

Figure 3. Tajima's D analysis across chromosome 15 in *Populus balsamifera* and *P. trichocarpa* individuals calculated in 50-kb windows. (Top) Tajima's D values across chromosome 15 are represented by blue and red continuous lines for *P. balsamifera* and *P. trichocarpa* respectively, and introgressed regions B and C are shown (see Figure 2). Values representing the top 95% of the distribution are shown in blue and red dashed lines for *P. balsamifera* and *P. trichocarpa* respectively; (Bottom) Tajima's D values in introgressed regions B of chromosome 15 (telomeric region from 0 to 880-kb) with straight solid blue and red lines representing the top 99% of the distribution for *P. balsamifera* and *P. trichocarpa* respectively. The Asterisk represents the chromosomal position of candidate gene *PRR5* (Potri.015G002300).

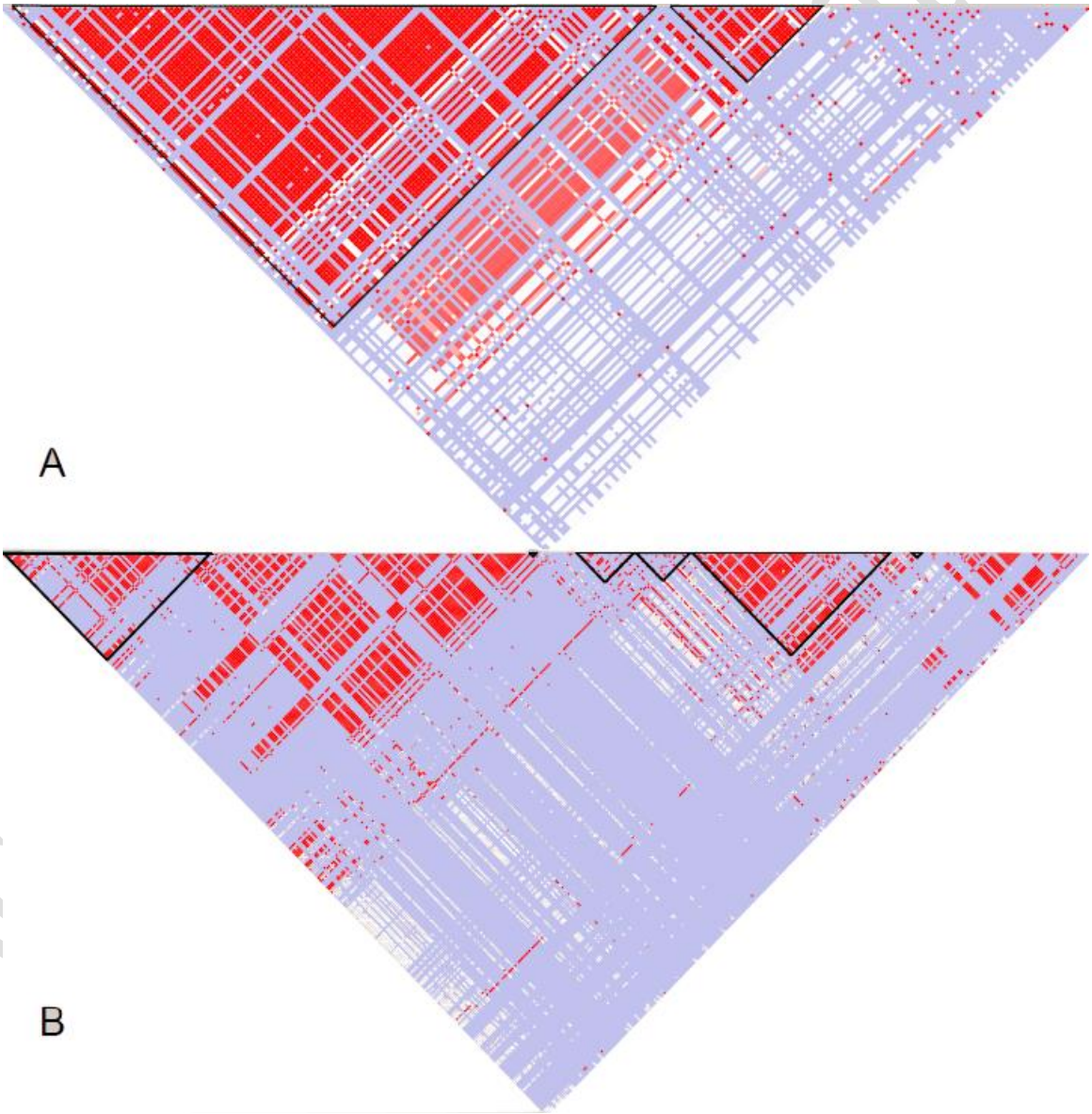

Figure 4. Linkage disequilibrium (LD) plot of the first 200-kb of chromosome 15 introgressed region in pure *P. trichocarpa* (B) and *P. balsamifera* (A). Red areas represent pairs of SNPs with high levels of LD (D'=1, LOD ≥2) and blue areas represent pairs of SNPs with LD comparisons with a low estimation confidence (LOD < 2). Dark triangles represent haplotype blocks based on Gabriel et al. (2002). In *P. balsamifera* a haplotype block at the start of chromosome 15 extends 130 -kb but in *P. trichocarpa* it extends to only 38-kb.

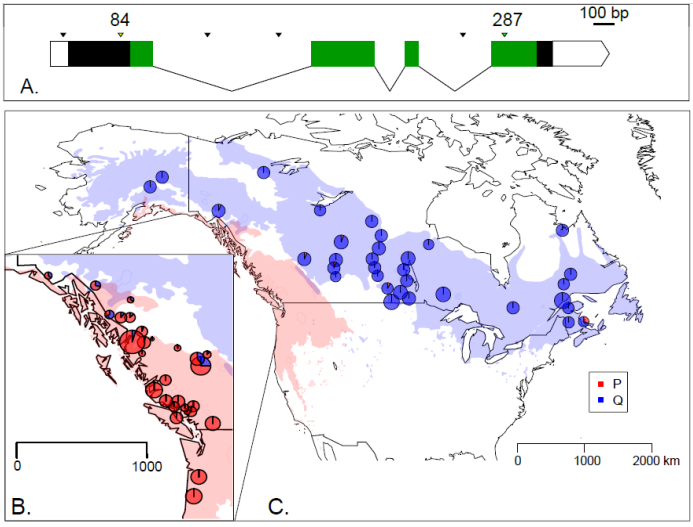

Figure 5. *COMT1* alleles and geographic distribution in *P. trichocarpa* and *P. balsamifera* populations. (A) Gene model of *COMT1* with arrows depicting SNPs with the top Fst values in the coding region, which were higher than the 99th percentile of the genome wide distribution (0.18) based on a previous analysis (Geraldes *et al.* 2014). The green arrow shows *nsSNP* P287Q (F_{ST}=0.23), the yellow arrow represents sSNP A84 (F_{ST}= 0.3) and black arrows depict SNPs in the non-coding region (5'UTR and introns). (B) Geographic distribution of *COMT1* haplotypes from 28 drainages in *Populus trichocarpa*, based on the nsSNPs with the highest Fst value (P287Q). (C) Geographic distribution of COMT1 haplotypes from 46 drainages in *P. balsamifera. P. balsamifera* individuals with P287 *COMT1* alleles (easternmost population) are admixed with *P. deltoides* (Geraldes *et. al.,* In preparation)

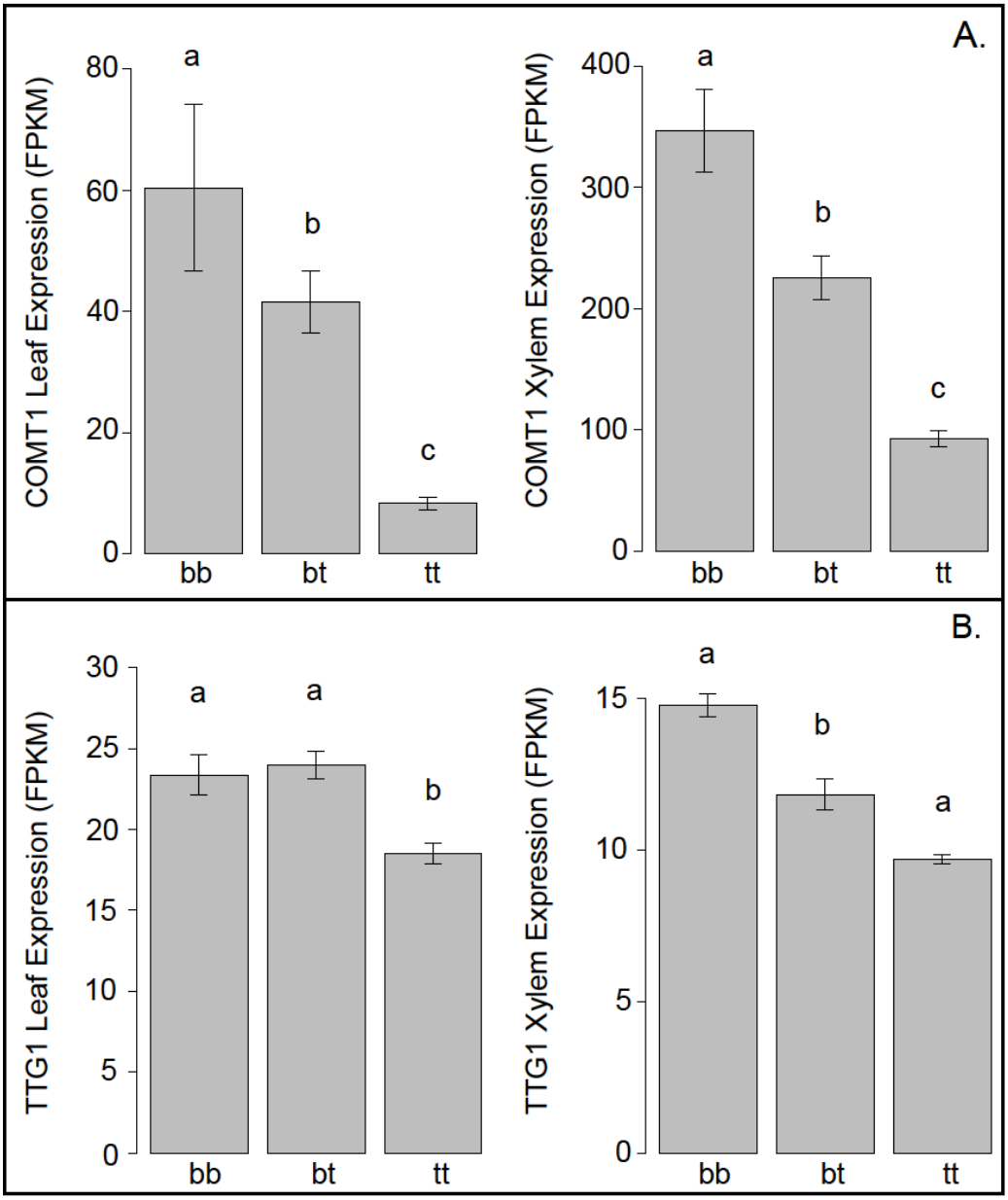

Figure 6. *COMT1* (A) and *TTG1* (B) gene expression levels in leaf and xylem of *P. trichocarpa* individuals with different haplotypes for introgressed region B from *P. balsamifera*. Gene expression is presented as FPMK (Fragments Per Kilobase of transcript per Million mapped reads) based on RNAseq data. Genotypes are based on the first 880-kb of chromosome 15 (see Figure 2): bb, homozygotes for the *P. balsamifera* introgressed region B [six samples from three genotypes]; bt, individuals heterozygous for the introgressed region [10 samples from five genotypes]; tt, individuals homozygous for *P. trichocarpa* haplotypes in the same region [65 samples from 24 genotypes]. The standard error (SE) within each genotypic class (bb, bt, tt) is represented by the bars. Shared letters above columns indicate that the average gene expression levels were not significantly different between those genotypes ($p<0.05$).

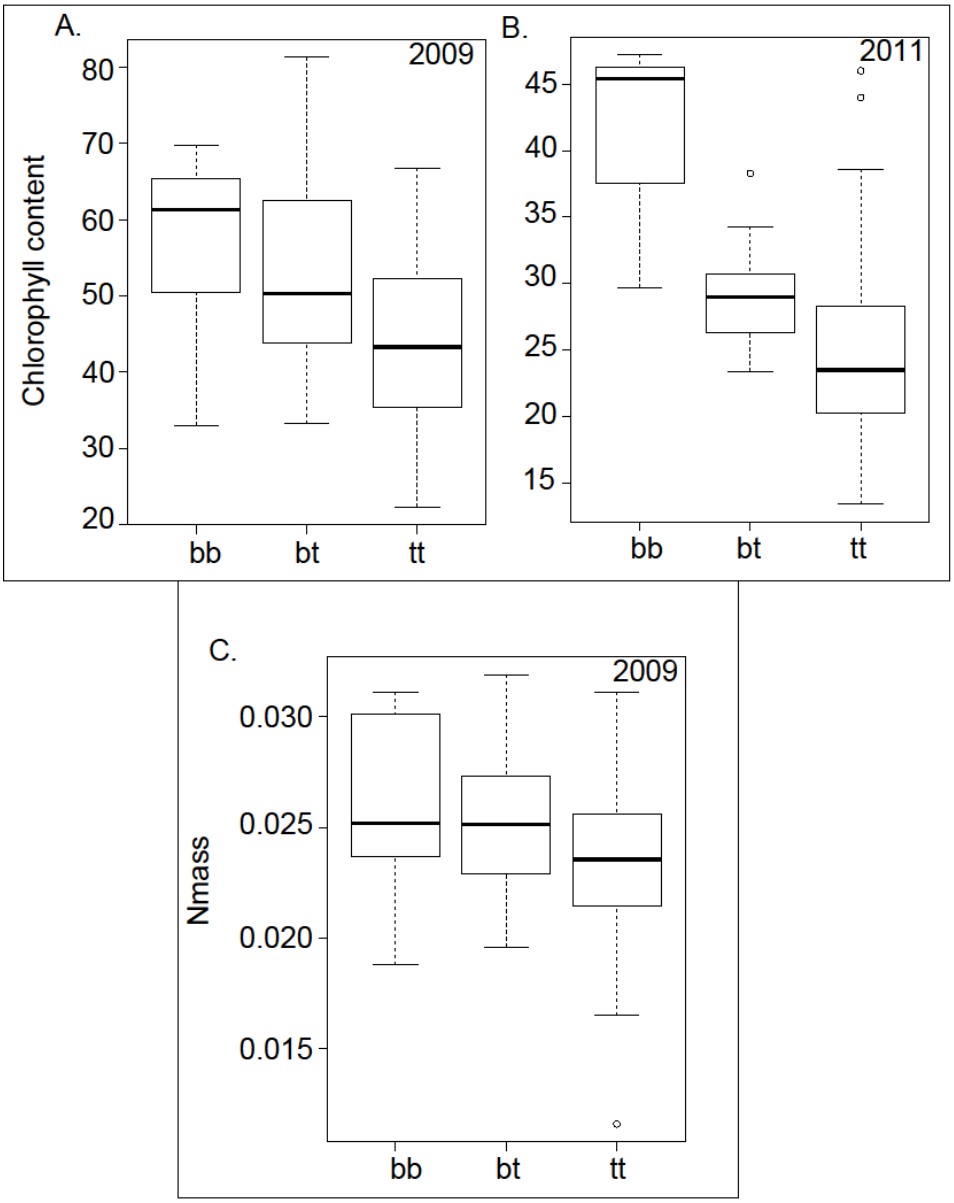

Figure 7. Boxplot diagrams depicting leaf chlorophyll content and leaf nitrogen content in *P. trichocarpa* individuals from northern and interior locations, with different haplotypes for introgressed region B from *P. balsamifera* (first 880-kb of chromosome 15, see Figure 2). bb, homozygotes for the *P. balsamifera* introgressed region B; bt, individuals heterozygous for the introgressed region; tt, individuals homozygous for *P. trichocarpa* haplotypes in the same region. (A) leaf chlorophyll content measured in 2009 [sample size: tt = 73, bt = 20, bb = 7], (B) leaf chlorophyll content measured in 2011 [tt = 47, bt = 9, bb = 3], (C) leaf nitrogen content measured in 2011 [tt = 100, bt = 30, bb = 8]. Each box shows the lower quartile, median and upper quartile values and the whiskers show the range of the phenotypic variation. Chlorophyll

content units are in Chlorophyll Concentration Index (CCI), and shared letters above columns indicate when differences between genotypes were not significant ($p<0.05$). Data from (McKown *et al.* 2013).

Supporting information: Figures and Tables

List of Supporting Figures

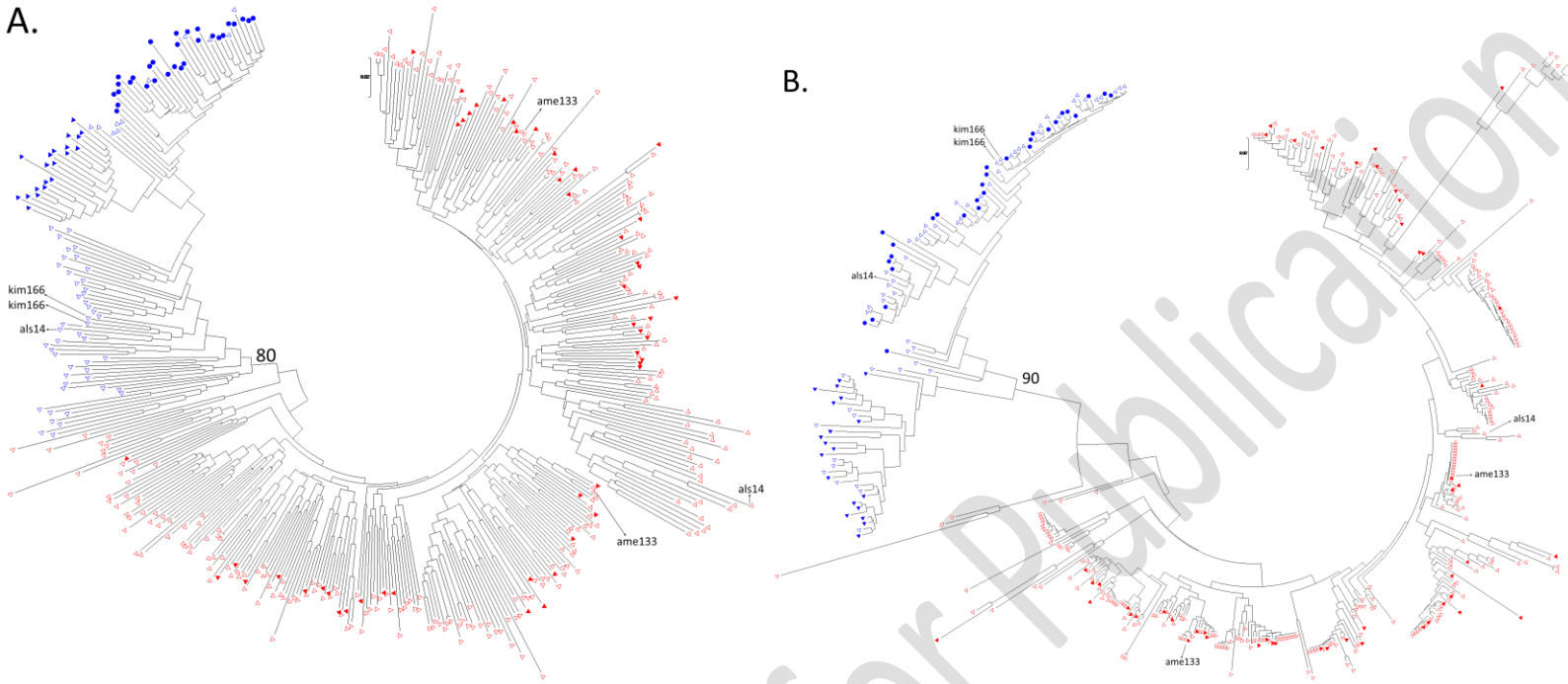

Figure S1. Neighbor-Joining (NJ) trees of 25 pure *P. balsamifera*, 25 pure *P. trichocarpa*, and 146 additional *P. trichocarpa* individuals from phased SNPs of an introgressed region of chromosome 15. (A) Tree based on the first 880 kb chromosome 15. (B) Tree based on the first 300 kb of chromosome 15. Pure *P. trichocarpa* accessions are shown by filled red triangles, pure *P. balsamifera* accessions are shown by filled blue triangles and circles and additional *P. trichocarpa* individuals accessions from northern and central regions of the range are shown by open blue or red triangles. The cluster of *P. balsamifera* haplotypes (open and filled blue triangles) had strong support in (A) and (B). The accession codes for haplotypes from three representative individuals are shown: one homozygote (bb) for *P. balsamifera* haplotypes (kim166), one heterozygote (bt; als14) and one homozygote (tt) for *P. trichocarpa* haplotypes (ame133). The NJ analyses were conducted in MEGA6.

Since we did not have information about the local ancestry patterns for all the 146 genotypes (in RASPberry we only included 36 *P. trichocarpa* admixed individuals), we used the phased introgressed region of chromosome 15 from all *P. trichocarpa* genotypes (146) as well as from the reference panel of individuals and implemented a NJ tree analysis - 1000 bootstrap replicates in MEGA (Tamura *et al.* 2007). These NJ trees, based on either the entire 880-kb chromosome 15 region B (A) or a smaller 300-kb portion at the start of the B region (B), revealed a well-defined cluster (bootstrap values: 80 and 99 based on 880-kb and 300 kb regions respectively) where haplotypes from pure *P. balsamifera* individuals grouped with haplotypes from admixed *P. trichocarpa* individuals. Based on these trees we identified eight genotypes homozygous for *P. balsamifera* haplotypes (bb: both haplotypes of the individual were found inside the *P. balsamifera* cluster), 32 heterozygous genotypes (bt: only one haplotype was found inside the *P. balsamifera* cluster) and 104 genotypes homozygous for *P. trichocarpa* haplotypes (tt: none of the haplotypes were inside the *P. balsamifera* cluster).

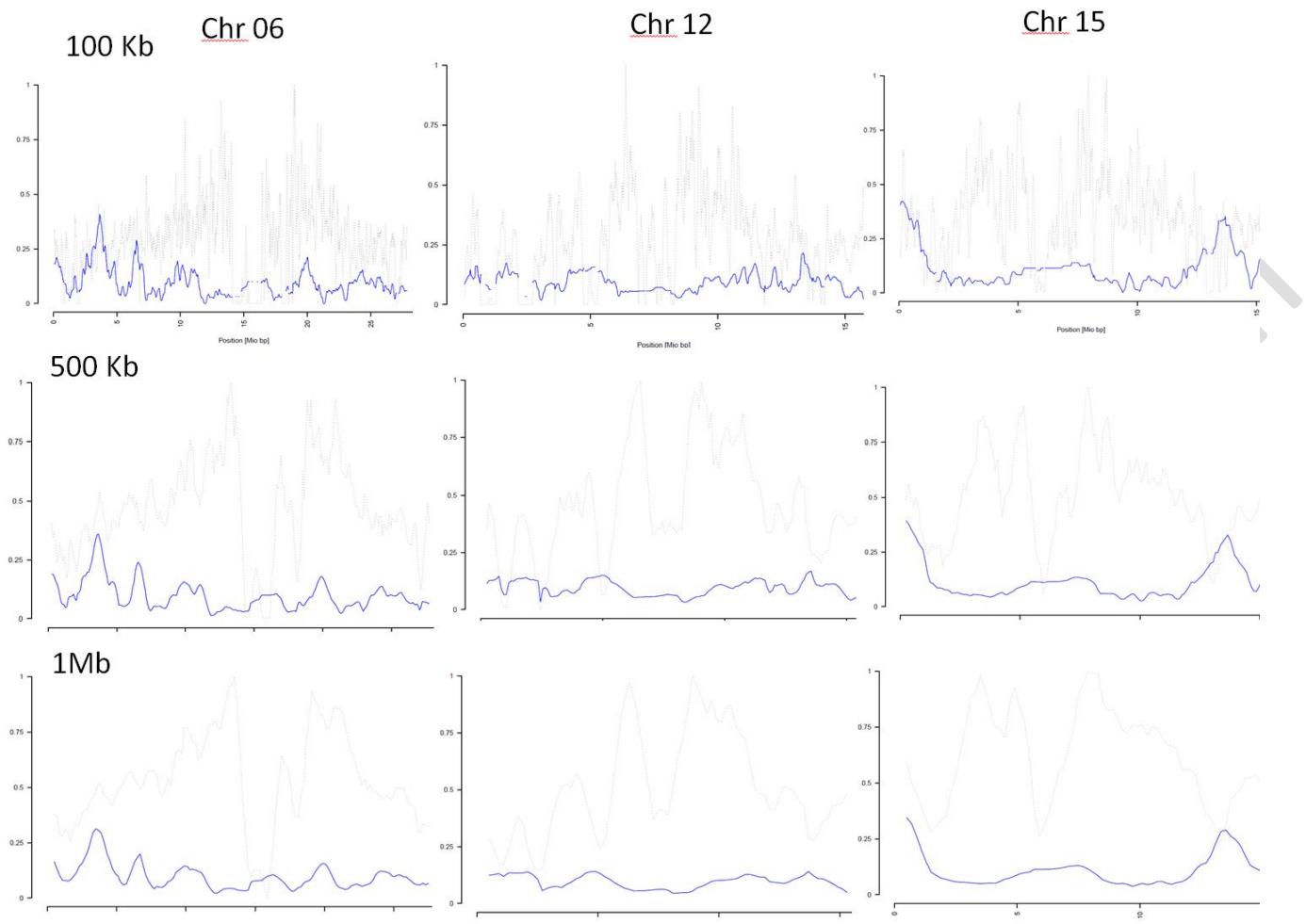

Figure S2. Proportion of *P. balsamifera* ancestry in admixed *P. trichocarpa* individuals analyzed in three sliding window sizes. *P. balsamifera* ancestry across (blue lines) chromosome 6, 12 and 15 is shown in three sliding window analyses (sizes: 100kb, 500kb and 1Mb with steps: 20kb, 100kb, 200kb respectively). Grey broken lines represent SNP density per window.

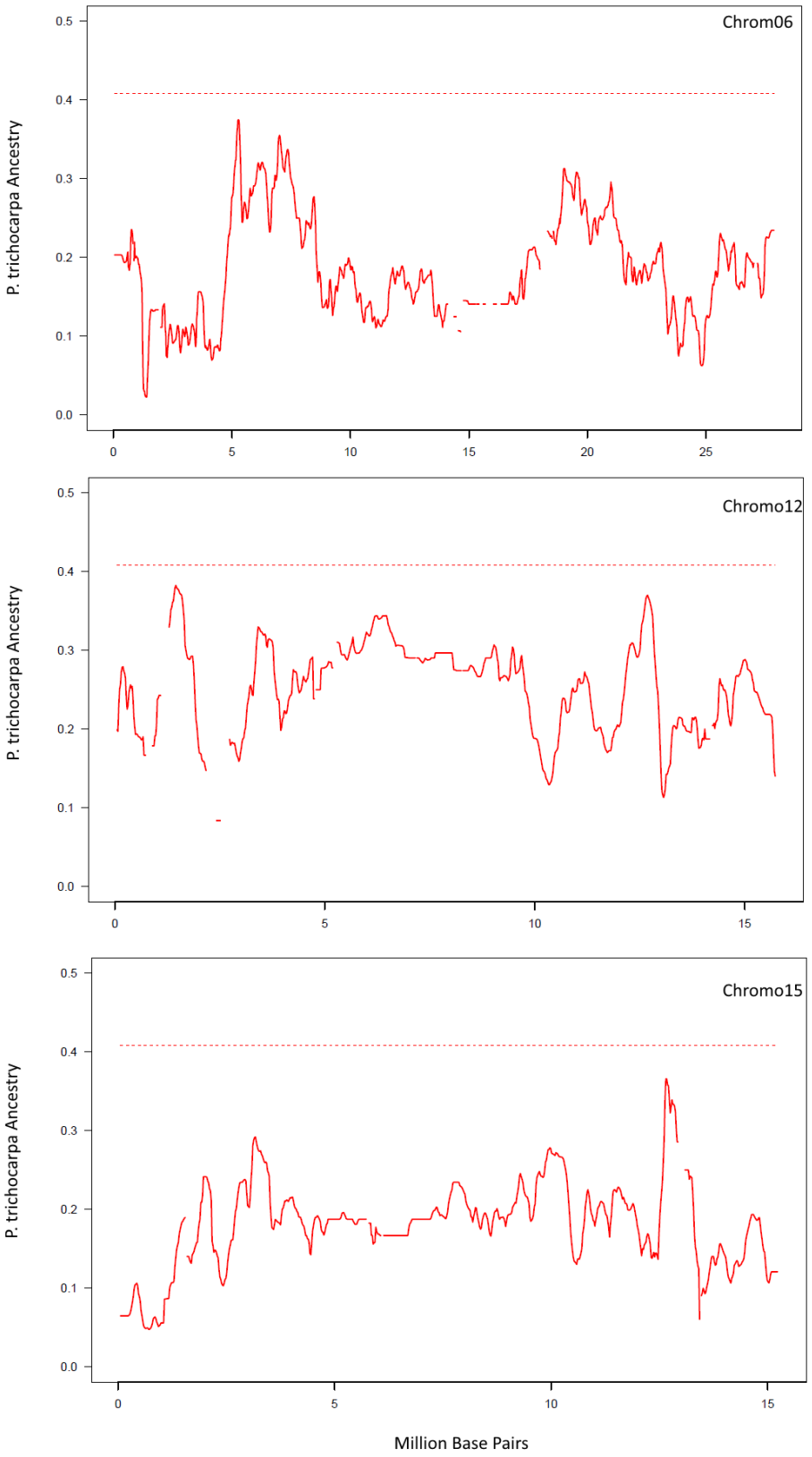

Figure S3. Proportion of *P. trichocarpa* ancestry in admixed *P. balsamifera* individuals across chromosomes 6, 12, and 15. Solid line: admixture in chromosomes 6, 12, and 15 based on sliding window analysis (size: 100kb, step: 20kb). Broken line: 3 standard deviations from the weighted mean across chromosomes 6, 12 and 15 based on SNP density per window.

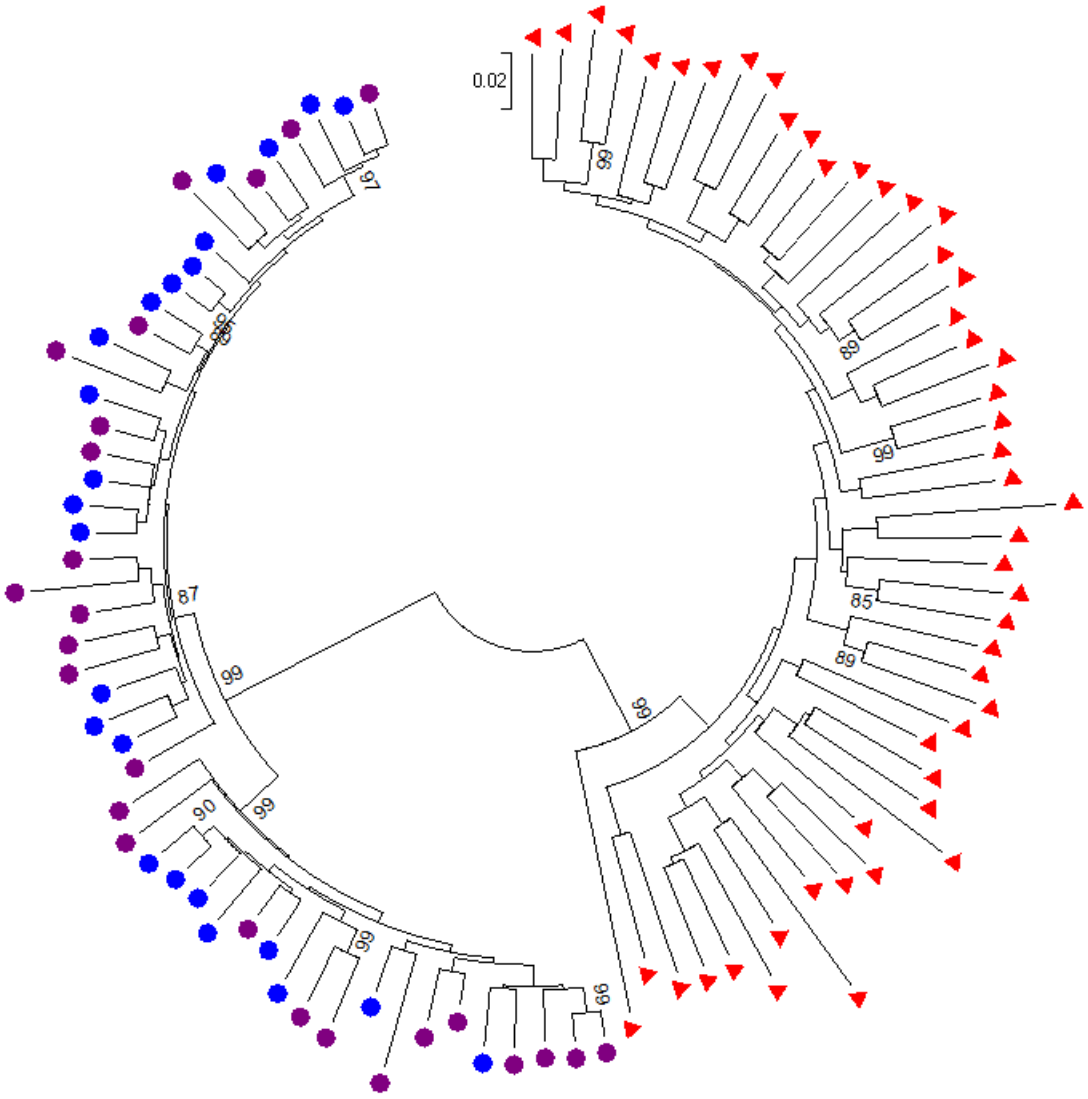

Figure S4. Neighbor-Joining (NJ) tree of parental linages based on the first 880 kb of chromosome 15. 25 *P. trichocarpa* accessions are shown in red and 25 *P. balsamifera* are shown in blue and purple. Branch lengths represent genetic distances using the p-distance method. For *P. balsamifera*, blue represents haplotypes from populations in the northwestern parts of the range and purple represents haplotypes from central populations. The NJ analysis was conducted in MEGA6.

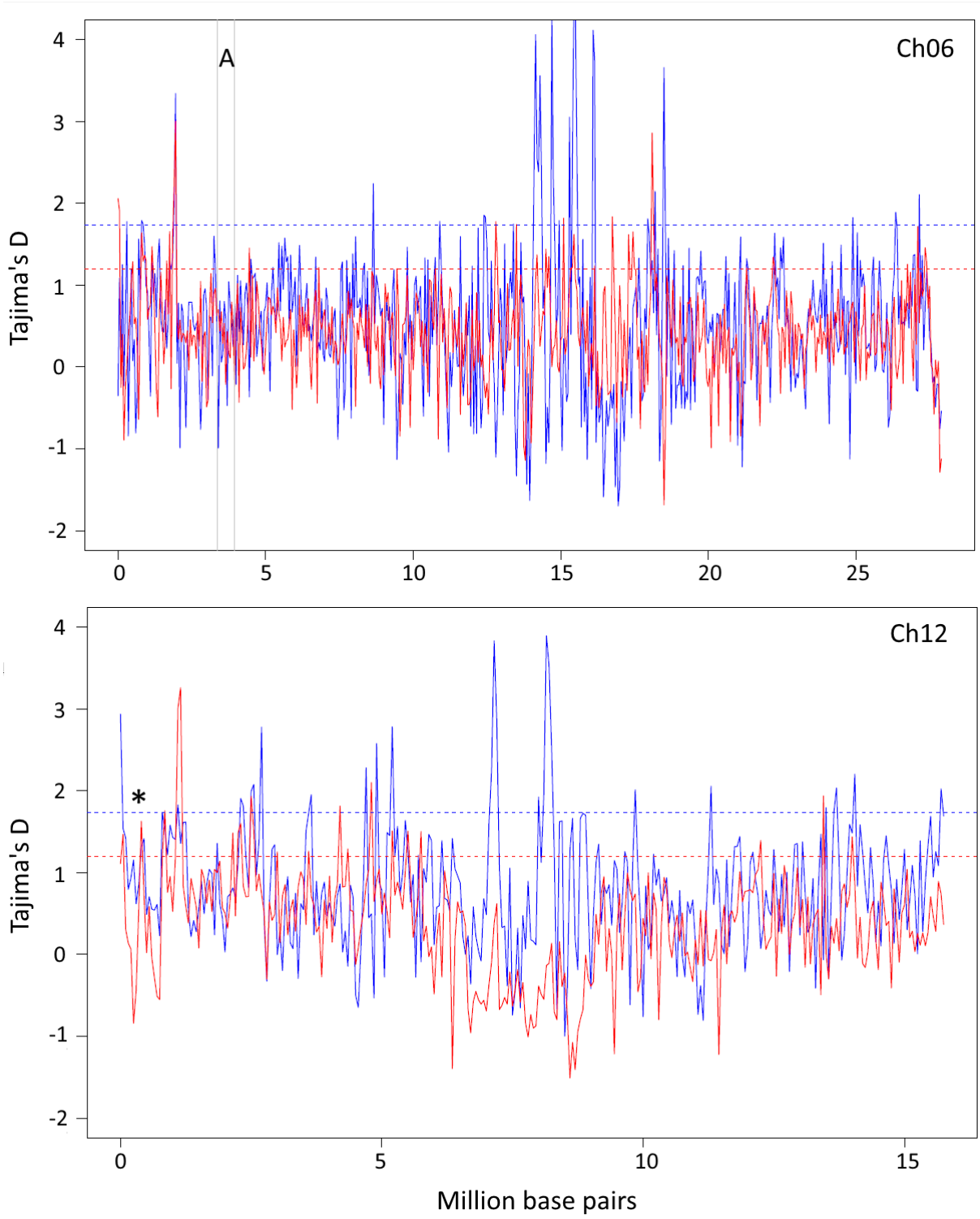

Figure S5. Tajima's D analysis in pure *P. balsamifera* and *P. trichocarpa* individuals in chromosome 6 and 12 based on 50-kb windows. *P. balsamifera* and *P. trichocarpa* Tajima's D values are represented by blue and red continuous lines respectively. The introgressed region in chromosome 6 is depicted by letter A; the paralog region of region B of chromosome 15 in chromosome 12 is represented by an asterisk (*) (see Figure 2 for details). Tajima's D values representing the 95% of the distribution are shown in blue and red broken lines for *P. balsamifera* and *P. trichocarpa* respectively.

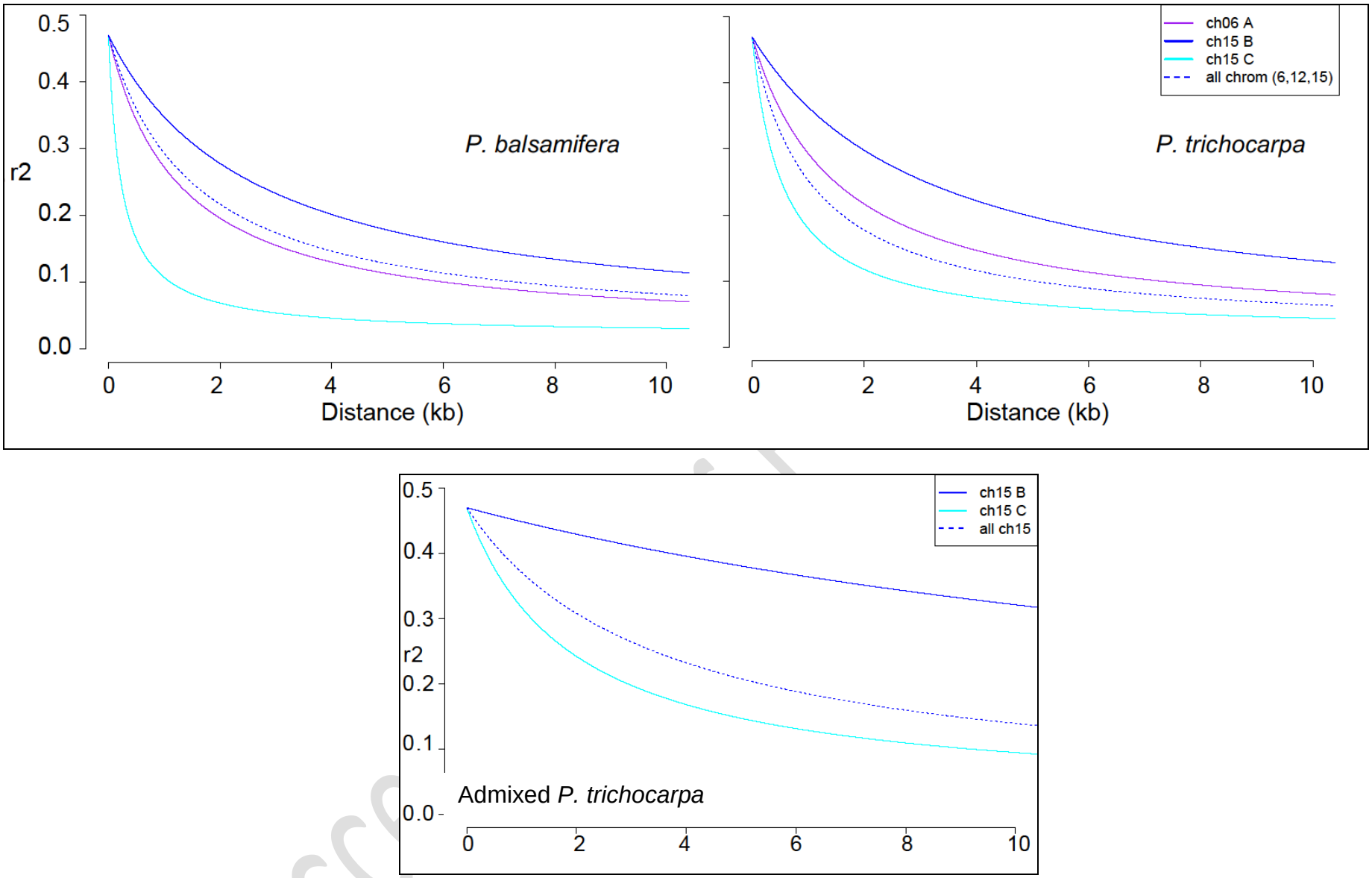

Figure S6.Top: Linkage disequilibrium (LD) decay with distance in *P. balsamifera* and *P. trichocarpa* based on single-nucleotide polymorphisms (SNPs) across three chromosomes (6, 12, 15 – dotted line) and three introgressed regions (region A in chromosome 6 – purple, region B in chromosome 15 – blue, region C in chromosome 15 – cyan). Bottom: LD decay with distance in a set of admixed *P. trichocarpa* individuals (see Supplementary M&M) based on SNPs across chromosomes (15 – dotted line) and two introgressed regions in chromosome 15 (region B– blue, region C– cyan).

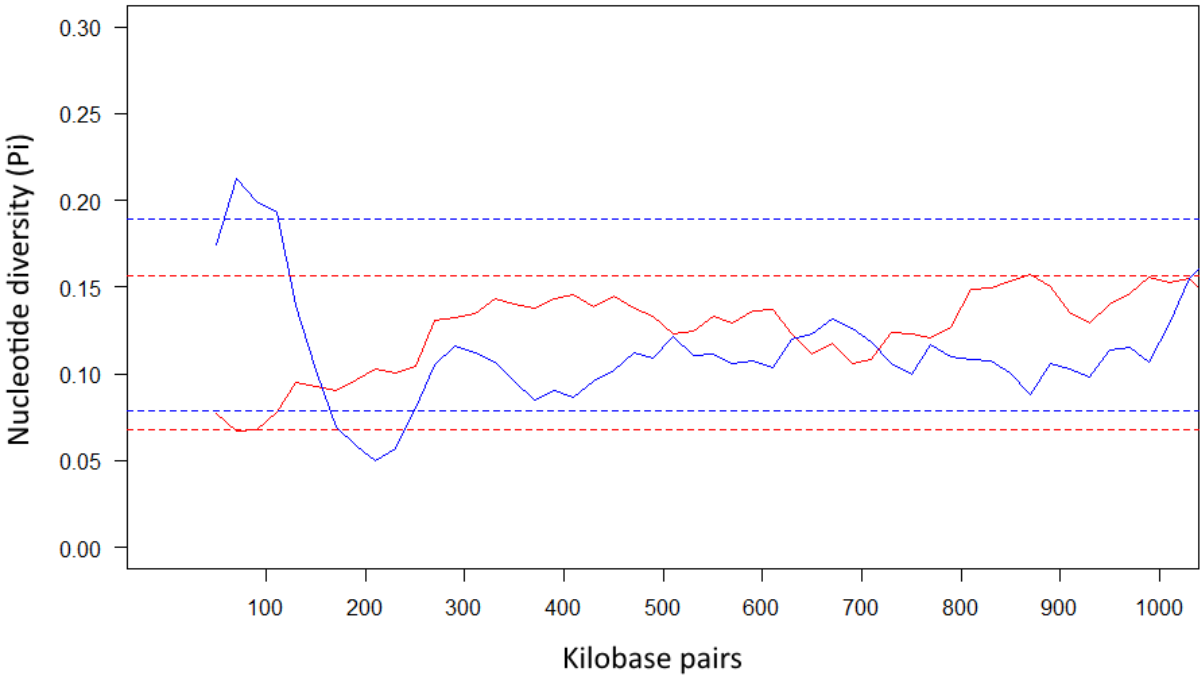

Figure S7. Nucleotide diversity (π) levels across the first 1 MB of chromosome 15. π was assessed in sliding windows (size: 100kb, step: 20kb) in pure *P. balsamifera* (blue continuous line) and pure *P. trichocarpa* (red continuous line) individuals. In admixed *P. trichocarpa* individuals, the first 880kb of chromosome 15 showed signals of introgression from *P. balsamifera*. Nucleotide diversity values representing the 95% and 5% of the distribution are shown in blue and red broken lines for *P. balsamifera* and *P. trichocarpa* respectively.

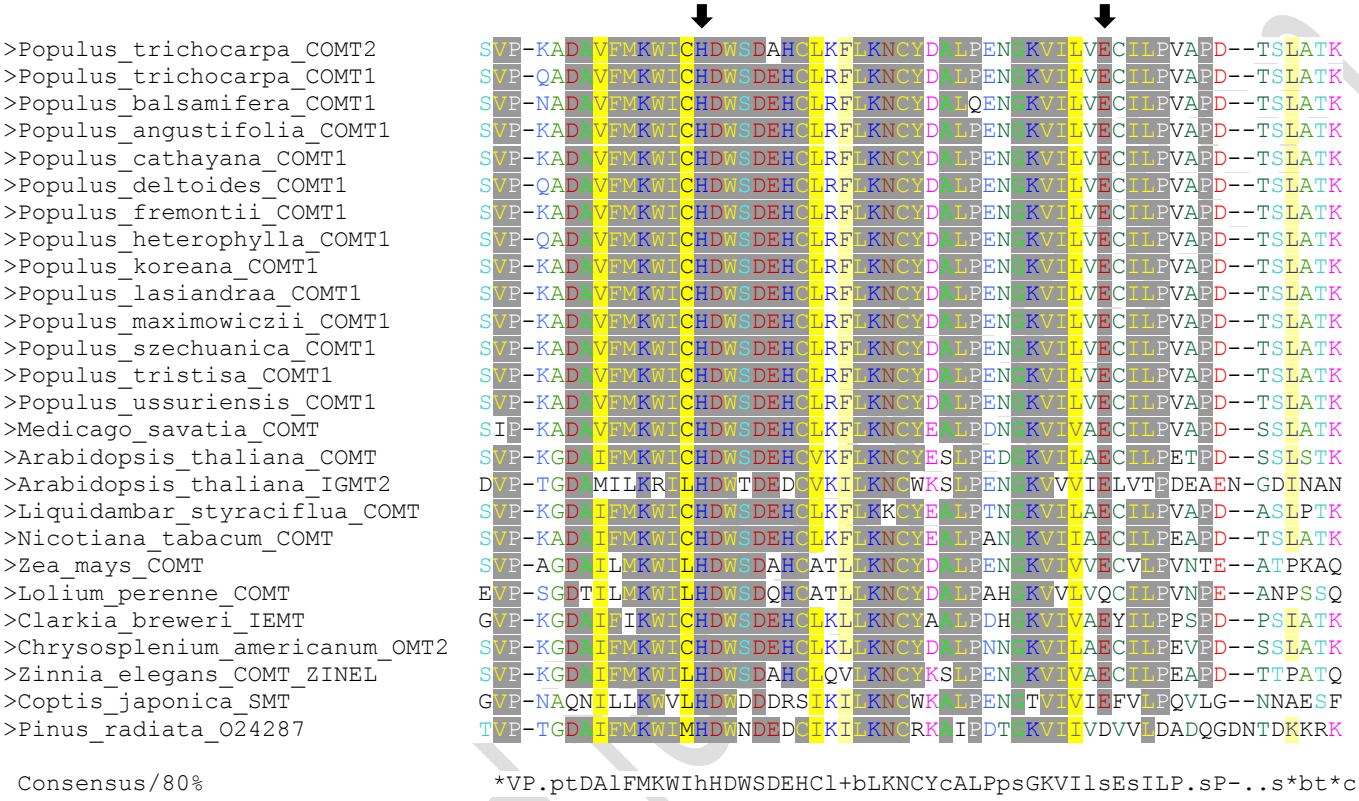

Figure S8. Partial protein alignment of different COMT1 homologs. All *P.* data were obtained from whole genome resequencing of the species indicated (Cronk et al., unpublished); other sequences are from Phytozome (http://www.phytozome.net). The alignment figure was created using CHROMA (http://www.llew.org.uk/chroma/). The star indicates the position of the Q287 variant in the *P. balsamifera* COMT1 sequence, a position occupied by a P287 in all other COMT sequences analyzed (indicted by red P in the consensus amino acid sequence). The arrows represent theconserved catalytic histidine (H) and glutamic acid (E) residues identified by Zubieta et al. (2002).

Figure S9. *TTG1* and *PRR5* alleles and geographic distribution of haplotypes in *P. trichocarpa* populations. Gene models and of *TTG1* (A) and *PRR5* (C) are shown with arrows depicting SNPs with the highest F_{ST} values across each whole gene sequence (top six). Yellow arrows represent synonymous SNPs, green arrows represent non \synonymous SNPs and black arrows depict SNPs in the non-coding region (UTRs and introns). Geographic distribution of *TTG1* (B) and *PRR5* (D) haplotypes from 28 drainages in *P. trichocarpa*, based on the SNPs with the highest F_{ST} values in the coding region. In *TTG1* (B) the highest F_{ST} values in the coding region was for two sSNP (L238, L323, F_{ST}= 0.25) with alleles restricted to the north and interior. In *PRR5* (D), the highest F_{ST} value in the coding region was for one nsSNP (R396W, F_{ST}=0.24).

Figure S10. Relative gene expression (based on 2–ΔCT) of *COMT1* among *P. trichocarpa* individuals with different *COMT1* alleles

Figure S11. Box plot of the mean-centered FPKM values for the expression of the top 25 genes co-expressed with PRR5 in xylem. Genes had Pearson coexpression coefficients of > 0.66 with PRR5 across 389 samples. Data is from *P. trichocarpa* individuals homozygotes for *P. balsamifera PRR5* alleles (WW), heterozygotes (WR) and homozygotes for *P. trichocarpa PRR5* alleles (RR). ANOVA revealed a significantly lower expression in WW individuals compared to either WR or RR individuals ($p<0.05$). Top 25 genes coexpressed with PRR5 (PCC > 0.66): Potri.001G205800; Potri.002G178200; Potri.003G194000; Potri.004G177000; Potri.004G217600; Potri.006G004700; Potri.006G067700; Potri.006G143300; Potri.006G184800; Potri.006G279900; Potri.007G050100; Potri.008G004300; Potri.008G077100; Potri.008G206300; Potri.009G015000; Potri.009G137200; Potri.010G086700; Potri.011G043200; Potri.011G082600; Potri.012G003700; Potri.012G005900; Potri.012G082600; Potri.013G046300; Potri.018G107000; Potri.018G129700.

Figure S12. LD plot of *COMT1* in individuals from northern and central parts of *P. trichocarpa's* range. Red diamonds represent pairs of SNPs with high levels of LD (D'=1, LOD ≥2). Green triangle represents nsSNP P287Q; purple triangle represent site 240301 (*P. trichocarpa* version 3 - v3.0 genome) in the intergenic region upstream of the 5'UTR region. Asterisk (*) represent LD between these two sites (D'=1; r^2=1). Red areas represent pairs of SNPs with high levels of LD (D'=1, LOD ≥2) and blue areas representing pairs of SNPs with LD comparisons with a low estimation confidence (LOD < 2). Dark triangles represent haplotype blocks based on Gabriel et al. (2002).

Figure S13. Three-dimensional protein model of *P. trichocarpa* COMT1 based on template 1KYW. The homology model (in blue) was constructed using UCSF Chimera (http://www.cgl.ucsf.edu/chimera/) interface and Modeller based on template 1KYW (in beige) (Zubieta *et al.* 2002).

References:

Tamura K, Dudley J, Nei M, Kumar S (2007) MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) Software Version 4.0. *Molecular Biology and Evolution,* 24, 1596-1599.

Zubieta C, Kota P, Ferrer J, Dixon RA, Noel JP (2002) Structural Basis for the Modulation of Lignin Monomer Methylation by Caffeic Acid/5-Hydroxyferulic Acid 3/5-O-Methyltransferase. *The Plant Cell,* 14, 1265-1277.

List of Supporting Tables

Table S1. List of *P. trichocarpa* and *P. balsamifera* accessions used in this study and biogeographical data (latitude, longitude, elevation). Data generated by this study is highlighted in orange (i.e.SNPs for local ancestry analysis, RASPberry; and gene sequence analysis. See M&M and Supplementary Figure 2). Data previously published is highlighted in blue (i.e. phenotypic data, McKown et at. 2013, DOI: 10.1111/nph.12601, S2 in nph12601-sup-0002-TablesS1-S8.xlsx) and that in preparation is highlighted in purple (RNA-seq, O. Corea, S. Biswas et al., preparation; PCA and preliminary RASPberry analysis, Geraldes et al in preparation)

Table S2. Parameters for the RASPberry model with the highest log likelihood value, based on a whole genome SNP data set (see supplementary M&M) in 25 pure P. balsamifera, 25 pure *P. trichocarpa* and 68 admixed individuals.

Table S3. Candidate genes for local adaptation across P. trichocarpa's range, in chromosome 6 and 15 based on FST outlier tests and/or association analysis with environmental variables and phenotypic traits (Geraldes et al. 2014; McKnown et al. 2014), and using a 34k SNP chip.

Table S4. Quantitive reverse transcription PCR (qTt-PCR) to test the levels of expression of COMT1 genes in different *P. trichocarpa* genotypes

Table S5. List of genes in introgressed region from chromosome 6 and 15 based on local ancestry analysis in RASPberry.

Table S6. A Introgressed genes from *P. balsamifera* in *P. trichocarpa* in a telomeric region of chromosome 15, corresponding Arabidopsis ortholog gene code, GO term or protein group enriched in the introgressed regions, Tajima's D values higher than 99% of the distribution, genes with significant positive values of alpha and nucleotide diversity values higher than 95% of the distribution in P. balsamifera
Table S6B Genes from 280 kb to 880 kb from region B in chromosome 15 and region A in chromosome 6 associated with GO terms and protein groups enriched in the introgressed regions from P.balsamifera into P. trichocarpa

Table S7. List of genes in introgressed region B in chromosome 15 that showed significantly different levels of expression in admixed (bb, bt) individuals compared to pure *P. trichocarpa* individuals

Table S8. A Genes from the first introgressed region of chromosome 15 that showed associations with traits related to phenology, ecophysiology and biomass (McKown et at. 2014)

Table S1. List of *P. trichocarpa* and *P. balsamifera* accessions used in this study and biogeographical data (latitude, longitude, elevation). Data generated by this study is highlighted in orange (i.e.SNPs for local ancestry analysis, RASPberry; and gene sequence analysis. See M&M and Supplementary Figure 2). Data previously published is highlighted in blue (i.e. phenotypic data, McKown et at. 2013, DOI: 10.1111/nph.12601, S2 in nph12601-sup-0002-TablesS1-S8.xlsx) and that in preparation is highlighted in purple (RNA-seq, O. Corea, S. Biswas et al., preparation; PCA and preliminary RASPberry analysis, Geraldes et al in preparation)

**P. trichocarpa* individuals were classified in one of three genotypic categories: homozygotes for *P. balsamifera* haplotypes (bb), heterozygotes (bt) and homozygotes for *P. trichocarpa* haplotypes (tt), based on phased genomic sequences of one introgressed region in chromosome 15

† We mined a population-wide RNA-seq dataset derived from 385 RNA samples isolated from developing xylem in 197 accessions (most in at least duplicate), and from 389 RNA samples isolated from expanding leaves of defined developmental stage in 191 accessions (most in at least duplicate) grown at Totem Field (O. Corea, S. Biswas et al., preparation). Levels of gene expression (measured by FPKM values) were compared among the three genotypic categories (bb, bt and tt).

AP individuals are genotypes from Alberta Pacific breeding program, supplied by Dr. Barbara Thomas. They do not belong to the core AgCanBaP collection.

Accession	Species code	Drainage/Location name	Lat	Long	Elevation	Included in RASPberry analysis	Gene sequence analysis	Genotypic Categories*	RNA-seq_replicates†	Phenotype data
AP-31-1004	*P. balsamifera*	Muskeg Creek, AB	55.24	114.36	630.00	Yes (admixed)	No	NA	No	No
AP-31-1006	*P. balsamifera*	Muskeg Creek, AB	55.11	114.03	625.00	Yes (admixed)	No	NA	No	No
AP-31-2298	*P. balsamifera*	Fort Nelson River, BC	59.11	122.46	266.00	Yes (admixed)	No	NA	No	No
AP-31-2446	*P. balsamifera*	Muskeg Creek, AB	55.24	114.36	630.00	Yes (admixed)	No	NA	No	No
AP-31-5230	*P. balsamifera*	Muskeg Creek, AB	55.24	114.36	630.00	Yes (admixed)	No	NA	No	No
AP-31-5451	*P. balsamifera*	Poplar Creek Road, AB	56.56	111.32	316.00	Yes (admixed)	No	NA	No	No
AP-31-5452	*P. balsamifera*	Calling Lake, AB	55.09	113.15	653.00	Yes (admixed)	No	NA	No	No
AP-31-5454	*P. balsamifera*	Marten Hills, AB	55.26	114.31	841.00	Yes (admixed)	No	NA	No	No
BOY-31-1	*P. balsamifera*	Boyle	54.55	-112.65	649.00	No	Yes	NA	No	No
BOY-31-11	*P. balsamifera*	Boyle	54.55	-112.65	649.00	No	Yes	NA	No	No
BOY-31-12	*P. balsamifera*	Boyle	54.55	-112.65	649.00	No	Yes	NA	No	No
BOY-31-2	*P. balsamifera*	Boyle	54.55	-112.65	649.00	No	Yes	NA	No	No

BOY-31-3	*P. balsamifera*	Boyle	54.55	-112.65	649.00	No	Yes	NA	No	No
BOY-31-4	*P. balsamifera*	Boyle	54.55	-112.65	649.00	No	Yes	NA	No	No
BOY-31-6	*P. balsamifera*	Boyle	54.55	-112.65	649.00	No	Yes	NA	No	No
BOY-31-8	*P. balsamifera*	Boyle	54.55	-112.65	649.00	No	Yes	NA	No	No
CAR-31-1	*P. balsamifera*	Carnduff	49.18	-101.83	558.00	No	Yes	NA	No	No
CAR-31-11	*P. balsamifera*	Carnduff	49.18	-101.83	558.00	No	Yes	NA	No	No
CAR-31-12	*P. balsamifera*	Carnduff	49.18	-101.83	558.00	No	Yes	NA	No	No
CAR-31-13	*P. balsamifera*	Carnduff	49.18	-101.83	558.00	No	Yes	NA	No	No
CAR-31-14	*P. balsamifera*	Carnduff	49.18	-101.83	558.00	No	Yes	NA	No	No
CAR-31-2	*P. balsamifera*	Carnduff	49.18	-101.83	558.00	No	Yes	NA	No	No
CAR-31-20	*P. balsamifera*	Carnduff	49.18	-101.83	558.00	No	Yes	NA	No	No
CAR-31-24	*P. balsamifera*	Carnduff	49.18	-101.83	558.00	No	Yes	NA	No	No
CAR-31-4	*P. balsamifera*	Carnduff	49.18	-101.83	558.00	No	Yes	NA	No	No
CAR-31-7	*P. balsamifera*	Carnduff	49.18	-101.83	558.00	No	Yes	NA	No	No
CAR-31-8	*P. balsamifera*	Carnduff	49.18	-101.83	558.00	No	Yes	NA	No	No
DEN-31-1	*P. balsamifera*	Denali National Park	63.39	-148.51	594.00	No	Yes	NA	No	No
DEN-31-10	*P. balsamifera*	Denali National Park	63.39	-148.51	594.00	No	Yes	NA	No	No
DEN-31-13	*P. balsamifera*	Denali National Park	63.39	-148.51	594.00	Yes (admixed)	Yes	NA	No	No
DEN-31-3	*P. balsamifera*	Denali National Park	63.39	-148.51	594.00	No	Yes	NA	No	No
DEN-31-4	*P. balsamifera*	Denali National Park	63.39	-148.51	594.00	Yes (admixed)	Yes	NA	No	No
DEN-31-5	*P. balsamifera*	Denali National Park	63.39	-148.51	594.00	No	Yes	NA	No	No
DEN-31-7	*P. balsamifera*	Denali National Park	63.39	-148.51	594.00	No	Yes	NA	No	No
DESD-31-22	*P. balsamifera*	Dease	59.45	-129.02	674.00	Yes (admixed)	No	NA	No	No
DUN-31-1	*P. balsamifera*	Dunlop	54.51	-98.35	223.00	No	Yes	NA	No	No
DUN-31-10	*P. balsamifera*	Dunlop	54.51	-98.35	223.00	No	Yes	NA	No	No

DUN-31-11	*P. balsamifera*	Dunlop	54.51	-98.35	223.00	No	Yes	NA	No	No
DUN-31-13	*P. balsamifera*	Dunlop	54.51	-98.35	223.00	Yes (pure)	Yes	NA	No	No
DUN-31-14	*P. balsamifera*	Dunlop	54.51	-98.35	223.00	Yes (pure)	Yes	NA	No	No
DUN-31-2	*P. balsamifera*	Dunlop	54.51	-98.35	223.00	No	Yes	NA	No	No
DUN-31-4	*P. balsamifera*	Dunlop	54.51	-98.35	223.00	Yes (pure)	Yes	NA	No	No
DUN-31-6	*P. balsamifera*	Dunlop	54.51	-98.35	223.00	No	Yes	NA	No	No
DUN-31-8	*P. balsamifera*	Dunlop	54.51	-98.35	223.00	No	Yes	NA	No	No
EDM-31-1	*P. balsamifera*	Edmonton	53.55	-113.32	719.00	No	Yes	NA	No	No
EDM-31-10	*P. balsamifera*	Edmonton	53.55	-113.32	719.00	No	Yes	NA	No	No
EDM-31-11	*P. balsamifera*	Edmonton	53.55	-113.32	719.00	No	Yes	NA	No	No
EDM-31-3	*P. balsamifera*	Edmonton	53.55	-113.32	719.00	No	Yes	NA	No	No
EDM-31-5	*P. balsamifera*	Edmonton	53.55	-113.32	719.00	No	Yes	NA	No	No
EDM-31-6	*P. balsamifera*	Edmonton	53.55	-113.32	719.00	No	Yes	NA	No	No
EDM-31-9	*P. balsamifera*	Edmonton	53.55	-113.32	719.00	No	Yes	NA	No	No
FBK-31-10	*P. balsamifera*	Fairbanks	64.90	-146.35	248.00	No	Yes	NA	No	No
FBK-31-11	*P. balsamifera*	Fairbanks	64.90	-146.35	248.00	Yes (pure)	Yes	NA	No	No
FBK-31-3	*P. balsamifera*	Fairbanks	64.90	-146.35	248.00	No	Yes	NA	No	No
FBK-31-4	*P. balsamifera*	Fairbanks	64.90	-146.35	248.00	No	Yes	NA	No	No
FBK-31-5	*P. balsamifera*	Fairbanks	64.90	-146.35	248.00	No	Yes	NA	No	No
FBK-31-6	*P. balsamifera*	Fairbanks	64.90	-146.35	248.00	Yes (pure)	Yes	NA	No	No
FBK-31-9	*P. balsamifera*	Fairbanks	64.90	-146.35	248.00	No	Yes	NA	No	No
FRE-31-12	*P. balsamifera*	Frederiction	46.40	-67.25	147.00	No	Yes	NA	No	No
FRE-31-14	*P. balsamifera*	Frederiction	46.40	-67.25	147.00	No	Yes	NA	No	No
FRE-31-5	*P. balsamifera*	Frederiction	46.40	-67.25	147.00	No	Yes	NA	No	No
FRE-31-6	*P. balsamifera*	Frederiction	46.40	-67.25	147.00	No	Yes	NA	No	No
FRE-31-8	*P. balsamifera*	Frederiction	46.40	-67.25	147.00	No	Yes	NA	No	No
FRE-31-9	*P. balsamifera*	Frederiction	46.40	-67.25	147.00	No	Yes	NA	No	No
FTM-31-1	*P. balsamifera*	Fort McMurray	56.56	-111.36	338.00	No	Yes	NA	No	No

FTM-31-13	*P. balsamifera*	Fort McMurray	56.56	-111.36	338.00	No	Yes	NA	No	No
FTM-31-2	*P. balsamifera*	Fort McMurray	56.56	-111.36	338.00	No	Yes	NA	No	No
FTM-31-3	*P. balsamifera*	Fort McMurray	56.56	-111.36	338.00	No	Yes	NA	No	No
FTM-31-4	*P. balsamifera*	Fort McMurray	56.56	-111.36	338.00	No	Yes	NA	No	No
FTM-31-5	*P. balsamifera*	Fort McMurray	56.56	-111.36	338.00	Yes (admixed)	Yes	NA	No	No
FTM-31-6	*P. balsamifera*	Fort McMurray	56.56	-111.36	338.00	Yes (admixed)	Yes	NA	No	No
FTM-31-8	*P. balsamifera*	Fort McMurray	56.56	-111.36	338.00	Yes (admixed)	Yes	NA	No	No
FTM-31-9	*P. balsamifera*	Fort McMurray	56.56	-111.36	338.00	No	Yes	NA	No	No
GIL-31-1	*P. balsamifera*	Gillam	56.35	-94.63	126.00	Yes (pure)	No	NA	No	No
GIL-31-10	*P. balsamifera*	Gillam	56.25	-94.36	126.00	Yes (pure)	No	NA	No	No
GIL-31-14	*P. balsamifera*	Gillam	56.25	-94.36	126.00	No	Yes	NA	No	No
GIL-31-3	*P. balsamifera*	Gillam	56.25	-94.36	126.00	No	Yes	NA	No	No
GIL-31-4	*P. balsamifera*	Gillam	56.25	-94.36	126.00	No	Yes	NA	No	No
GIL-31-7	*P. balsamifera*	Gillam	56.25	-94.36	126.00	No	Yes	NA	No	No
GIL-31-8	*P. balsamifera*	Gillam	56.25	-94.36	126.00	No	Yes	NA	No	No
GPR-31-1	*P. balsamifera*	Grande Prairie	54.75	-118.63	769.00	Yes (admixed)	Yes	NA	No	No
GPR-31-10	*P. balsamifera*	Grande Prairie	54.75	-118.63	769.00	Yes (admixed)	No	NA	No	No
GPR-31-11	*P. balsamifera*	Grande Prairie	54.75	-118.63	769.00	Yes (admixed)	Yes	NA	No	No
GPR-31-12	*P. balsamifera*	Grande Prairie	54.75	-118.63	769.00	Yes (admixed)	Yes	NA	No	No
GPR-31-13	*P. balsamifera*	Grande Prairie	54.75	-118.63	769.00	Yes (admixed)	Yes	NA	No	No
GPR-31-14	*P. balsamifera*	Grande Prairie	54.75	-118.63	769.00	Yes (admixed)	No	NA	No	No
GPR-31-2	*P. balsamifera*	Grande Prairie	54.75	-118.63	769.00	Yes (admixed)	Yes	NA	No	No
GPR-31-3	*P. balsamifera*	Grande Prairie	54.75	-118.63	769.00	Yes (admixed)	Yes	NA	No	No
GPR-31-4	*P. balsamifera*	Grande Prairie	54.75	-118.63	769.00	Yes	No	NA	No	No

						(admixed)				
GPR-31-5	*P. balsamifera*	Grande Prairie	54.75	-118.63	769.00	Yes (admixed)	Yes	NA	No	No
GPR-31-6	*P. balsamifera*	Grande Prairie	54.75	-118.63	769.00	Yes (admixed)	No	NA	No	No
GPR-31-7	*P. balsamifera*	Grande Prairie	54.75	-118.63	769.00	Yes (admixed)	Yes	NA	No	No
GPR-31-8	*P. balsamifera*	Grande Prairie	54.75	-118.63	769.00	Yes (admixed)	No	NA	No	No
GPR-31-9	*P. balsamifera*	Grande Prairie	54.75	-118.63	769.00	Yes (admixed)	No	NA	No	No
GRA-31-10	*P. balsamifera*	Grand Rapids	53.20	-99.35	254.00	No	Yes	NA	No	No
GRA-31-3	*P. balsamifera*	Grand Rapids	53.20	-99.35	254.00	No	Yes	NA	No	No
GRA-31-4	*P. balsamifera*	Grand Rapids	53.20	-99.35	254.00	No	Yes	NA	No	No
GRA-31-5	*P. balsamifera*	Grand Rapids	53.20	-99.35	254.00	No	Yes	NA	No	No
GRA-31-6	*P. balsamifera*	Grand Rapids	53.20	-99.35	254.00	No	Yes	NA	No	No
GRA-31-7	*P. balsamifera*	Grand Rapids	53.20	-99.35	254.00	No	Yes	NA	No	No
GRA-31-8	*P. balsamifera*	Grand Rapids	53.20	-99.35	254.00	No	Yes	NA	No	No
GYP-31-1	*P. balsamifera*	Gypsumville	51.77	-98.62	253.00	No	Yes	NA	No	No
GYP-31-10	*P. balsamifera*	Gypsumville	51.77	-98.62	253.00	Yes (pure)	Yes	NA	No	No
GYP-31-12	*P. balsamifera*	Gypsumville	51.77	-98.62	253.00	No	Yes	NA	No	No
GYP-31-13	*P. balsamifera*	Gypsumville	51.77	-98.62	253.00	Yes (pure)	No	NA	No	No
GYP-31-2	*P. balsamifera*	Gypsumville	51.77	-98.62	253.00	No	Yes	NA	No	No
GYP-31-3	*P. balsamifera*	Gypsumville	51.77	-98.62	253.00	No	Yes	NA	No	No
GYP-31-4	*P. balsamifera*	Gypsumville	51.77	-98.62	253.00	No	Yes	NA	No	No
GYP-31-7	*P. balsamifera*	Gypsumville	51.77	-98.62	253.00	No	Yes	NA	No	No
GYP-31-9	*P. balsamifera*	Gypsumville	51.77	-98.62	253.00	Yes (pure)	No	NA	No	No
HAY-31-1	*P. balsamifera*	Hay River	60.80	-115.78	168.00	No	Yes	NA	No	No
HAY-31-11	*P. balsamifera*	Hay River	60.80	-115.78	168.00	No	Yes	NA	No	No
HAY-31-12	*P. balsamifera*	Hay River	60.80	-115.78	168.00	No	Yes	NA	No	No

HAY-31-3	*P. balsamifera*	Hay River	60.80	-115.78	168.00	No	Yes	NA	No	No
HAY-31-4	*P. balsamifera*	Hay River	60.80	-115.78	168.00	No	Yes	NA	No	No
HAY-31-5	*P. balsamifera*	Hay River	60.80	-115.78	168.00	No	Yes	NA	No	No
INU-31-9	*P. balsamifera*	Inuvik	68.38	-133.77	7.00	Yes (pure)	No	NA	No	No
KUU-31-09	*P. balsamifera*	Kuujjuaq	58.02	-68.65	17.00	No	Yes	NA	No	No
KUU-31-1	*P. balsamifera*	Kuujjuaq	58.02	-68.65	17.00	No	Yes	NA	No	No
KUU-31-10	*P. balsamifera*	Kuujjuaq	58.02	-68.65	17.00	No	Yes	NA	No	No
KUU-31-13	*P. balsamifera*	Kuujjuaq	58.02	-68.65	17.00	No	Yes	NA	No	No
KUU-31-2	*P. balsamifera*	Kuujjuaq	58.02	-68.65	17.00	No	Yes	NA	No	No
KUU-31-3	*P. balsamifera*	Kuujjuaq	58.02	-68.65	17.00	No	Yes	NA	No	No
KUU-31-5	*P. balsamifera*	Kuujjuaq	58.02	-68.65	17.00	No	Yes	NA	No	No
LAB-31-1	*P. balsamifera*	Labrador City	52.93	-67.25	554.00	No	Yes	NA	No	No
LAB-31-12	*P. balsamifera*	Labrador City	52.93	-67.25	554.00	No	Yes	NA	No	No
LAB-31-4	*P. balsamifera*	Labrador City	52.93	-67.25	554.00	No	Yes	NA	No	No
LAB-31-5	*P. balsamifera*	Labrador City	52.93	-67.25	554.00	No	Yes	NA	No	No
LAB-31-6	*P. balsamifera*	Labrador City	52.93	-67.25	554.00	No	Yes	NA	No	No
LAB-31-7	*P. balsamifera*	Labrador City	52.93	-67.25	554.00	No	Yes	NA	No	No
LAB-31-8	*P. balsamifera*	Labrador City	52.93	-67.25	554.00	No	Yes	NA	No	No
LAR-31-11	*P. balsamifera*	La Ronge	54.45	-105.33	471.00	No	Yes	NA	No	No
LAR-31-12	*P. balsamifera*	La Ronge	54.45	-105.33	471.00	Yes (pure)	No	NA	No	No
LAR-31-15	*P. balsamifera*	La Ronge	54.45	-105.33	471.00	No	Yes	NA	No	No
LAR-31-2	*P. balsamifera*	La Ronge	54.45	-105.33	471.00	No	Yes	NA	No	No
LAR-31-3	*P. balsamifera*	La Ronge	54.45	-105.33	471.00	No	Yes	NA	No	No
LAR-31-5	*P. balsamifera*	La Ronge	54.45	-105.33	471.00	No	Yes	NA	No	No
LAR-31-6	*P. balsamifera*	La Ronge	54.45	-105.33	471.00	No	Yes	NA	No	No
LAR-31-9	*P. balsamifera*	La Ronge	54.45	-105.33	471.00	No	Yes	NA	No	No
LOV-31-1	*P. balsamifera*	Love	53.63	-105.50	419.00	No	Yes	NA	No	No
LOV-31-	*P. balsamifera*	Love	53.63	-105.50	419.00	No	Yes	NA	No	No

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LOV-31-2	*P. balsamifera*	Love	53.63	-105.50	419.00	No	Yes	NA	No	No
LOV-31-3	*P. balsamifera*	Love	53.63	-105.50	419.00	No	Yes	NA	No	No
LOV-31-4	*P. balsamifera*	Love	53.63	-105.50	419.00	No	Yes	NA	No	No
LOV-31-6	*P. balsamifera*	Love	53.63	-105.50	419.00	No	Yes	NA	No	No
LOV-31-7	*P. balsamifera*	Love	53.63	-105.50	419.00	No	Yes	NA	No	No
MAN-31-2	*P. balsamifera*	Manicougan	49.30	-68.32	180.00	No	Yes	NA	No	No
MAN-31-4	*P. balsamifera*	Manicougan	49.30	-68.32	180.00	No	Yes	NA	No	No
MAN-31-5	*P. balsamifera*	Manicougan	49.30	-68.32	180.00	No	Yes	NA	No	No
MAN-31-7	*P. balsamifera*	Manicougan	49.30	-68.32	180.00	No	Yes	NA	No	No
MAN-31-9	*P. balsamifera*	Manicougan	49.30	-68.32	180.00	No	Yes	NA	No	No
MAT-31-11	*P. balsamifera*	Matapedia	48.22	-67.18	98.00	No	Yes	NA	No	No
MAT-31-12	*P. balsamifera*	Matapedia	48.22	-67.18	98.00	No	Yes	NA	No	No
MAT-31-14	*P. balsamifera*	Matapedia	48.22	-67.18	98.00	No	Yes	NA	No	No
MAT-31-2	*P. balsamifera*	Matapedia	48.22	-67.18	98.00	No	Yes	NA	No	No
MAT-31-3	*P. balsamifera*	Matapedia	48.22	-67.18	98.00	No	Yes	NA	No	No
MAT-31-4	*P. balsamifera*	Matapedia	48.22	-67.18	98.00	No	Yes	NA	No	No
MAT-31-7	*P. balsamifera*	Matapedia	48.22	-67.18	98.00	No	Yes	NA	No	No
MEL-31-11	*P. balsamifera*	Melville	51.35	-102.62	541.00	No	Yes	NA	No	No
MEL-31-12	*P. balsamifera*	Melville	51.35	-102.62	541.00	No	Yes	NA	No	No
MEL-31-2	*P. balsamifera*	Melville	51.35	-102.62	541.00	Yes (pure)	No	NA	No	No
MEL-31-4	*P. balsamifera*	Melville	51.35	-102.62	541.00	No	Yes	NA	No	No
MEL-31-5	*P. balsamifera*	Melville	51.35	-102.62	541.00	No	Yes	NA	No	No
MEL-31-6	*P. balsamifera*	Melville	51.35	-102.62	541.00	No	Yes	NA	No	No
MEL-31-7	*P. balsamifera*	Melville	51.35	-102.62	541.00	No	Yes	NA	No	No
MGR-31-	*P. balsamifera*	Mount Groulx	51.33	68.09	na	No	Yes	NA	No	No

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MGR-31-3	*P. balsamifera*	Mount Groulx	51.33	68.09	na	No	Yes	NA	No	No
MGR-31-4	*P. balsamifera*	Mount Groulx	51.33	68.09	na	No	Yes	NA	No	No
MGR-31-5	*P. balsamifera*	Mount Groulx	51.33	68.09	na	No	Yes	NA	No	No
MGR-31-8	*P. balsamifera*	Mount Groulx	51.33	68.09	na	No	Yes	NA	No	No
MGR-31-9	*P. balsamifera*	Mount Groulx	51.33	68.09	na	No	Yes	NA	No	No
MIN-31-1	*P. balsamifera*	Minnedosa	50.32	-99.85	592.00	Yes (pure)	Yes	NA	No	No
MIN-31-10	*P. balsamifera*	Minnedosa	50.32	-99.85	592.00	No	Yes	NA	No	No
MIN-31-11	*P. balsamifera*	Minnedosa	50.32	-99.85	592.00	No	Yes	NA	No	No
MIN-31-13	*P. balsamifera*	Minnedosa	50.32	-99.85	592.00	No	Yes	NA	No	No
MIN-31-14	*P. balsamifera*	Minnedosa	50.32	-99.85	592.00	No	Yes	NA	No	No
MIN-31-2	*P. balsamifera*	Minnedosa	50.32	-99.85	592.00	No	Yes	NA	No	No
MIN-31-3	*P. balsamifera*	Minnedosa	50.32	-99.85	592.00	No	Yes	NA	No	No
MIN-31-4	*P. balsamifera*	Minnedosa	50.32	-99.85	592.00	No	Yes	NA	No	No
MIN-31-9	*P. balsamifera*	Minnedosa	50.32	-99.85	592.00	No	Yes	NA	No	No
MTN-31-10	*P. balsamifera*	Matane	48.57	-67.35	119.00	No	Yes	NA	No	No
MTN-31-11	*P. balsamifera*	Matane	48.57	-67.35	119.00	No	Yes	NA	No	No
MTN-31-13	*P. balsamifera*	Matane	48.57	-67.35	119.00	No	Yes	NA	No	No
MTN-31-2	*P. balsamifera*	Matane	48.57	-67.35	119.00	No	Yes	NA	No	No
MTN-31-3	*P. balsamifera*	Matane	48.57	-67.35	119.00	No	Yes	NA	No	No
MTN-31-9	*P. balsamifera*	Matane	48.57	-67.35	119.00	No	Yes	NA	No	No
NWL-31-1	*P. balsamifera*	Norman Wells	65.16	-126.44	84.00	Yes (pure)	No	NA	No	No
NWL-31-10	*P. balsamifera*	Norman Wells	65.16	-126.44	84.00	Yes (pure)	Yes	NA	No	No

NWL-31-11	*P. balsamifera*	Norman Wells	65.16	-126.44	84.00	Yes (pure)	No	NA	No	No
NWL-31-112	*P. balsamifera*	Norman Wells	65.16	-126.44	84.00	Yes (pure)	No	NA	No	No
NWL-31-12	*P. balsamifera*	Norman Wells	65.16	-126.44	84.00	Yes (pure)	Yes	NA	No	No
NWL-31-16	*P. balsamifera*	Norman Wells	65.16	-126.44	84.00	No	Yes	NA	No	No
NWL-31-2	*P. balsamifera*	Norman Wells	65.16	-126.44	84.00	No	Yes	NA	No	No
NWL-31-3	*P. balsamifera*	Norman Wells	65.16	-126.44	84.00	No	Yes	NA	No	No
NWL-31-5	*P. balsamifera*	Norman Wells	65.16	-126.44	84.00	No	Yes	NA	No	No
NWL-31-7	*P. balsamifera*	Norman Wells	65.16	-126.44	84.00	Yes (pure)	No	NA	No	No
NWL-31-8	*P. balsamifera*	Norman Wells	65.16	-126.44	84.00	No	Yes	NA	No	No
NWL-31-9	*P. balsamifera*	Norman Wells	65.23	-126.67	84.00	Yes (pure)	No	NA	No	No
POR-31-1	*P. balsamifera*	Portage	49.57	-98.18	283.00	No	Yes	NA	No	No
POR-31-11	*P. balsamifera*	Portage	49.57	-98.18	283.00	No	Yes	NA	No	No
POR-31-12	*P. balsamifera*	Portage	49.57	-98.18	283.00	No	Yes	NA	No	No
POR-31-14	*P. balsamifera*	Portage	49.57	-98.18	283.00	No	Yes	NA	No	No
POR-31-4	*P. balsamifera*	Portage	49.57	-98.18	283.00	No	Yes	NA	No	No
POR-31-5	*P. balsamifera*	Portage	49.57	-98.18	283.00	No	Yes	NA	No	No
POR-31-6	*P. balsamifera*	Portage	49.57	-98.18	283.00	Yes (pure)	Yes	NA	No	No
POR-31-7	*P. balsamifera*	Portage	49.57	-98.18	283.00	No	Yes	NA	No	No
RNA-31-1	*P. balsamifera*	Rouyn-Noranda	48.60	-78.67	310.00	No	Yes	NA	No	No
RNA-31-11	*P. balsamifera*	Rouyn-Noranda	48.60	-78.67	310.00	No	Yes	NA	No	No
RNA-31-13	*P. balsamifera*	Rouyn-Noranda	48.60	-78.67	310.00	No	Yes	NA	No	No
RNA-31-14	*P. balsamifera*	Rouyn-Noranda	48.60	-78.67	310.00	No	Yes	NA	No	No
RNA-31-2	*P. balsamifera*	Rouyn-Noranda	48.60	-78.67	310.00	No	Yes	NA	No	No
RNA-31-3	*P. balsamifera*	Rouyn-Noranda	48.60	-78.67	310.00	No	Yes	NA	No	No
RNA-31-6	*P. balsamifera*	Rouyn-Noranda	48.60	-78.67	310.00	No	Yes	NA	No	No
ROS-31-1	*P. balsamifera*	Roseville	47.33	-64.37	25.00	No	Yes	NA	No	No

ROS-31-14	*P. balsamifera*	Roseville	47.33	-64.37	25.00	No	Yes	NA	No	No
ROS-31-4	*P. balsamifera*	Roseville	47.33	-64.37	25.00	No	Yes	NA	No	No
ROS-31-6	*P. balsamifera*	Roseville	47.33	-64.37	25.00	No	Yes	NA	No	No
ROS-31-9	*P. balsamifera*	Roseville	47.33	-64.37	25.00	No	Yes	NA	No	No
SOU-31-1	*P. balsamifera*	Sioux Lookout	50.08	-91.90	384.00	No	Yes	NA	No	No
SOU-31-12	*P. balsamifera*	Sioux Lookout	50.08	-91.90	384.00	No	Yes	NA	No	No
SOU-31-14	*P. balsamifera*	Sioux Lookout	50.08	-91.90	384.00	No	Yes	NA	No	No
SOU-31-15	*P. balsamifera*	Sioux Lookout	50.08	-91.90	384.00	No	Yes	NA	No	No
SOU-31-2	*P. balsamifera*	Sioux Lookout	50.08	-91.90	384.00	No	Yes	NA	No	No
SOU-31-3	*P. balsamifera*	Sioux Lookout	50.08	-91.90	384.00	No	Yes	NA	No	No
SOU-31-4	*P. balsamifera*	Sioux Lookout	50.08	-91.90	384.00	No	Yes	NA	No	No
SOU-31-5	*P. balsamifera*	Sioux Lookout	50.08	-91.90	384.00	No	Yes	NA	No	No
SOU-31-7	*P. balsamifera*	Sioux Lookout	50.08	-91.90	384.00	No	Yes	NA	No	No
SOU-31-9	*P. balsamifera*	Sioux Lookout	50.08	-91.90	384.00	No	Yes	NA	No	No
SRD-31-11	*P. balsamifera*	South Reindeer	56.27	-104.23	419.00	No	Yes	NA	No	No
SRD-31-12	*P. balsamifera*	South Reindeer	56.27	-104.23	419.00	No	Yes	NA	No	No
SRD-31-2	*P. balsamifera*	South Reindeer	56.27	-104.23	419.00	No	Yes	NA	No	No
SRD-31-4	*P. balsamifera*	South Reindeer	56.27	-104.23	419.00	No	Yes	NA	No	No
SRD-31-5	*P. balsamifera*	South Reindeer	56.27	-104.23	419.00	No	Yes	NA	No	No
SRD-31-7	*P. balsamifera*	South Reindeer	56.27	-104.23	419.00	No	Yes	NA	No	No
SRD-31-8	*P. balsamifera*	South Reindeer	56.27	-104.23	419.00	No	Yes	NA	No	No
SRD-31-9	*P. balsamifera*	South Reindeer	56.27	-104.23	419.00	Yes (admixed)	Yes	NA	No	No
STL-31-1	*P. balsamifera*	Stettler	52.35	-112.73	795.00	No	Yes	NA	No	No
STL-31-10	*P. balsamifera*	Stettler	52.35	-112.73	795.00	No	Yes	NA	No	No
STL-31-13	*P. balsamifera*	Stettler	52.35	-112.73	795.00	No	Yes	NA	No	No
STL-31-14	*P. balsamifera*	Stettler	52.35	-112.73	795.00	No	Yes	NA	No	No
STL-31-8	*P. balsamifera*	Stettler	52.35	-112.73	795.00	No	Yes	NA	No	No
STO-31-1	*P. balsamifera*	Stony Rapids	59.23	-105.72	306.00	No	Yes	NA	No	No

STO-31-12	*P. balsamifera*	Stony Rapids	59.23	-105.72	306.00	No	Yes	NA	No	No
STO-31-13	*P. balsamifera*	Stony Rapids	59.23	-105.72	306.00	No	Yes	NA	No	No
STO-31-2	*P. balsamifera*	Stony Rapids	59.23	-105.72	306.00	No	Yes	NA	No	No
STO-31-4	*P. balsamifera*	Stony Rapids	59.23	-105.72	306.00	No	Yes	NA	No	No
STO-31-7	*P. balsamifera*	Stony Rapids	59.23	-105.72	306.00	No	Yes	NA	No	No
STO-31-8	*P. balsamifera*	Stony Rapids	59.23	-105.72	306.00	No	Yes	NA	No	No
TNZA-4-1	*P. balsamifera*	Upper Stikine	58.30	-130.47	567.00	Yes (admixed)	Yes	NA	No	No
WAD-31-1	*P. balsamifera*	Wadena	52.37	-104.27	543.00	No	Yes	NA	No	No
WAD-31-1	*P. balsamifera*	Wadena	52.37	-104.27	543.00	Yes (pure)	No	NA	No	No
WAD-31-12	*P. balsamifera*	Wadena	52.37	-104.27	543.00	No	Yes	NA	No	No
WAD-31-14	*P. balsamifera*	Wadena	52.37	-104.27	543.00	No	Yes	NA	No	No
WAD-31-3	*P. balsamifera*	Wadena	52.37	-104.27	543.00	No	Yes	NA	No	No
WAD-31-5	*P. balsamifera*	Wadena	52.37	-104.27	543.00	No	Yes	NA	No	No
WAD-31-8	*P. balsamifera*	Wadena	52.37	-104.27	543.00	No	Yes	NA	No	No
WHR-31-1	*P. balsamifera*	Whitehorse	60.70	-135.33	770.00	No	Yes	NA	No	No
WHR-31-11	*P. balsamifera*	Whitehorse	60.70	-135.33	770.00	No	Yes	NA	No	No
WHR-31-11	*P. balsamifera*	Whitehorse	60.70	-135.33	770.00	Yes (admixed)	No	NA	No	No
WHR-31-12	*P. balsamifera*	Whitehorse	60.70	-135.33	770.00	No	Yes	NA	No	No
WHR-31-15	*P. balsamifera*	Whitehorse	60.70	-135.33	770.00	No	Yes	NA	No	No
WHR-31-2	*P. balsamifera*	Whitehorse	60.70	-135.33	770.00	No	Yes	NA	No	No
WHR-31-	*P. balsamifera*	Whitehorse	60.70	-135.33	770.00	No	Yes	NA	No	No

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WHR-31-3	*P. balsamifera*	Whitehorse	60.70	-135.33	770.00	Yes (pure)	No	NA	No	No
WHR-31-4	*P. balsamifera*	Whitehorse	60.70	-135.33	770.00	No	Yes	NA	No	No
WHR-31-4	*P. balsamifera*	White Horse	60.70	-135.33	770.00	Yes (pure)	No	NA	No	No
WHR-31-9	*P. balsamifera*	Whitehorse	60.70	-135.33	770.00	No	Yes	NA	No	No
WOL-31-1	*P. balsamifera*	Wollaston Lake	57.58	-103.93	423.00	No	Yes	NA	No	No
WOL-31-14	*P. balsamifera*	Wollaston Lake	57.58	-103.93	423.00	No	Yes	NA	No	No
WOL-31-15	*P. balsamifera*	Wollaston Lake	57.58	-103.93	423.00	No	Yes	NA	No	No
WOL-31-2	*P. balsamifera*	Wollaston Lake	57.58	-103.93	423.00	No	Yes	NA	No	No
WOL-31-3	*P. balsamifera*	Wollaston Lake	57.58	-103.93	423.00	No	Yes	NA	No	No
WOL-31-4	*P. balsamifera*	Wollaston Lake	57.58	-103.93	423.00	No	Yes	NA	No	No
WOL-31-6	*P. balsamifera*	Wollaston Lake	57.58	-103.93	423.00	Yes (admixed)	Yes	NA	No	No
ALAA-20-1	*P. trichocarpa*	Klinaklini	50.98	-126.12	0.00	Yes (pure)	Yes	NA	No	No
ALAA-20-3	*P. trichocarpa*	Klinaklini	50.98	-126.12	0.00	No	Yes	NA	No	No
ALAA-20-4	*P. trichocarpa*	Klinaklini	50.98	-126.12	0.00	No	Yes	NA	No	No
ALAA-20-5	*P. trichocarpa*	Klinaklini	50.98	-126.12	0.00	No	Yes	NA	No	No
ALSC-1-4	*P. trichocarpa*	Alsek	59.62	-137.92	107.00	Yes (admixed)	Yes	bt	No	Yes
ALSC-1-5	*P. trichocarpa*	Alsek	59.62	-137.92	107.00	Yes (admixed)	Yes	bt	No	Yes
AMER-13-1	*P. trichocarpa*	Stuart	54.63	-124.97	701.00	Yes (pure)	Yes	tt	14	No
AMER-13-3	*P. trichocarpa*	Stuart	54.63	-124.97	701.00	No	Yes	tt	No	No
BELA-18-1	*P. trichocarpa*	Bella Coola river	52.42	-126.17	152.00	No	Yes	NA	No	No

BELA-18-2	*P. trichocarpa*	Bella Coola river	52.42	-126.17	152.00	No	Yes	NA	No	No
BELA-18-3	*P. trichocarpa*	Bella Coola river	52.42	-126.17	152.00	No	Yes	NA	No	No
BELA-18-5	*P. trichocarpa*	Bella Coola river	52.42	-126.17	152.00	No	Yes	NA	No	No
BELC-18-1	*P. trichocarpa*	Bella Coola river	52.38	-126.60	135.00	No	Yes	NA	No	No
BELC-18-2	*P. trichocarpa*	Bella Coola river	52.38	-126.60	135.00	No	Yes	NA	No	No
BELC-18-3	*P. trichocarpa*	Bella Coola river	52.38	-126.60	135.00	No	Yes	NA	No	No
BELC-18-4	*P. trichocarpa*	Bella Coola river	52.38	-126.60	135.00	No	Yes	NA	No	No
BELC-18-5	*P. trichocarpa*	Bella Coola river	52.38	-126.60	135.00	No	Yes	NA	No	No
BULA-11-4	*P. trichocarpa*	Bulkley	55.25	-127.50	311.00	Yes (admixed)	Yes	bt	No	Yes
BULB-11-1	*P. trichocarpa*	Bulkley	55.12	-127.35	427.00	No	Yes	tt	No	Yes
BULF-11-2	*P. trichocarpa*	Bulkley	54.55	-126.83	561.00	No	Yes	tt	No	Yes
BULF-11-3	*P. trichocarpa*	Bulkley	54.55	-126.83	561.00	No	Yes	tt	No	Yes
BULF-11-4	*P. trichocarpa*	Bulkley	54.55	-126.83	561.00	No	Yes	tt	No	Yes
BULF-11-5	*P. trichocarpa*	Bulkley	54.55	-126.83	561.00	No	Yes	tt	No	Yes
BULG-11-2	*P. trichocarpa*	Bulkley	54.45	-126.80	579.00	No	Yes	bt	No	Yes
BULG-11-4	*P. trichocarpa*	Bulkley	54.45	-126.80	579.00	No	Yes	tt	No	Yes
BULG-11-5	*P. trichocarpa*	Bulkley	54.45	-126.80	579.00	No	Yes	tt	No	Yes
CARS-29-2	*P. trichocarpa*	Columbia	45.75	-122.83	650.00	No	Yes	NA	No	No
CARS-29-3	*P. trichocarpa*	Columbia	45.75	-122.83	650.00	No	Yes	NA	No	No
CARS-29-4	*P. trichocarpa*	Columbia	45.75	-122.83	650.00	No	Yes	NA	No	No
CARS-29-5	*P. trichocarpa*	Columbia	45.75	-122.83	650.00	No	Yes	NA	No	No

CDRE-10-1	*P. trichocarpa*	Skeena	55.02	-128.33	152.00	No	Yes	tt	No	Yes
CDRE-10-3	*P. trichocarpa*	Skeena	55.02	-128.33	152.00	No	Yes	tt	No	Yes
CEDA-10-2	*P. trichocarpa*	Skeena	54.95	-128.92	274.00	No	Yes	tt	No	Yes
CEDA-10-4	*P. trichocarpa*	Skeena	54.95	-128.92	274.00	No	Yes	tt	No	Yes
CHIL-14-2	*P. trichocarpa*	Nechako	54.88	-122.98	183.00	No	Yes	tt	No	Yes
CHKC-19-1	*P. trichocarpa*	Chuckwall	51.73	-127.32	67.00	No	Yes	NA	No	No
CHKC-19-2	*P. trichocarpa*	Chuckwall	51.73	-127.32	67.00	No	Yes	NA	No	No
CHKC-19-3	*P. trichocarpa*	Chuckwall	51.73	-127.32	67.00	No	Yes	NA	No	No
CHKC-19-4	*P. trichocarpa*	Chuckwall	51.77	-127.20	79.00	Yes (pure)	Yes	NA	No	No
CHKD-19-1	*P. trichocarpa*	Chuckwall	51.77	-127.20	79.00	No	Yes	NA	No	No
CHKD-19-2	*P. trichocarpa*	Chuckwall	51.77	-127.20	79.00	No	Yes	NA	No	No
CHKD-19-3	*P. trichocarpa*	Chuckwall	51.77	-127.20	79.00	No	Yes	NA	No	No
CHKD-19-4	*P. trichocarpa*	Chuckwall	51.77	-127.20	79.00	No	Yes	NA	No	No
CHKD-19-5	*P. trichocarpa*	Chuckwall	51.77	-127.20	79.00	No	Yes	NA	No	No
CHNH-27-4	*P. trichocarpa*	Fraser	49.08	-121.72	280.00	No	Yes	NA	No	No
CHWJ-27-2	*P. trichocarpa*	Fraser	49.08	-121.72	280.00	Yes (pure)	No	NA	No	No
CNYH-28-1	*P. trichocarpa*	Vancouver Island	49.67	-125.07	76.00	No	Yes	NA	No	No
CNYH-28-2	*P. trichocarpa*	Vancouver Island	49.67	-125.07	76.00	Yes (pure)	No	NA	No	No
CSYJ-28-1	*P. trichocarpa*	Vancouver Island	49.07	-123.87	20.00	No	Yes	NA	No	No
CSYJ-28-2	*P. trichocarpa*	Vancouver Island	49.07	-123.87	20.00	No	Yes	NA	No	No

CSYJ-28-3	*P. trichocarpa*	Vancouver Island	49.07	-123.87	20.00	No	Yes	NA	No	No
CSYJ-28-4	*P. trichocarpa*	Vancouver Island	49.07	-123.87	20.00	No	Yes	NA	No	No
DENB-17-2	*P. trichocarpa*	Dean	52.83	-126.70	152.00	Yes (pure)	No	NA	No	No
ELAD-25-1	*P. trichocarpa*	Squamish	50.25	-123.58	305.00	No	Yes	NA	No	No
ELAD-25-2	*P. trichocarpa*	Squamish	50.25	-123.58	305.00	No	Yes	NA	No	No
ELAD-25-3	*P. trichocarpa*	Squamish	50.25	-123.58	305.00	No	Yes	NA	No	No
ELAD-25-4	*P. trichocarpa*	Squamish	50.25	-123.58	305.00	No	Yes	NA	No	No
ELAD-25-5	*P. trichocarpa*	Squamish	50.25	-123.58	305.00	No	Yes	NA	No	No
FKRB-6-1	*P. trichocarpa*	Iskut	56.73	-130.63	280.00	No	Yes	tt	No	Yes
GLCB-26-3	*P. trichocarpa*	Lillooet	50.10	-123.00	579.00	Yes (pure)	No	NA	No	No
HALS-30-1	*P. trichocarpa*	Willamette	44.42	-123.33	300.00	No	Yes	NA	No	No
HALS-30-2	*P. trichocarpa*	Willamette	44.42	-123.33	300.00	No	Yes	NA	No	No
HALS-30-4	*P. trichocarpa*	Willamette	44.42	-123.33	300.00	No	Yes	NA	No	No
HALS-30-6	*P. trichocarpa*	Willamette	44.42	-123.33	300.00	No	Yes	NA	No	No
HAZH-10-1	*P. trichocarpa*	Skeena	55.22	-127.67	238.00	No	Yes	tt	No	Yes
HAZH-10-2	*P. trichocarpa*	Skeena	55.22	-127.67	238.00	No	Yes	tt	2	Yes
HAZH-10-3	*P. trichocarpa*	Skeena	55.22	-127.67	238.00	No	Yes	bt	No	Yes
HAZH-10-5	*P. trichocarpa*	Skeena	55.22	-127.67	238.00	No	Yes	bt	No	Yes
HIRD-12-2	*P. trichocarpa*	Kitimat	54.07	-128.45	335.00	No	No	tt	2	Yes
HIXN-16-1	*P. trichocarpa*	Quesnel	53.40	-122.63	518.00	Yes (admixed)	Yes	tt	2	Yes

HIXN-16-5	*P. trichocarpa*	Quesnel	53.40	-122.63	518.00	Yes (admixed)	Yes	tt	No	Yes
HOMB-21-1	*P. trichocarpa*	Homathko	51.23	-124.95	88.00	Yes (pure)	Yes	NA	No	No
HOMB-21-5	*P. trichocarpa*	Homathko	50.95	-124.90	37.00	No	Yes	NA	No	No
HOMD-21-5	*P. trichocarpa*	Homathko	51.28	-124.83	152.00	No	Yes	NA	No	No
HOPF-27-2	*P. trichocarpa*	Fraser	49.43	-121.43	61.00	No	Yes	NA	No	No
HOPF-27-4	*P. trichocarpa*	Fraser	49.43	-121.43	61.00	No	Yes	NA	No	No
HOPG-27-1	*P. trichocarpa*	Fraser	49.40	-121.55	500.00	No	Yes	NA	No	No
HRSP-27-3	*P. trichocarpa*	Fraser	49.23	-121.85	30.00	No	Yes	NA	No	No
IRVC-7-1	*P. trichocarpa*	Bell-Irving	56.73	-129.73	579.00	No	Yes	tt	No	Yes
IRVC-7-4	*P. trichocarpa*	Bell-Irving	56.73	-129.73	579.00	No	Yes	tt	No	Yes
IRVC-7-5	*P. trichocarpa*	Bell-Irving	56.73	-129.73	579.00	No	Yes	bt	No	Yes
IRVC-7-6	*P. trichocarpa*	Bell-Irving	56.73	-129.73	579.00	No	Yes	tt	No	Yes
IRVD-7-4	*P. trichocarpa*	Bell-Irving	56.85	-129.62	677.00	Yes (admixed)	Yes	bt	No	Yes
ISKA-6-1	*P. trichocarpa*	Iskut	56.70	-131.15	73.00	No	Yes	tt	No	Yes
ISKA-6-2	*P. trichocarpa*	Iskut	56.70	-131.15	73.00	No	Yes	tt	No	Yes
ISKA-6-4	*P. trichocarpa*	Iskut	56.70	-131.15	73.00	No	Yes	tt	No	Yes
ISKA-6-5	*P. trichocarpa*	Iskut	56.70	-131.15	73.00	No	Yes	bt	No	No
ISKC-6-1	*P. trichocarpa*	Iskut	56.93	-130.33	317.00	No	Yes	bt	No	No
ISKC-6-2	*P. trichocarpa*	Iskut	56.93	-130.33	317.00	No	Yes	NA	No	No
ISKC-6-3	*P. trichocarpa*	Iskut	56.93	-130.33	317.00	No	Yes	tt	No	Yes
ISKC-6-5	*P. trichocarpa*	Iskut	56.93	-130.33	317.00	No	Yes	tt	No	Yes
JASP-30-1	*P. trichocarpa*	Willamette	44.00	-122.92	150.00	No	Yes	NA	No	No
JASP-30-3	*P. trichocarpa*	Willamette	44.00	-122.92	150.00	No	Yes	NA	No	No
JASP-30-4	*P. trichocarpa*	Willamette	44.00	-122.92	150.00	No	Yes	NA	No	No
JASP-30-5	*P. trichocarpa*	Willamette	44.00	-122.92	150.00	No	Yes	NA	No	No
JEFF-30-1	*P. trichocarpa*	Willamette	44.73	-123.08	100.00	No	Yes	NA	No	No

JEFF-30-2	*P. trichocarpa*	Willamette	44.73	-123.08	100.00	No	Yes	NA	No	No
JEFF-30-3	*P. trichocarpa*	Willamette	44.73	-123.08	100.00	No	Yes	NA	No	No
JEFF-30-4	*P. trichocarpa*	Willamette	44.73	-123.08	100.00	No	Yes	NA	No	No
KIMB-16-1	*P. trichocarpa*	Quesnel	52.93	-121.17	823.00	Yes (admixed)	Yes	tt	No	Yes
KIMB-16-2	*P. trichocarpa*	Quesnel	52.93	-121.17	823.00	Yes (pure)	Yes	tt	2	Yes
KIMB-16-3	*P. trichocarpa*	Quesnel	52.93	-121.17	823.00	Yes (admixed)	Yes	bt	2	Yes
KIMB-16-4	*P. trichocarpa*	Quesnel	52.93	-121.17	823.00	No	Yes	bt	No	Yes
KIMB-16-5	*P. trichocarpa*	Quesnel	52.93	-121.17	823.00	Yes (admixed)	Yes	tt	No	Yes
KIMB-16-6	*P. trichocarpa*	Quesnel	52.93	-121.17	823.00	Yes (admixed)	Yes	bb	No	Yes
KLNE-20-1	*P. trichocarpa*	Klinaklini	51.73	-125.57	427.00	No	Yes	NA	No	No
KLNE-20-2	*P. trichocarpa*	Klinaklini	51.73	-125.57	427.00	No	Yes	NA	No	No
KSPA-9-3	*P. trichocarpa*	Kispiox	55.77	-128.53	518.00	No	Yes	tt	No	Yes
KTMA-12-1	*P. trichocarpa*	Kitimat	54.25	-128.52	122.00	Yes (pure)	No	tt	2	Yes
KTMA-12-2	*P. trichocarpa*	Kitimat	54.25	-128.52	122.00	Yes (pure)	No	NA	No	No
KTMA-12-3	*P. trichocarpa*	Kitimat	54.25	-128.52	122.00	No	No	tt	No	Yes
KTMA-12-4	*P. trichocarpa*	Kitimat	54.25	-128.52	122.00	No	No	tt	2	Yes
KTMA-12-5	*P. trichocarpa*	Kitimat	54.25	-128.52	122.00	No	Yes	tt	No	Yes
KTMB-12-1	*P. trichocarpa*	Kitimat	54.15	-128.58	61.00	No	Yes	tt	No	No
KTMB-12-3	*P. trichocarpa*	Kitimat	54.15	-128.58	61.00	No	Yes	tt	No	No
KTMB-12-5	*P. trichocarpa*	Kitimat	54.15	-128.58	61.00	No	Yes	tt	No	No
KTMC-12-	*P. trichocarpa*	Kitimat	54.05	-128.68	18.00	No	No	tt	No	Yes

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KTMC-12-2	*P. trichocarpa*	Kitimat	54.05	-128.68	18.00	No	No	tt	No	Yes
KTMC-12-3	*P. trichocarpa*	Kitimat	54.05	-128.68	18.00	No	No	tt	2	Yes
KTMC-12-5	*P. trichocarpa*	Kitimat	54.05	-128.68	18.00	No	No	tt	2	Yes
KTSG-10-5	*P. trichocarpa*	Skeena	55.10	-127.92	213.00	No	Yes	tt	No	Yes
KTWF-10-3	*P. trichocarpa*	Skeena	55.08	-128.18	177.00	No	Yes	tt	No	Yes
LAFY-30-1	*P. trichocarpa*	Willamette	45.20	-123.08	100.00	No	Yes	NA	No	No
LAFY-30-2	*P. trichocarpa*	Willamette	45.20	-123.08	100.00	No	Yes	NA	No	No
LAFY-30-3	*P. trichocarpa*	Willamette	45.20	-123.08	100.00	No	Yes	NA	No	No
LAFY-30-5	*P. trichocarpa*	Willamette	45.20	-123.08	100.00	No	Yes	NA	No	No
LILA-26-3	*P. trichocarpa*	Lillooet	50.62	-123.38	411.00	No	Yes	NA	No	No
LILB-26-2	*P. trichocarpa*	Lillooet	50.55	-123.20	274.00	No	Yes	NA	No	No
LNZK-28-2	*P. trichocarpa*	Vancouver Island	49.23	-124.07	60.00	No	Yes	NA	No	No
LNZK-28-3	*P. trichocarpa*	Vancouver Island	49.23	-124.07	60.00	No	Yes	NA	No	No
LNZK-28-4	*P. trichocarpa*	Vancouver Island	49.23	-124.07	60.00	No	Yes	NA	No	No
LNZK-28-5	*P. trichocarpa*	Vancouver Island	49.23	-124.07	60.00	No	Yes	NA	No	No
LONG-29-1	*P. trichocarpa*	Columbia	46.08	-123.92	100.00	No	Yes	NA	No	No
LONG-29-2	*P. trichocarpa*	Columbia	46.08	-123.92	100.00	No	Yes	NA	No	No
LONG-29-3	*P. trichocarpa*	Columbia	46.08	-123.92	100.00	No	Yes	NA	No	No
LONG-29-4	*P. trichocarpa*	Columbia	46.08	-123.92	100.00	No	Yes	NA	No	No
LONG-29-5	*P. trichocarpa*	Columbia	46.08	-123.92	100.00	No	Yes	NA	No	No
MCFA-20-	*P. trichocarpa*	Klinaklini	51.32	-126.23	275.00	No	Yes	NA	No	No

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MCFA-20-2	*P. trichocarpa*	Klinaklini	51.32	-126.23	275.00	No	Yes	NA	No	No
MCFA-20-3	*P. trichocarpa*	Klinaklini	51.32	-126.23	275.00	No	Yes	NA	No	No
MCFA-20-4	*P. trichocarpa*	Klinaklini	51.32	-126.23	275.00	No	Yes	NA	No	No
MCFA-20-5	*P. trichocarpa*	Klinaklini	51.32	-126.23	275.00	No	Yes	NA	No	No
MCFA-20-6	*P. trichocarpa*	Klinaklini	51.32	-126.23	275.00	No	Yes	NA	No	No
MCGR-15-4	*P. trichocarpa*	McGregor	54.18	-122.00	579.00	No	Yes	tt	No	Yes
MCGR-15-6	*P. trichocarpa*	McGregor	54.18	-122.00	579.00	No	Yes	bt	No	Yes
MCGR-15-7	*P. trichocarpa*	McGregor	54.18	-122.00	579.00	No	Yes	tt	No	Yes
MCGR-15-8	*P. trichocarpa*	McGregor	54.18	-122.00	579.00	Yes (admixed)	Yes	bb	No	Yes
MCHA-19-1	*P. trichocarpa*	Chuckwall	51.63	-126.68	70.00	No	Yes	NA	No	No
MCHA-19-2	*P. trichocarpa*	Chuckwall	51.63	-126.68	70.00	No	Yes	NA	No	No
MCHA-19-3	*P. trichocarpa*	Chuckwall	51.63	-126.68	70.00	No	Yes	NA	No	No
MCHA-19-4	*P. trichocarpa*	Chuckwall	51.63	-126.68	70.00	No	Yes	NA	No	No
MCHA-19-5	*P. trichocarpa*	Chuckwall	51.63	-126.68	70.00	No	Yes	NA	No	No
MCHB-19-1	*P. trichocarpa*	Chuckwall	51.62	-126.58	122.00	No	Yes	NA	No	No
MCHB-19-2	*P. trichocarpa*	Chuckwall	51.62	-126.58	122.00	No	Yes	NA	No	No
MCHB-19-3	*P. trichocarpa*	Chuckwall	51.62	-126.58	122.00	No	Yes	NA	No	No
MCHB-19-4	*P. trichocarpa*	Chuckwall	51.62	-126.58	122.00	Yes (pure)	No	NA	No	No

MCHB-19-4	*P. trichocarpa*	Chuckwall	51.62	-126.58	122.00	No	Yes	NA	No	No
MCHB-19-5	*P. trichocarpa*	Chuckwall	51.62	-126.58	122.00	No	Yes	NA	No	No
MCMN-27-3	*P. trichocarpa*	Fraser	49.18	-122.58	15.00	Yes (pure)	No	NA	No	No
MEMA-28-1	*P. trichocarpa*	Vancouver Island	50.22	-125.80	30.00	No	Yes	NA	No	No
MEMA-28-3	*P. trichocarpa*	Vancouver Island	50.22	-125.80	30.00	No	Yes	NA	No	No
MEMA-28-4	*P. trichocarpa*	Vancouver Island	50.22	-125.80	30.00	No	Yes	NA	No	No
MEMA-28-5	*P. trichocarpa*	Vancouver Island	50.22	-125.80	30.00	No	Yes	NA	No	No
MTSM-27-2	*P. trichocarpa*	Fraser	49.12	-122.33	8.00	No	Yes	NA	No	No
MTSM-27-5	*P. trichocarpa*	Fraser	49.12	-122.33	8.00	No	Yes	NA	No	No
NASC-8-2	*P. trichocarpa*	Nass	55.05	-129.50	24.00	No	Yes	tt	No	Yes
NASC-8-5	*P. trichocarpa*	Nass	55.05	-129.50	24.00	No	Yes	bt	No	Yes
NASD-8-2	*P. trichocarpa*	Nass	55.05	-129.50	24.00	No	Yes	NA	No	No
NASD-8-4	*P. trichocarpa*	Nass	55.22	-129.13	58.00	No	Yes	tt	No	Yes
NASD-8-5	*P. trichocarpa*	Nass	55.22	-129.13	58.00	No	Yes	tt	No	Yes
NASF-8-2	*P. trichocarpa*	Nass	55.57	-128.78	152.00	No	Yes	tt	No	Yes
NASH-8-1	*P. trichocarpa*	Nass	55.72	-128.82	183.00	No	Yes	tt	No	Yes
NASH-8-4	*P. trichocarpa*	Nass	55.72	-128.82	183.00	No	Yes	tt	No	Yes
NASH-8-5	*P. trichocarpa*	Nass	55.72	-128.82	183.00	Yes (pure)	Yes	tt	No	Yes
NBON-29-1	*P. trichocarpa*	Columbia	45.58	-122.00	300.00	No	Yes	NA	No	No
NBON-29-2	*P. trichocarpa*	Columbia	45.58	-122.00	300.00	No	Yes	NA	No	No
NBON-29-4	*P. trichocarpa*	Columbia	45.58	-122.00	300.00	No	Yes	NA	No	No
NECA-14-1	*P. trichocarpa*	Nechako	54.10	-124.43	655.00	Yes (pure)	Yes	tt	No	No
NECB-14-	*P. trichocarpa*	Nechako	53.95	-124.43	671.00	Yes (pure)	Yes	tt	3	No

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NHTB-27-2	*P. trichocarpa*	Fraser	49.97	-121.82	335.00	No	Yes	NA	No	No
NHTB-27-5	*P. trichocarpa*	Fraser	49.97	-121.82	335.00	No	Yes	NA	No	No
NKND-3-2	*P. trichocarpa*	Taku	58.93	-133.18	122.00	Yes (admixed)	Yes	tt	No	Yes
NPLN-30-3	*P. trichocarpa*	Willamette	45.57	-123.00	100.00	No	Yes	NA	No	No
NPLN-30-4	*P. trichocarpa*	Willamette	45.57	-123.00	100.00	No	Yes	NA	No	No
NPLN-30-5	*P. trichocarpa*	Willamette	45.57	-123.00	100.00	No	Yes	NA	No	No
PHLA-22-1	*P. trichocarpa*	Philips	50.60	-125.32	5.00	Yes (pure)	Yes	NA	No	No
PHLA-22-2	*P. trichocarpa*	Philips	50.60	-125.32	5.00	No	Yes	NA	No	No
PHLA-22-3	*P. trichocarpa*	Philips	50.60	-125.32	5.00	No	Yes	NA	No	No
PHLA-22-4	*P. trichocarpa*	Philips	50.60	-125.32	5.00	No	Yes	NA	No	No
PHLA-22-5	*P. trichocarpa*	Philips	50.60	-125.32	5.00	No	Yes	NA	No	No
PHLC-22-1	*P. trichocarpa*	Philips	50.68	-125.25	58.00	No	Yes	NA	No	No
PHLC-22-2	*P. trichocarpa*	Philips	50.68	-125.25	58.00	No	Yes	NA	No	No
PHLC-22-3	*P. trichocarpa*	Philips	50.68	-125.25	58.00	No	Yes	NA	No	No
PHLC-22-4	*P. trichocarpa*	Philips	50.68	-125.25	58.00	No	Yes	NA	No	No
PHLC-22-5	*P. trichocarpa*	Philips	50.68	-125.25	58.00	No	Yes	NA	No	No
PITS-29-1	*P. trichocarpa*	Columbia	45.83	-123.12	900.00	No	Yes	NA	No	No
PITS-29-2	*P. trichocarpa*	Columbia	45.83	-123.12	900.00	No	Yes	NA	No	No
PITS-29-3	*P. trichocarpa*	Columbia	45.83	-123.12	900.00	No	Yes	NA	No	No
PITS-29-4	*P. trichocarpa*	Columbia	45.83	-123.12	900.00	No	Yes	NA	No	No

PITS-29-5	*P. trichocarpa*	Columbia	45.83	-123.12	900.00	No	Yes	NA	No	No
QAUS-16-1	*P. trichocarpa*	Quesnel	52.72	-122.47	442.00	No	Yes	bt	No	Yes
QAUS-16-3	*P. trichocarpa*	Quesnel	52.72	-122.47	442.00	Yes (admixed)	Yes	bb	2	Yes
QAUS-16-4	*P. trichocarpa*	Quesnel	52.72	-122.47	442.00	No	Yes	bt	No	Yes
QAUS-16-7	*P. trichocarpa*	Quesnel	52.72	-122.47	442.00	No	Yes	bt	No	Yes
QBKR-16-2	*P. trichocarpa*	Quesnel	52.95	-122.87	823.00	No	Yes	tt	2	Yes
QBKR-16-3	*P. trichocarpa*	Quesnel	52.95	-122.87	823.00	Yes (admixed)	Yes	bt	2	Yes
QBKR-16-4	*P. trichocarpa*	Quesnel	52.95	-122.87	823.00	Yes (admixed)	Yes	tt	2	Yes
QBKR-16-5	*P. trichocarpa*	Quesnel	52.95	-122.87	823.00	Yes (admixed)	Yes	bt	No	Yes
QCTN-16-1	*P. trichocarpa*	Quesnel	53.03	-122.15	823.00	No	Yes	bt	2	Yes
QCTN-16-3	*P. trichocarpa*	Quesnel	53.03	-122.15	823.00	No	Yes	tt	No	Yes
QCTN-16-4	*P. trichocarpa*	Quesnel	53.03	-122.15	823.00	No	Yes	tt	2	Yes
QFRS-16-1	*P. trichocarpa*	Quesnel	53.07	-122.52	472.00	No	Yes	bt	2	Yes
QFRS-16-2	*P. trichocarpa*	Quesnel	53.07	-122.52	472.00	No	Yes	tt	No	Yes
QFRS-16-3	*P. trichocarpa*	Quesnel	53.07	-122.52	472.00	Yes (admixed)	Yes	bt	No	Yes
QFRS-16-4	*P. trichocarpa*	Quesnel	53.07	-122.52	472.00	Yes (admixed)	Yes	bt	No	Yes
QFRS-16-5	*P. trichocarpa*	Quesnel	53.07	-122.52	472.00	Yes (admixed)	Yes	tt	2	Yes
QLKE-16-1	*P. trichocarpa*	Quesnel	52.97	-122.32	488.00	Yes (admixed)	Yes	bt	2	Yes
QLKE-16-2	*P. trichocarpa*	Quesnel	52.97	-122.32	488.00	Yes (admixed)	Yes	tt	No	Yes

QLKE-16-3	*P. trichocarpa*	Quesnel	52.97	-122.32	488.00	Yes (admixed)	Yes	tt	2	Yes
QLKE-16-4	*P. trichocarpa*	Quesnel	52.97	-122.32	488.00	No	Yes	tt	2	Yes
SHEL-15-1	*P. trichocarpa*	McGregor	54.03	-122.60	564.00	Yes (admixed)	Yes	bb	2	Yes
SHEL-15-2	*P. trichocarpa*	McGregor	54.03	-122.60	564.00	No	Yes	bt	No	Yes
SHEL-15-3	*P. trichocarpa*	McGregor	54.03	-122.60	564.00	Yes (admixed)	Yes	bb	No	Yes
SHEL-15-4	*P. trichocarpa*	McGregor	54.03	-122.60	564.00	Yes (admixed)	Yes	bb	2	Yes
SHEL-15-5	*P. trichocarpa*	McGregor	54.03	-122.60	564.00	No	Yes	tt	2	Yes
SHEL-15-6	*P. trichocarpa*	McGregor	54.03	-122.60	564.00	Yes (admixed)	Yes	tt	No	Yes
SKNB-10-1	*P. trichocarpa*	Skeena	54.68	-128.38	122.00	No	Yes	tt	No	Yes
SKNB-10-2	*P. trichocarpa*	Skeena	54.68	-128.38	122.00	No	Yes	tt	No	Yes
SKNC-10-1	*P. trichocarpa*	Skeena	54.77	-128.27	122.00	No	Yes	tt	No	Yes
SKNC-10-2	*P. trichocarpa*	Skeena	54.77	-128.27	122.00	No	Yes	tt	2	Yes
SKNC-10-4	*P. trichocarpa*	Skeena	54.77	-128.27	122.00	No	Yes	tt	No	Yes
SKND-10-2	*P. trichocarpa*	Skeena	54.85	-128.33	140.00	Yes (pure)	Yes	tt	No	Yes
SKNL-10-1	*P. trichocarpa*	Skeena	54.45	-128.75	61.00	No	Yes	tt	No	Yes
SKNL-10-3	*P. trichocarpa*	Skeena	54.45	-128.75	61.00	No	Yes	tt	No	Yes
SKNL-10-4	*P. trichocarpa*	Skeena	54.45	-128.75	61.00	No	Yes	tt	No	Yes
SKNM-10-1	*P. trichocarpa*	Skeena	54.40	-128.98	43.00	Yes (pure)	Yes	tt	No	Yes
SKNM-10-2	*P. trichocarpa*	Skeena	54.40	-128.98	43.00	No	Yes	tt	No	Yes
SKNM-10-	*P. trichocarpa*	Skeena	54.40	-128.98	43.00	No	Yes	tt	No	Yes

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SKNM-10-5	*P. trichocarpa*	Skeena	54.40	-128.98	43.00	No	Yes	tt	No	No
SKNM-10-6	*P. trichocarpa*	Skeena	54.40	-128.98	43.00	No	Yes	tt	No	Yes
SKNN-10-2	*P. trichocarpa*	Skeena	54.40	-128.98	43.00	Yes (pure)	Yes	tt	2	Yes
SKNN-10-3	*P. trichocarpa*	Skeena	54.40	-128.98	43.00	No	Yes	bt	No	Yes
SKNN-10-4	*P. trichocarpa*	Skeena	54.40	-128.98	43.00	No	Yes	tt	No	Yes
SKNN-10-5	*P. trichocarpa*	Skeena	54.40	-128.98	43.00	No	Yes	tt	No	Yes
SKNO-10-2	*P. trichocarpa*	Skeena	54.40	-128.98	43.00	No	Yes	tt	No	Yes
SKNO-10-3	*P. trichocarpa*	Skeena	54.40	-128.98	43.00	No	Yes	tt	No	Yes
SKNO-10-4	*P. trichocarpa*	Skeena	54.40	-128.98	43.00	No	Yes	tt	No	Yes
SKNP-10-10	*P. trichocarpa*	Skeena	54.40	-128.98	43.00	No	Yes	tt	No	No
SKNP-10-11	*P. trichocarpa*	Skeena	54.40	-128.98	43.00	No	Yes	tt	No	Yes
SKNP-10-2	*P. trichocarpa*	Skeena	54.40	-128.98	43.00	No	Yes	tt	No	Yes
SKNP-10-3	*P. trichocarpa*	Skeena	54.40	-128.98	43.00	No	Yes	tt	No	Yes
SKNP-10-4	*P. trichocarpa*	Skeena	54.40	-128.98	43.00	No	Yes	tt	No	Yes
SKNP-10-8	*P. trichocarpa*	Skeena	54.40	-128.98	43.00	Yes (pure)	Yes	tt	4	Yes
SKNP-10-9	*P. trichocarpa*	Skeena	54.40	-128.98	43.00	No	Yes	tt	4	Yes
SKNQ-10-1	*P. trichocarpa*	Skeena	54.40	-128.98	43.00	No	Yes	tt	No	No
SKNQ-10-3	*P. trichocarpa*	Skeena	54.40	-128.98	43.00	No	Yes	tt	No	Yes

SKNQ-10-4	*P. trichocarpa*	Skeena	54.40	-128.98	43.00	No	Yes	tt	No	No
SKNR-10-1	*P. trichocarpa*	Skeena	54.68	-128.35	244.00	No	Yes	tt	No	Yes
SKWB-24-4	*P. trichocarpa*	Jervis	50.23	-124.00	115.00	No	Yes	NA	No	No
SKWC-24-3	*P. trichocarpa*	Jervis	50.25	-124.00	152.00	No	Yes	NA	No	No
SKWC-24-4	*P. trichocarpa*	Jervis	50.25	-124.00	152.00	No	Yes	NA	No	No
SKWF-24-2	*P. trichocarpa*	Jervis	50.25	-123.93	244.00	No	Yes	NA	No	No
SLMD-28-5	*P. trichocarpa*	Vancouver Island	50.28	-125.87	30.00	No	Yes	NA	No	No
SQMA-25-3	*P. trichocarpa*	Squamish	49.87	-123.23	61.00	No	Yes	NA	No	No
SQMA-25-5	*P. trichocarpa*	Squamish	49.87	-123.23	61.00	No	Yes	NA	No	No
SQMC-25-1	*P. trichocarpa*	Squamish	50.10	-123.37	177.00	Yes (pure)	No	NA	No	No
SQMC-25-2	*P. trichocarpa*	Squamish	50.10	-123.37	177.00	No	Yes	NA	No	No
STEL-14-1	*P. trichocarpa*	Nechako	54.03	-124.92	701.00	Yes (admixed)	Yes	bt	No	Yes
STHA-21-2	*P. trichocarpa*	Homathko	50.82	-124.48	239.00	No	Yes	NA	No	No
STHA-21-3	*P. trichocarpa*	Homathko	50.82	-124.48	239.00	No	Yes	NA	No	No
STHA-21-4	*P. trichocarpa*	Homathko	50.82	-124.48	239.00	No	Yes	NA	No	No
STHA-21-5	*P. trichocarpa*	Homathko	50.82	-124.48	239.00	No	Yes	NA	No	No
STHB-21-1	*P. trichocarpa*	Homathko	50.88	-124.73	91.00	No	Yes	NA	No	No
STHB-21-2	*P. trichocarpa*	Homathko	50.88	-124.73	91.00	No	Yes	NA	No	No
STHB-21-	*P. trichocarpa*	Homathko	50.88	-124.73	91.00	No	Yes	NA	No	No

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STHB-21-4	*P. trichocarpa*	Homathko	50.88	-124.73	91.00	No	Yes	NA	No	No
STHB-21-5	*P. trichocarpa*	Homathko	50.88	-124.73	91.00	No	Yes	NA	No	No
STKB-5-3	*P. trichocarpa*	Lower Stikine	56.93	-131.78	31.00	No	Yes	bb	No	No
STKB-5-4	*P. trichocarpa*	Lower Stikine	56.93	-131.78	31.00	Yes (admixed)	Yes	bb	No	Yes
STKD-5-1	*P. trichocarpa*	Lower Stikine	57.33	-131.78	49.00	No	Yes	tt	No	Yes
STKD-5-3	*P. trichocarpa*	Lower Stikine	57.33	-131.78	49.00	No	Yes	bt	No	Yes
STKE-5-3	*P. trichocarpa*	Lower Stikine	57.52	-131.78	61.00	No	Yes	bb	No	Yes
STKF-5-1	*P. trichocarpa*	Lower Stikine	57.65	-131.57	85.00	Yes (admixed)	Yes	bt	No	Yes
STKG-4-4	*P. trichocarpa*	Upper Stikine	57.95	-129.67	732.00	No	Yes	tt	No	Yes
TAKA-3-1	*P. trichocarpa*	Taku	58.60	-133.57	31.00	No	Yes	bt	No	No
TAKA-3-2	*P. trichocarpa*	Taku	58.60	-133.57	31.00	No	Yes	tt	No	No
TAKA-3-3	*P. trichocarpa*	Taku	58.60	-133.57	31.00	No	Yes	tt	No	Yes
TAKB-3-3	*P. trichocarpa*	Taku	58.70	-133.40	49.00	Yes (admixed)	Yes	tt	No	Yes
TAKB-3-4	*P. trichocarpa*	Taku	58.70	-133.40	49.00	Yes (admixed)	Yes	bt	No	Yes
TAKB-3-5	*P. trichocarpa*	Taku	58.70	-133.40	49.00	Yes (admixed)	Yes	bt	No	Yes
TATB-1-4	*P. trichocarpa*	Alsek	59.43	-137.83	34.00	Yes (admixed)	Yes	bt	No	Yes
TATB-1-7	*P. trichocarpa*	Alsek	59.43	-137.83	34.00	Yes (admixed)	Yes	bt	No	Yes
TLKH-11-1	*P. trichocarpa*	Bulkley	54.67	-127.12	567.00	No	Yes	tt	No	Yes
TLKH-11-5	*P. trichocarpa*	Bulkley	54.67	-127.12	567.00	Yes (pure)	Yes	tt	2	Yes
TLKI-11-1	*P. trichocarpa*	Bulkley	54.67	-127.12	567.00	No	Yes	tt	No	No
TNZA-4-3	*P. trichocarpa*	Upper Stikine	58.30	-130.47	567.00	Yes (pure)	Yes	bb	2	Yes
TOBA-23-2	*P. trichocarpa*	Toba	50.52	-124.23	67.00	No	Yes	NA	No	No
TOBA-23-	*P. trichocarpa*	Toba	50.52	-124.23	67.00	No	Yes	NA	No	No

3										
TOBA-23-4	*P. trichocarpa*	Toba	50.52	-124.23	67.00	No	Yes	NA	No	No
TOBA-23-5	*P. trichocarpa*	Toba	50.52	-124.23	67.00	No	Yes	NA	No	No
TOBB-23-2	*P. trichocarpa*	Toba	50.57	-124.08	73.00	No	Yes	NA	No	No
TOBB-23-3	*P. trichocarpa*	Toba	50.57	-124.08	73.00	No	Yes	NA	No	No
TOBB-23-4	*P. trichocarpa*	Toba	50.57	-124.08	73.00	No	Yes	NA	No	No
TOBB-23-5	*P. trichocarpa*	Toba	50.57	-124.08	73.00	No	Yes	NA	No	No
TRTB-7-5	*P. trichocarpa*	Bell-Irving	56.57	-129.82	640.00	No	Yes	bt	No	Yes
TRTB-7-6	*P. trichocarpa*	Bell-Irving	56.57	-129.82	640.00	No	Yes	tt	No	Yes
TRTB-7-7	*P. trichocarpa*	Bell-Irving	56.57	-129.82	640.00	No	Yes	tt	No	Yes
WELC-27-3	*P. trichocarpa*	Fraser	49.67	-121.42	91.00	Yes (pure)	No	NA	No	No
WFSH-13-6	*P. trichocarpa*	Stuart	54.60	-124.77	686.00	Yes (admixed)	Yes	tt	No	Yes
WHTE-28-2	*P. trichocarpa*	Vancouver Island	50.13	-126.05	213.00	No	Yes	NA	No	No
WHTE-28-5	*P. trichocarpa*	Vancouver Island	50.13	-126.05	213.00	No	Yes	NA	No	No
WLOW-15-1	*P. trichocarpa*	McGregor	53.92	-122.28	640.00	No	Yes	bt	No	Yes
WLOW-15-3	*P. trichocarpa*	McGregor	53.92	-122.28	640.00	No	Yes	tt	2	Yes
WLOW-15-4	*P. trichocarpa*	McGregor	53.92	-122.28	640.00	No	Yes	tt	No	Yes
WLOW-15-5	*P. trichocarpa*	McGregor	53.92	-122.28	640.00	Yes (admixed)	Yes	bt	No	Yes
YALD-27-3	*P. trichocarpa*	Fraser	49.57	-121.47	549.00	No	Yes	NA	No	No
YALD-27-4	*P. trichocarpa*	Fraser	49.57	-121.47	549.00	No	Yes	NA	No	No
ZYMJ-10-	*P. trichocarpa*	Skeena	54.47	-127.93	305.00	No	Yes	tt	No	Yes

1										
ZYMJ-10-5	*P. trichocarpa*	Skeena	54.47	-127.93	305.00	No	Yes	tt	2	Yes

Table S2. Parameters for the RASPberry model with the highest log likelihood value, based on a whole genome SNP data set (see supplementary M&M) in 25 pure P. balsamifera, 25 pure *P. trichocarpa* and 68 admixed individuals.

Parameter*	Model
defaultRate	5 //cM per Megabase
timeSinceAdmixture	10
ancestryPropFile	**
ancestralRate_tricho (Levsen)†	300
ancestralRate_balsamifera (Levsen)†	200
miscopyRate	0.05
mutation1	0.0079365
mutation2	0.0079365
miscopyMutation	0.01
recomputeWindowSize	2
collapsingDistance	3

*See Price et al 2009 and Wegmann et al 2011

**used whole genome stimation from 900K SNP data set which is highly correlated to that based on chromosome 6,12 and 15 using whole SNP scanning

† Based on Levsen et al. 2012

Table S3. Candidate genes for local adaptation across P. trichocarpa's range, in chromosome 6 and 15 based on F_{ST} outlier tests and/or association analysis with environmental

variables and phenotypic traits (Geraldes et al. 2014; McKnown *et al.* 2014), and using a 34k SNP chip.

Selected candidates*	Chr	Gene model[a]	Start kb[b]	Annotation[c]	Fst test[d]		Geo/Env correlation test[e]	Trait associa. test[f]	Introgressed Region¶
					Fdist	Bayescan			
Yes	6	Potri.006G020600	1448.9	FAR1	***	***			
Yes	6	Potri.006G020700	1454.7	FHY3	***	***	Lat,Long		
No	6	Potri.006G048500	3475.9	Glycosyltransferase	***	***	Lat,MAT,MCMT,DD_0,DD_18		A
No	6	Potri.006G049700	3580.3	AP2	***				A
No	6	Potri.006G053800	3923.9	Zinc finger	**	**	MWMT		A
Yes	15	Potri.015G000200	12.7	ABCB19	***				B
Yes	15	Potri.015G000500	26.5	LSU4	**				B
Yes	15	Potri.015G002300	137.8	PRR5	***	***	Lat,MAT,MCMT,TD,DD_0,DD_18,EMT	Phenology - Biomass- Ecophysiology	B
Yes	15	Potri.015G002600	162.0	TTG1	***	***	Lat,MAT,MCMT,TD,DD_0,DD_18,EMT	Phenology - Biomass- Ecophysiology	B
Yes	15	Potri.015G003100	236.7	COMT1	***		Lat		B
Yes	15	Potri.015G004100	276.7	NAC062	**		Lat,MCMT,TD,DD_0,EMT	Phenology - Ecophysiology	B
Yes	15	Potri.015G006500	406.8	Unknown	***	***	Lat,MCMT,TD,DD_0,EMT		B
Yes	15	Potri.015G009100	597.6	Yippee	***	***	Lat,MCMT,DD_0	Phenology	B
Yes	15	Potri.015G009300	611.5	Dof- zinc finger	**	***	Lat,MAT,MCMT,TD,DD_0,DD_18,EMT	Phenology - Ecophysiology	B
No	15	Potri.015G125500	13870.2	MADS box				Phenology - Biomass	C

Table S4. Quantitive reverse transcription PCR (qTt-PCR) to test the levels of expression of COMT1 genes in different *P. trichocarpa* genotypes.

Table S4A. Primers used in qRT-PCR

Primer	Sequence
CO1-rt-F	GTTGATGCCATAATGCTGGCACAT
CO1-rt-R	CACGTACGTATTGAATGCACAGCACATC
18S-F	AATTGTTGGTCTTCAACGAGGAA
18S-R	AAAGGGCAGGGACGTAGTCAA

*For qRT-PCR analyses, 5 individuals from each poplar genotypes were randomly selected: homozygotes for balsamifera COMT1 (QQ), homozygotes for trichocarpa COMT1 (PP) and heterozygotes (QP). RNA was isolated from leaf tissue harvested on August 2013 from 11:00 am to 1:00 pm, following the protocol of Kolosova et al. (2004) (1). RNA was quantified based on absorption at 260 nm and then reverse-transcribed into cDNA using the SuperScript First-Strand Synthesis system (Invitrogen). Primers for the target gene (COMT1: CO1-rt-F, CO1-rt-R) were designed using Primer-Blast (2) and primers from for the reference gene (18S) were obtained from (3) (18S-F, 18S-R). Using all cDNA samples and three technical replicates per sample, we performed quantitative PCR using SYBR® Select Master Mix with CFX Connect™ Real-Time PCR Detection System (Invitrogen). To analyze gene expression levels, the 2ΔCT method (4) was used. We subtracted the Ct (threshold cycle) value of the target gene (COMT1) by the Ct value of the reference housekeeping gene (18S) to standardize for the amounts of RNA template. Here, the larger the ΔCT value, the lower the mRNA level. The Ct values were then compared between genotype groups using ANOVA and multiple comparison Tukey test. We also converted ΔCT values to a linear form using the term 2–ΔCT.

Table S4B. Gene expression levels in different genotypes of *COMT1* based on qRT-PCR. QQ represents genotypes homozygotes for *P. balsamifera* haplotypes, QP represents heterozygotes and PP represents genotypes homozygotes for *P. trichocarpa* haplotypes.

Sample	COMT1_Genotype	Ct_18S_reference gene	Ct_COMT1	ΔCT (Cq_COMT1 - Cq_18S)	2–ΔCT
QQ22	QQ	15.94	27.73	11.80	0.000280444
QQ28	QQ	16.31	28.26	11.95	0.000252031
QQ25	QQ	18.37	28.51	10.14	0.000884204
QQ30	QQ	17.49	28.17	10.68	0.000610946
QQ23	QQ	15.27	27.33	12.06	0.000234737
QP27	PQ	14.9	27.03	12.13	0.000223103
QP14	PQ	16.00	27.92	11.92	0.000258061
QP44	PQ	14.57	27.40	12.83	0.000137654
QP8	PQ	17.22	30.14	12.92	0.000128733
QP9	PQ	15.47	28.37	12.90	0.00013053
PP2	PP	13.88	28.28	14.40	4.64E-05
PP26	PP	14.15	28.47	14.32	4.89E-05
PP35	PP	13.59	26.89	13.30	9.89E-05
PP5	PP	13.28	28.17	14.89	3.29E-05
PP6	PP	13.69	27.53	13.84	6.84E-05

Table S5. List of genes in introgressed region from chromosome 6 and 15 based on local ancestry analysis in RASPberry.

Gene model v3	Chromosome	Introgressed Region (see Figure 2)	Start bp
Potri.006G047300	6	A	3362926
Potri.006G047400	6	A	3367842
Potri.006G047500	6	A	3382904
Potri.006G047600	6	A	3387931
Potri.006G047700	6	A	3394337
Potri.006G047800	6	A	3412602
Potri.006G047900	6	A	3416251
Potri.006G048000	6	A	3428314
Potri.006G048100	6	A	3435767
Potri.006G048200	6	A	3441197
Potri.006G048300	6	A	3453082
Potri.006G048400	6	A	3455995
Potri.006G048500	6	A	3476876
Potri.006G048600	6	A	3479534
Potri.006G048700	6	A	3494410
Potri.006G048800	6	A	3502417
Potri.006G048900	6	A	3511577
Potri.006G049000	6	A	3516210
Potri.006G049100	6	A	3518027
Potri.006G049200	6	A	3534435
Potri.006G049300	6	A	3539405
Potri.006G049400	6	A	3572786
Potri.006G049500	6	A	3575352
Potri.006G049600	6	A	3577659
Potri.006G049700	6	A	3580290
Potri.006G049800	6	A	3584244
Potri.006G049900	6	A	3585352
Potri.006G050000	6	A	3590598
Potri.006G050100	6	A	3612871
Potri.006G050200	6	A	3620003

Gene model v3	Chromosome	Introgressed Region (see Figure 2)	Start bp
Potri.006G050300	6	A	3643063
Potri.006G050400	6	A	3648901
Potri.006G050500	6	A	3650962
Potri.006G050600	6	A	3652919
Potri.006G050700	6	A	3655561
Potri.006G050800	6	A	3666733
Potri.006G050900	6	A	3672741
Potri.006G051000	6	A	3681915
Potri.006G051100	6	A	3686833
Potri.006G051200	6	A	3693920
Potri.006G051300	6	A	3700986
Potri.006G051400	6	A	3706602
Potri.006G051500	6	A	3708051
Potri.006G051600	6	A	3712940
Potri.006G051700	6	A	3723120
Potri.006G051800	6	A	3728291
Potri.006G051900	6	A	3732757
Potri.006G052000	6	A	3734407
Potri.006G052100	6	A	3736693
Potri.006G052200	6	A	3749410
Potri.006G052300	6	A	3756829
Potri.006G052400	6	A	3760125
Potri.006G052500	6	A	3768101
Potri.006G052600	6	A	3768788
Potri.006G052700	6	A	3778059
Potri.006G052800	6	A	3786821
Potri.006G052900	6	A	3811387
Potri.006G053000	6	A	3824895
Potri.006G053100	6	A	3831484
Potri.006G053200	6	A	3841284

Potri.006G053300	6	A	3854946
Potri.006G053400	6	A	3875357
Potri.006G053500	6	A	3886219
Potri.006G053600	6	A	3899010
Potri.006G053700	6	A	3901982
Potri.006G053800	6	A	3923944
Potri.006G053900	6	A	3934404
Potri.015G000100	15	B	718
Potri.015G000200	15	B	12677
Potri.015G000300	15	B	18076
Potri.015G000400	15	B	21154
Potri.015G000500	15	B	26481
Potri.015G000600	15	B	32239
Potri.015G000700	15	B	37947
Potri.015G000800	15	B	40286
Potri.015G000900	15	B	42652
Potri.015G001000	15	B	62625
Potri.015G001100	15	B	70823
Potri.015G001200	15	B	72405
Potri.015G001300	15	B	76529
Potri.015G001400	15	B	84957
Potri.015G001500	15	B	95829
Potri.015G001600	15	B	106143
Potri.015G001700	15	B	113349
Potri.015G001800	15	B	119245
Potri.015G001900	15	B	120496
Potri.015G002000	15	B	125378
Potri.015G002100	15	B	126927
Potri.015G002200	15	B	133318
Potri.015G002300	15	B	137759
Potri.015G002400	15	B	146190
Potri.015G002500	15	B	149764
Potri.015G002600	15	B	162021
Potri.015G002700	15	B	169831

Potri.015G002800	15	B	183196
Potri.015G002900	15	B	203640
Potri.015G003000	15	B	209639
Potri.015G003100	15	B	236968
Potri.015G003200	15	B	240398
Potri.015G003300	15	B	244282
Potri.015G003400	15	B	246736
Potri.015G003500	15	B	247166
Potri.015G003600	15	B	251085
Potri.015G003700	15	B	253596
Potri.015G003800	15	B	262782
Potri.015G003900	15	B	268522
Potri.015G004000	15	B	273252
Potri.015G004100	15	B	276664
Potri.015G004200	15	B	281188
Potri.015G004300	15	B	289125
Potri.015G004400	15	B	292701
Potri.015G004500	15	B	297501
Potri.015G004600	15	B	301982
Potri.015G004700	15	B	310478
Potri.015G004800	15	B	313921
Potri.015G004900	15	B	317586
Potri.015G005000	15	B	318346
Potri.015G005100	15	B	324815
Potri.015G005200	15	B	329951
Potri.015G005300	15	B	334725
Potri.015G005400	15	B	342635
Potri.015G005500	15	B	349201
Potri.015G005600	15	B	355168
Potri.015G005700	15	B	360375
Potri.015G005800	15	B	362192
Potri.015G005900	15	B	367350
Potri.015G006000	15	B	375417
Potri.015G006100	15	B	388134

Potri.015G006200	15	B	394635
Potri.015G006300	15	B	401359
Potri.015G006400	15	B	404468
Potri.015G006500	15	B	406777
Potri.015G006600	15	B	409935
Potri.015G006700	15	B	412188
Potri.015G006800	15	B	422668
Potri.015G006900	15	B	440386
Potri.015G007000	15	B	444823
Potri.015G007100	15	B	448365
Potri.015G007200	15	B	452861
Potri.015G007300	15	B	458876
Potri.015G007400	15	B	466963
Potri.015G007500	15	B	472570
Potri.015G007600	15	B	474256
Potri.015G007700	15	B	480884
Potri.015G007800	15	B	488522
Potri.015G007900	15	B	491967
Potri.015G008000	15	B	494511
Potri.015G008100	15	B	502912
Potri.015G008200	15	B	507230
Potri.015G008300	15	B	521697
Potri.015G008400	15	B	526505
Potri.015G008500	15	B	527335
Potri.015G008600	15	B	549477
Potri.015G008700	15	B	571152
Potri.015G008800	15	B	585592
Potri.015G008900	15	B	590801
Potri.015G009000	15	B	592354
Potri.015G009100	15	B	597610
Potri.015G009200	15	B	601409
Potri.015G009300	15	B	611499
Potri.015G009400	15	B	621712
Potri.015G009500	15	B	629684
Potri.015G009600	15	B	640314
Potri.015G009700	15	B	655882
Potri.015G009800	15	B	659824
Potri.015G009900	15	B	665491
Potri.015G010000	15	B	670429
Potri.015G010100	15	B	673363
Potri.015G010200	15	B	679470
Potri.015G010300	15	B	686701
Potri.015G010400	15	B	692700
Potri.015G010500	15	B	703077
Potri.015G010600	15	B	707479
Potri.015G010700	15	B	710140
Potri.015G010800	15	B	713815
Potri.015G010900	15	B	721815
Potri.015G011000	15	B	725856
Potri.015G011100	15	B	729257
Potri.015G011200	15	B	735325
Potri.015G011300	15	B	742773
Potri.015G011400	15	B	745998
Potri.015G011500	15	B	753082
Potri.015G011600	15	B	754817
Potri.015G011700	15	B	756920
Potri.015G011800	15	B	758283
Potri.015G011900	15	B	761676
Potri.015G012000	15	B	765908
Potri.015G012100	15	B	775679
Potri.015G012200	15	B	780352
Potri.015G012300	15	B	787447
Potri.015G012400	15	B	792937
Potri.015G012500	15	B	804149
Potri.015G012600	15	B	814410
Potri.015G012700	15	B	823142
Potri.015G012800	15	B	829009
Potri.015G012900	15	B	840198

Potri.015G013000	15	B	849511
Potri.015G013100	15	B	859616
Potri.015G013200	15	B	866349
Potri.015G013300	15	B	869556
Potri.015G013400	15	B	879297
Potri.015G118500	15	C	13340589
Potri.015G118600	15	C	13347602
Potri.015G118700	15	C	13358567
Potri.015G118800	15	C	13363254
Potri.015G118900	15	C	13378867
Potri.015G119000	15	C	13381315
Potri.015G119100	15	C	13384217
Potri.015G119200	15	C	13387137
Potri.015G119300	15	C	13388708
Potri.015G119400	15	C	13420539
Potri.015G119500	15	C	13427881
Potri.015G119600	15	C	13437147
Potri.015G119700	15	C	13443181
Potri.015G119800	15	C	13450146
Potri.015G119900	15	C	13495791
Potri.015G120000	15	C	13497065
Potri.015G120100	15	C	13500740
Potri.015G120200	15	C	13504131
Potri.015G120300	15	C	13513875
Potri.015G120400	15	C	13517154
Potri.015G120500	15	C	13524911
Potri.015G120600	15	C	13534933
Potri.015G120700	15	C	13538777
Potri.015G120800	15	C	13542174
Potri.015G120900	15	C	13543412
Potri.015G121000	15	C	13547456
Potri.015G121100	15	C	13555980
Potri.015G121200	15	C	13557989
Potri.015G121300	15	C	13565623
Potri.015G121400	15	C	13574575
Potri.015G121500	15	C	13583571
Potri.015G121600	15	C	13584454
Potri.015G121700	15	C	13588790
Potri.015G121800	15	C	13592871
Potri.015G121900	15	C	13604850
Potri.015G122000	15	C	13605985
Potri.015G122100	15	C	13609021
Potri.015G122200	15	C	13611137
Potri.015G122300	15	C	13618881
Potri.015G122400	15	C	13627969
Potri.015G122500	15	C	13635414
Potri.015G122600	15	C	13638401
Potri.015G122700	15	C	13639994
Potri.015G122800	15	C	13653311
Potri.015G122900	15	C	13660828
Potri.015G123000	15	C	13672157
Potri.015G123100	15	C	13683044
Potri.015G123200	15	C	13691247
Potri.015G123300	15	C	13696202
Potri.015G123400	15	C	13697565
Potri.015G123500	15	C	13707245
Potri.015G123600	15	C	13711820
Potri.015G123700	15	C	13729143
Potri.015G123800	15	C	13741366
Potri.015G123900	15	C	13749090
Potri.015G124000	15	C	13752932
Potri.015G124100	15	C	13757991
Potri.015G124200	15	C	13767796
Potri.015G124300	15	C	13781891
Potri.015G124400	15	C	13798542
Potri.015G124500	15	C	13806271
Potri.015G124600	15	C	13824535
Potri.015G124700	15	C	13829810

Potri.015G124800	15	C	13834878
Potri.015G124900	15	C	13840486
Potri.015G125000	15	C	13841314
Potri.015G125100	15	C	13848997
Potri.015G125200	15	C	13854295
Potri.015G125300	15	C	13855993
Potri.015G125400	15	C	13861692
Potri.015G125500	15	C	13870204
Potri.015G125600	15	C	13874217
Potri.015G125700	15	C	13878009
Potri.015G125800	15	C	13884264
Potri.015G125900	15	C	13887037
Potri.015G126000	15	C	13889098
Potri.015G126100	15	C	13892764
Potri.015G126200	15	C	13893781
Potri.015G126300	15	C	13897845
Potri.015G126400	15	C	13898667
Potri.015G126500	15	C	13904779
Potri.015G126600	15	C	13907143
Potri.015G126700	15	C	13910051
Potri.015G126800	15	C	13913898

Table S6. A Introgressed genes from *P. balsamifera* in *P. trichocarpa* in a telomeric region of chromosome 15, corresponding Arabidopsis ortholog gene code, GO term or protein group enriched in the introgressed regions, Tajima's D values higher than 99% of the distribution, genes with significant positive values of alpha and nucleotide diversity values higher than 95% of the distribution in P. balsamifera

Gene model v3	Description	start	end	Arabidopsis best hit	GO term enriched	Tajima's D	Positive selection (alpha)*	Pi-balsamifera
Potri.015G000100	VIT family	718	7519			Tajima > 99%		
Potri.015G000200	ABCB19; ATPase, coupled to transmembrane movement of substances / auxin efflux transmembrane transporter	12677	18022	AT3G28860	GO:0048466;GO:0048443;SM00382:AAA;GO:0016887;IPR003593;GO:0010218;;	Tajima > 99%		
Potri.015G000300	Peptidase family C78, Uncharacterized conserved protein	18076	20078			Tajima > 99%		
Potri.015G000400	Autophagy-related protein 13, Phosphoprotein involved in cytoplasm to vacuole targeting and autophagy	21154	24866			Tajima > 99%		

Potri.015G000500	NA- Ath 50% ~LSU4 response to low sulfur 4, similar to expressed protein in Arabidopsis thaliana%3B [co-ortholog (2of2) of At3g49580 C At5g24655 C At5g24660 C At3g49570 C]	26481	27392			Tajima > 99%	
Potri.015G000600	mitochondrial import inner membrane translocase subunit Tim17 FTim22 FTim23 family protein%3B [co-ortholog (1of2) of At3g49560 C At5g24650 C]	32239	35641			Tajima > 99%	
Potri.015G000700	NA*	37947	40110			Tajima > 99%	
Potri.015G000800	Thaumatin-like protein (Arabidopsis thaliana) GI:2435406 [co-ortholog (1of2) of At5g24620 C]	40286	41854			Tajima > 99%	
Potri.015G000900	NA	42652	45307			Tajima > 99%	
Potri.015G001000	Rpp14/Pop5 family RNase P/RNase MRP subunit POP5 LIPOATE-PROTEIN LIGASE B	62625	64009			Tajima > 99%	Pi > 95%
Potri.015G001100	Unknown function, DUF599 -At5g24600 C]	70823	71165			Tajima > 99%	Pi > 95%

Potri.015G001200	Rpp14 family protein3B ribonuclease P family protein At1g04635 C]	72405	76263	AT1G04635	GO:0006396;GO:0043228;GO:0043232;GO:0070013;GO:0043233;GO:0031981;GO:0031974;	Tajima > 99%	Pi > 95%
Potri.015G001300	Protein of unknown function, DUF599 - At5g24600 C]	76529	77962			Tajima > 99%	Pi > 95%
Potri.015G001400	NA	84957	85645			Tajima > 99%	Pi > 95%
Potri.015G001500	Protein of unknown function, DUF599 - At5g24600 C]	95829	97634			Tajima > 99%	Pi > 95%
Potri.015G001600	Rpp14/Pop5 family, LIPOATE-PROTEIN LIGASE B, ribonuclease activity	106143	107360			Tajima > 95%	Pi > 95%
Potri.015G001700	NA&	113349	114150			Tajima > 95%	Pi > 95%
Potri.015G001800	NA	119245	120097			Tajima > 95%	Pi > 95%
Potri.015G001900	SPFH stomatin-like band 7 family protein HFLC Prohibitins and stomatins of the PID superfamily	120496	124220			Tajima > 95%	Pi > 95%
Potri.015G002000	NA	125378	125545			Tajima > 95%	Pi > 95%
Potri.015G002100	F-box domain	126927	130749			Tajima > 95%	Pi > 95%
Potri.015G002200	Sigma 54 modulation protein / S30EA ribosomal protein	133327	136045	AT5G24490	GO:0043228;GO:0043232;	Tajima > 95%	Pi > 95%
Potri.015G002300	PRR5 PSEUDO-RESPONSE REGULATOR 5%3B [co-ortholog (2of3) of At5g24470 C]	137759	143403	AT5G24470	GO:0010218;	Tajima > 95%	Pi > 95%

Potri.015G002400	Late embryogenesis abundant protein	146192	147599			Tajima > 95%		Pi > 95%
Potri.015G002500	NA	149764	151121			Tajima > 95%		Pi > 95%
Potri.015G002600	TTG1, TRANSPARENT TESTA GLABRA 1, TTG, TTG1, UNARMED 23, URM23	162021	163539					
Potri.015G002700	NA	169831	169932					
Potri.015G002800	2OG-Fe(II) oxygenase superfamily, oxidoreductases	183196	190645				x	Pi < 5%
Potri.015G002900	NAC147 No apical meristem	203640	204896	AT1G71930	IPR003441;		x	Pi < 5%
Potri.015G003000	nuclear RNA polymerase C2	209639	235482				x	Pi < 5%
Potri.015G003100	COMT1 similar to Chain A%3B similar to Crystal Structure Analysis Of Caffeic Acid5-Hydroxyferulic Acid 35-O-Methyltransferase Ferulic Acid Complex. [ORG:Medicago sativa]%3B [co-ortholog (2of2) of CAA58218 C 1KYW_C C 1KYZ_A C At5g54160 C]	236720	239777				x	Pi < 5%
Potri.015G003200	NA^	240398	242448				x	Pi < 5%

Potri.015G003300	NAC-UBA/TS-N domain, NASCENT POLYPEPTIDE ASSOCIATED COMPLEX ALPHA SUBUNIT-RELATED	244282	246269				x	Pi < 5%
Potri.015G003400	NA	246736	247092				x	Pi < 5%
Potri.015G003500	Peroxidase, oxidation reduction, heme binding, response to oxidative stress	247166	249255				x	Pi < 5%
Potri.015G003600	Peroxidase, oxidation reduction, heme binding, response to oxidative stress	251085	252707				x	Pi < 5%
Potri.015G003700	NA#	253596	259375				x	Pi < 5%
Potri.015G003800	copper-binding protein-related%3B similar to low similarity to copper homeostasis factor gi:3168840 from Arabidopsis thaliana%3B [co-ortholog (1of2) of At4g27590 C]	262782	264158				x	Pi < 5%

Potri.015G003900	copper-binding family protein%3B similar to copper homeostasis factor gi:3168840 from Arabidopsis thaliana%3B copper-binding family protein%3B similar to copper homeostasis factor gi:3168840 from Ara%3B [co-ortholog (2of2) of At5g24580 C]	268522	271061				x	Pi < 5%
Potri.015G004000	Peptidase family M20/M25/M40, IAA-amino acid hydrolase	272966	276146				x	Pi < 5%
Potri.015G004100	anac062 (NAC62); TF	276664	279681	AT3G49530	IPR003441;		x	Pi < 5%

*Alpha estimates of a region comprising 14 genes within a 110-kb region (from 183 kb to 280 kb in chromosome 15) revealed signals of positive selection in 46% and 41% of all amino acid substitutions in *P. trichocarpa* and *P. balsamifera* respectively

Table S6B Genes from 280 kb to 880 kb from region B in chromosome 15 and region A in chromosome 6 associated with GO terms and protein groups enriched in the introgressed regions from P.balsamifera into P. trichocarpa.

Gene model v3	Description	start	Arabidopsis best hit	GO enriched
Potri.015G004300	Unknown function, DUF623	289125	AT4G18830	GO:0031981;GO:0031974;GO:0043228; GO:0043232;GO:0070013;GO:0043233;
Potri.015G004600	RNA recognition motif (RRM, RBD,RNP domain) Alternative splicing factor ASF/SF2 (RRM superfamily)	301982	AT3G49430	GO:0031981;GO:0031974;GO:0006396; GO:0043228;GO:0043232;GO:0070013; GO:0043233
Potri.015G004700	60S acidic ribosomal protein P1.%3B [co-ortholog (2of2) of At4g00810 C At5g47700 C At1g01100 C]	310478	AT5G24510	GO:0043228;GO:0043232;
Potri.015G005200	similar to mitochondrial transcription termination factor-related%3B similar to mTERF-related%3B [co-ortholog (1of2) of At5g54180 C]	329951	AT5G54180	GO:0043228;GO:0043232;
Potri.015G006000		375417	AT3G53480	IPR003593;SM00382:AAA;GO:0016887
Potri.015G006200	QLQ regulation of transcription, DNA-dependent in Ath growth-regulating factor 7	394635	AT5G53660	GO:0010218
Potri.015G006300		401359	AT5G51660	GO:0006396
Potri.015G007000	No apical meristem (NAM) protein	444823	AT5G17260	IPR003441
Potri.015G007100	UBIQUITIN EXTENSION PROTEIN 1%3B [co-ortholog (2of4) of At3g52590 C At2g36170 C]	448365	AT3G52590	GO:0031981;GO:0031974;GO:0043228; GO:0043232;GO:0070013;GO:0043233;

Potri.015G007700	MSP1 protein%3B putative%3B similar to intramitochondrial sorting protein%3B putative%3B similar to Swiss-Prot:P28737 MSP1 protein (TAT-binding homolog 4) (Saccharomyces cerevisiae)%3B similar to AAA family%3B [co-ortholog (1of5) of At4g27680 C At5g53540 C	480884	AT4G27680	IPR003593;SM00382:AAA;GO:0016887
Potri.015G007800		488522	AT2G46620	IPR003593;SM00382:AAA;GO:0016887
Potri.015G008700	similar to RNA helicase%3B putative%3B similar to SP%7CQ14562%7CATP dependent-helicase DDX8 RNA (helicase HRH1 DEAH) (box-protein 8 %7BHomo) %7Bsapiens%7D %3B [ortholog of At1g32490 CAt4g16680 CAt2g35340 C]	571152	AT1G32490	GO:0006396;GO:0016887;
Potri.015G009100	Yippee putative zinc-binding protein	597610	AT4G27740	PIRSF028804
Potri.015G009200	Yippee-like protein At4g27740.%3B [co-ortholog (2of5) of At4g27740 C], FAD NAD BINDING OXIDOREDUCTASES	601409	AT4G27745	PIRSF028804
Potri.015G009600	PHD finger family protein%3B similar to SET domain-containing protein%3B [co-ortholog (2of2) of At5g24330 C]	640314	AT5G24330	GO:0048466;GO:0048443;
Potri.015G009900		665491	AT5G53490.3	GO:0070013;GO:0043233;GO:0031974
Potri.015G010600	similar to Protein phosphatase 2C PPH1 (EC 3.36) (PP2C).%3B [ortholog of At4g27800 C]	707479	AT4G27800	GO:0043228;GO:0043232;GO:0031981; GO:0031974;GO:0070013;GO:0043233;
Potri.015G010700		710140	AT5G24314	GO:0043228;GO:0043232;
Potri.015G012900		840198	AT5G53350	IPR003593;GO:0070013;GO:0043233;GO:0031974;SM00382:AAA;GO:0016887;
Potri.006G045300	PF00240-Ubiquitin family	3200269	AT3G52590	GO:0031981;GO:0031974;GO:0043228; GO:0043232;;;
Potri.006G048000	PF00154-recA bacterial DNA recombination protein	3428314	AT3G10140	IPR003593;SM00382:AAA;GO:0016887
Potri.006G048300	PF00076-RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	3453082	AT1G51510	GO:0006396;GO:0043228;GO:0043232; GO:0031981;GO:0031974;GO:0070013; GO:0043233
Potri.006G048400	PF08271-TFIIB zinc-binding;PF00382-Transcription factor TFIIB repeat	3455995	AT3G10330	GO:0070013;GO:0043233;GO:0031981; GO:0031974;;;

Potri.006G048600	PF00225-Kinesin motor domain;PF00307-Calponin homology (CH) domain	3479534	AT3G10310	GO:0043228;GO:0043232;
Potri.006G049000		3516210	AT3G21090	IPR003593;SM00382:AAA;GO:0016887
Potri.006G049300	PF00005-ABC transporter	3539405	AT2G41700	GO:0016887
Potri.006G050200	PF00626-Gelsolin repeat;PF02209-Villin headpiece domain	3620003	AT2G41740	GO:0043228;GO:0043232;
Potri.006G051200	PF01138-3' exoribonuclease family, domain 1	3693920	AT1G60080	GO:0006396
Potri.006G051300	PF10288-Protein of unknown function (DUF2392)	3700986	AT4G35910	GO:0006396
Potri.006G051400	PF02365-No apical meristem (NAM) protein	3706602	AT3G04070	IPR003441
Potri.006G052400	PF03719-Ribosomal protein S5, C-terminal domain;PF00333-Ribosomal protein S5, N-terminal domain	3760125	AT3G57490	GO:0043228;GO:0043232;
Potri.006G052700	PF00295-Glycosyl hydrolases family 28	3778059	AT3G07970	GO:0048466;GO:0048443;
Potri.006G053500	PF02045-CCAAT-binding transcription factor (CBF-B/NF-YA) subunit B	3886219	AT3G14020	GO:0031981;GO:0070013;GO:0043233; GO:0031974;;;

Supplementary Table 6C List of GO terms enriched in the introgressed regions from *P. balsamifera* into *P. trichocarpa*.

GO:0006396~RNA processing
GO:0010218~response to far red light
GO:0016887~ATPase activity
GO:0031974~membrane-enclosed lumen
GO:0031981~nuclear lumen
GO:0043228~non-membrane-bounded organelle
GO:0043232~intracellular non-membrane-bounded organelle
GO:0043233~organelle lumen
GO:0048443~stamen development
GO:0048466~androecium development
GO:0070013~intracellular organelle lumen
IPR003441:No apical meristem (NAM) protein
IPR003593:ATPase, AAA+ type, core
PIRSF028804:protein yippee-like
SM00382:AAA

Table S7. List of genes in introgressed region B in chromosome 15 that showed significantly different levels of expression in admixed (bb, bt) individuals compared to pure *P. trichocarpa* individuals.

			Anova		Tukey tests		Anova		Tukey tests
Gene model v3	**Description**	**Leaf Mean FPKM**	**F-value**	**p-value**	***Leaf Expression**	**Xylem Mean FPKM**	**Fvalue**	**pvalue**	***Xylem Expression**
Potri.015G001200	Major Facilitator Superfamily, ET TRANSLATION PRODUCT-RELATED, Uncharacterized conserved protein	9.577835	30.65	1.51E-10	tt>bt>bb	22.81604	31.62	2.33E-10	tt>bt=bb
Potri.015G001500		0.07304318	15.42	2.28E-06	bb>bt=tt	0.002600863	ns	ns	
Potri.015G002100	F-box domain	13.62576	29.91	2.29E-10	tt>bt>bb	7.238503	29.7	6.31E-10	tt>bt>bb
Potri.015G002600	TTG1, TRANSPARENT TESTA GLABRA 1, TTG, TTG1, UNARMED 23, URM23	18.45906	7.873	0.000768	bb=bt>tt	9.671041	50.61	4.74E-14	bb>bt>tt
Potri.015G003100	COMT1	9.53016	72.54	<2e-16	bb>bt>tt	102.9831	72.48	<2e-16	bb>bt>tt
Potri.015G003200		0.3963508	47.86	2.73E-14	bt>bb=tt	1.090179	ns	ns	
Potri.015G003800		0.1366683	14.23	5.39E-06	bt>tt	0.006370198	ns	ns	
Potri.015G004200	CCR4 Endonuclease/Exonuclease/phosphatase family, CARBON CATABOLITE REPRESSOR PROTEIN 4	1.341835	7.833	0.000794	bt=bb>tt	0.327882	52.36	2.39E-14	bb>bt>tt
Potri.015G005900		0.1446214	21.76	3.09E-08	bt>bb=tt	0.01141833	ns	ns	
Potri.015G006000		0.01184041	6.481	0.00249	bt>bb=tt	0.007379346	10.67	9.67E-05	bt>bb=tt
Potri.015G007200		28.90136	ns	ns		51.09009	14.89	4.60E-06	bb>bt=tt
Potri.015G011300	alpha/beta hydrolase fold,Soluble epoxide hydrolase	6.392737	7.771	0.000837	bb>tt	2.703451	12.2	3.11E-05	bb=bt>tt
Potri.015G012300		4.513397	ns	ns		9.047215	19.31	2.50E-07	bb>bt=tt
Potri.015G012700		13.73239	12.19	2.47E-05	bt=bb>tt	17.03197	ns	ns	

*RNAseq data was obtained from developing xylem in 197 accessions (385 samples including replicates), and from expanding leaves of defined developmental stage in 191 accessions (389 samples including replicates) grown at Totem Field. For the nearly 800 samples, RNA-seq reads were mapped to the ~40,000 genes in the poplar reference genome, and FPKM (Fragments Per Kilobase of transcript per Million mapped reads) were estimated (Corea, et al. In preparation). We compared levels of gene expression (measured by FPKM values) among the three genotypic categories (bb, bt and tt) using ANOVAs correcting p-values for multiple testing. Among the 134 genes. : bb and bt represent admixed homozygotes and heterozygote genotypes for balsam alleles respectively. tt represents genotypes homozygotes for trichocarpa alleles. ns= pvalue >0.05

Table S8. A Genes from the first introgressed region of chromosome 15 that showed associations with traits related to phenology, ecophysiology and biomass (McKown et at. 2014)

		Phenology				Biomass			Ecophysiology	
Gene model v3	Gene name	Bud set	Leaf drop	Post-bud set period	100% Yellowing	Growth period	Height	Height growth cessation	Chlsummer	Nmass
Potri.015G002300	PRR5	x	x	x			x		x	
Potri.015G002600	TTG1	x	x	x		x	x	x	x	
Potri.015G004100	ANAC062	x	x		x	x		x	x	x
Potri.015G009100	Yippee								x	
Potri.015G009300	Dof-type zinc finger	x	x	x	x	x			x	

Table S8. B. List of traits used in ANOVAs to determine if admixed individuals with balsamifera introgressed region are phenotypically different to those trichocarpa individuals without balsamifera genes. Chlsummer: Chlorophyll content summer, Nmass: Leaf nitrogen content per unit dry mass, Post.bud_set: Post bud set period, Yellowing_100%: total canopy leaf yellowing. The complete data set can be found in McKown et al. 2013 - Supporting information STable 2

Trait type	Traits from 2008	Traits from 2009	Traits from 2010	Traits from 2011	Total datasets
Phenology	Bud_set_08	Bud_set_09	Bud_set_10		3
	Leaf_drop_08	Leaf_drop_09	Leaf_drop_10		3
		Post.bud_set._09	Post.bud_set._10		2
			Yellowing_100%_10		1
Biomass		Height_09	Height_10	Height_11	3
			Growth_period_10		1
		Height_growth_cessation_09			1
Ecophysiology		Chsummer_09		Chsummer_11	2
		Nmass_09	Nmass_10		2
				Total tests:	**18**

Table S8. C List of F-values and p-values from ANOVAs comparing genotypes homozygous for introgressed *P. balsamifera* alleles, heterozygotes and homozygous for *P. trichocarpa* alleles in the first 880kb of chromosome 15.

Trait type	Trait	Fvalue	p-value
Phenology	Bud_set_08	3.974	0.021
	Bud_set_09	1.554	0.215
	Bud_set_10	1.644	0.197
	Leaf_drop_08	4.747	0.0101
	Leaf_drop_09	1.719	0.183
	Leaf_drop_10	3.542	0.0316
	Post.bud_set._09	0.317	0.729
	Post.bud_set._10	0.34	0.712
	Yellowing_100%_10	0.707	0.495
Biomass	Height_09	5.053	0.0076
	Height_10	0.787	0.457
	Height_11	1.098	0.336
	Height_growth_cessation_09	2.022	0.136
	Growth_period_10	0.608	0.546
Ecophysiology	**Chsummer_09**	**7.999**	**0.000609***
	Chsummer_11	**9.242**	**0.000347***
	Nmass_09	**6.225**	**0.00259***
	Nmass_10	2.983	0.0585

*significant differences after p-values were adjusted with Bonferroni correction (<0.0028)

Supporting information: Materials and Methods

Data sets used in this study including those generated here as well as those already published or in preparation for publication are presented in Table 1.

Table A1. List of the data sets used in this study, including those generated here as well as those already published or in preparation for publication. Data generated by this study is highlighted in orange (i.e. SNPs for local ancestry analysis, RASPberry; and gene sequence anaysis. See M&M and Supplementary Figure 2). Data previously published is highlighted in blue (i.e. phenotypic data, McKown et at. 2014) and in preparation for publication is highlighted in purple (RNA-seq, O. Corea, S. Biswas et al., preparation; PCA and preliminary RASPberry analysis, Geraldes et al in preparation). Data has now been archived in SRA and dryad.

Data set	Details	Individuals	Usage	Repository
Whole genome data set (971k_SNPs)*	Geraldes et al., in preparation	435 P. trichocarpa, 448 P. balsamifera	PCA analysis (Appendix S1, SI; Geraldes et al., In preparation) to select reference and admixed individuals (25 pure P. balsamifera, 25 pure P. trichocarpa, 68 admixed)	In preparation
Whole genome data set (from 971k_SNPs)*		25 pure P. balsamifera, 25 pure P. trichocarpa, 68 admixed	Preliminary analysis in RASPberry to select the model with the highest log likelihood value	†Dryad, ~SRA
Whole genome data set (from 971k_SNPs)*		68 admixed	Individual ancestries used in the input files for RASPberry analysis (ANCESTRY)	†Dryad, ~SRA
SNPs chromosome 6, 12, 15	Suarez et al (this MS)	25 pure P. balsamifera, 25 pure P. trichocarpa, 68 admixed	Local ancestry analysis(RASPberry). For the pure individuals only, Tajima's D, nucleotide diversity (π) (vcftools) and LD (Haploview, R) - in chromosome 15 - were estimated	†Dryad, ~SRA
SNPs chromosome 15	Suarez et al (this MS)	435 P. trichocarpa	Used to identify admixed individuals from northern populations (161) using NJ analysis (Mega). Also used to estimate LD (Haploview, R) - in 36 admixed individuals	†Dryad, ~SRA
Gene sequence analysis (COMT1, COMT2)	Suarez et al (this MS)	301 P. trichocarpa, 242 P. balsamifera	F_{ST} value per SNP (Arlequin), haplotype distribution	†Dryad, ~SRA
Gene sequence analysis (TTG1)	Suarez et al (this MS)	297 P. trichocarpa	F_{ST} value per SNP (Arlequin), haplotype distribution	†Dryad, ~SRA
Gene sequence analysis (PRR5)	Suarez et al (this MS)	302 P. trichocarpa	F_{ST} value per SNP (Arlequin), haplotype distribution	†Dryad, ~SRA

RNA-seq data	Corea et al., preparation	385 RNA samples from developing xylem in 197 accessions (most in at least duplicate), and 389 RNA samples isolated from expanding leaves of defined developmental stage in 191 accessions (most in at least duplicate)	We mined a population-wide RNA-seq dataset grown at Totem Field (O. Corea, S. Biswas et al., preparation). Levels of gene expression (measured by FPKM values) were compared among the three genotypic categories (bb, bt and tt).	¶SRA
Phenotypic data †	McKown et at. 2014			

~SRA: Accession: PRJNA276056; ID: 276056
¶SRA: Bioproject ID 300564
†Dryad: doi:10.5061/dryad.0817m

The input files and data used for the analyses implemented in this study have been archive in dryad: doi:10.5061/dryad.0817m (Table 2).

Table A2. List of the input files and data used for the analyses implemented in this study and now archive in dryad (doi:10.5061/dryad.0817m)

Title	Original SNP data ch6 12 15_replace
Description	SNPs in three chromosomes (6, 12, 15) for 50 reference individuals (25 pure *P. balsamifera* and 25 pure P. trichocarpa) and 68 admixed individuals
Title	971Kb_filtered_dataset
Description	Filtered dataset(MAF >0.1, GR 0.95), for 50 pure and 68 admixed individuals. The initial dataset consisted of 971K SNPs (3691 genes, 19 chromosomes)
Title	alpha estimates in introgressed regions
Description	Data from Table 2. Alpha estimate for three introgressed *P. balsamifera* regions in P. trichocarpa, one in chromosome (Chr) 06 (region A) and two in chromosome 15 (B and C).
Title	Tajima and Nucleotide Diversity estimates
Downloaded	1 time
Description	Data for Figure 2, Figure 4 Supporting Information (Tajimas' D) and Figure 7 Supporting Information (Nucleotide diversity).
Title	RASPberry
Description	Data for Figure 1, Figure 2 supportive information and Figure 3 supportive information.
Title	LD_Haploview
Description	Data for Figure 3 and Figure 6 supportive information.
Title	NJ analysis

Description	Data from Figure 1 Supporting information and Figure 5 Supporting information
Title	Gene_sequences
Description	Data for Figure 4, Figure 8 supportive information and Figure 9 supportive information.

For local ancestry analysis in RASPberry, we selected 50 reference individuals (25 pure *P. balsamifera* and 25 pure *P. trichocarpa*) and 68 admixed individuals (36 *P. trichocarpa* individuals with *P. balsamifera* admixture, and 32 *P. balsamifera* individuals with *P. trichocarpa* admixture) from a collection of 435 *P. trichocarpa* and 448 *P. balsamifera* genotypes, using a previous genome wide admixture analysis and a PCA based on 971K SNPs from 3691 genes in all 19 chromosomes (Geraldes et al in preparation). This analysis also included other *P.* species (i.e. *P. deltoides, P. fremontii, P. heterophylla, P. angustifolia*).

Figure 1 shows eigenvector 1 (67.78%) separating *P. balsamifera* from *P. trichocarpa* and revealing admixed individuals, while eigenvector 10 (4.9%) separates *P. trichocarpa* samples along a north-south axis. Additional eigenvectors separated *P. balsamifera* and *P. trichocarpa* from other *P.* species (Geraldes et al in preparation). Based on eigenvector 1 values, we identified 25 pure *P. trichocarpa* (0.034 to 0.037), 25 pure *P. balsamifera* (-0.039 to -0.035), 36 admixed *P. trichocarpa* (0.019 to 0.029) and 32 admixed *P. balsamifera* (-0.031 to 0.006).
Figure 2 shows a detailed section of Figure 1 with *P. trichocarpa* admixed individuals selected for RASPberry analysis (orange), and those selected for LD decay estimates (black). The latter were selected within a set of admixed individuals with eigenvector 1 values raging from 0.024 0.029, to avoid pure *P. trichocarpa* and early generation hybrids.

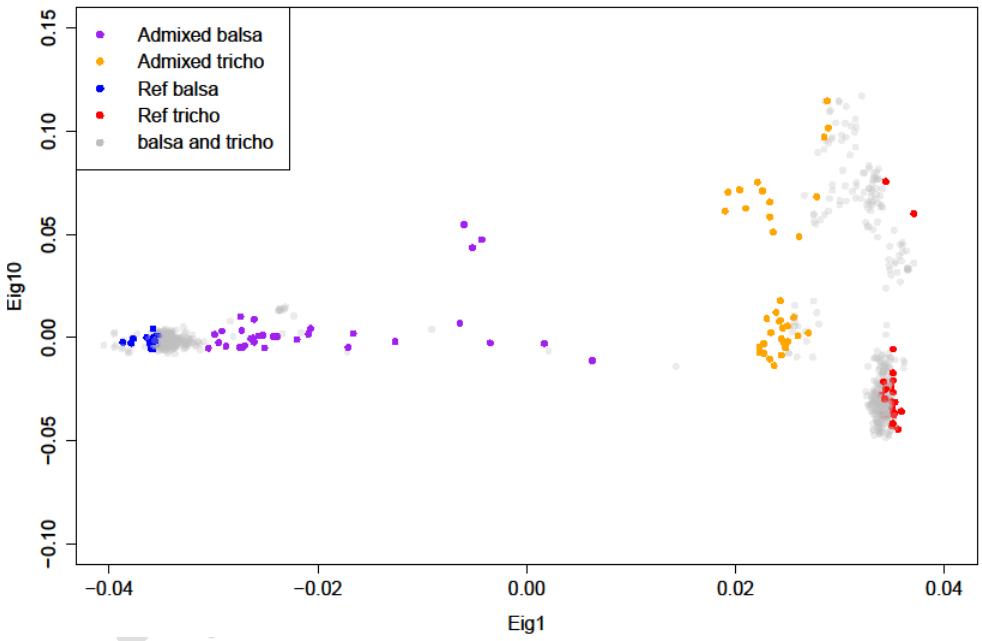

Figure A1. Principal Component Analysis (PCA) plot of SNPs from *P. trichocarpa* and *P. balsamifera* accessions. The plot shows Eigenvector 1 vs Eigenvector 10 from a PCA based on 50 pure individuals (25 pure *P. balsamifera* and 25 pure *P. trichocarpa*) and 68 admixed individuals (32 admixed *P. balsamifera* and 36 admixed *P. trichocarpa*). SNPs from pure *P. balsamifera* (blue), pure *P. trichocarpa* (red) and *P. trichocarpa* admixed with *P. balsamifera* SNPs (yellow) were used in ancestry analaysis. This analysis is based on a previous genome wide admixture analysis based on 900K SNPs from 3691 genes in all 19 chromosomes (Geraldes et al in preparation).

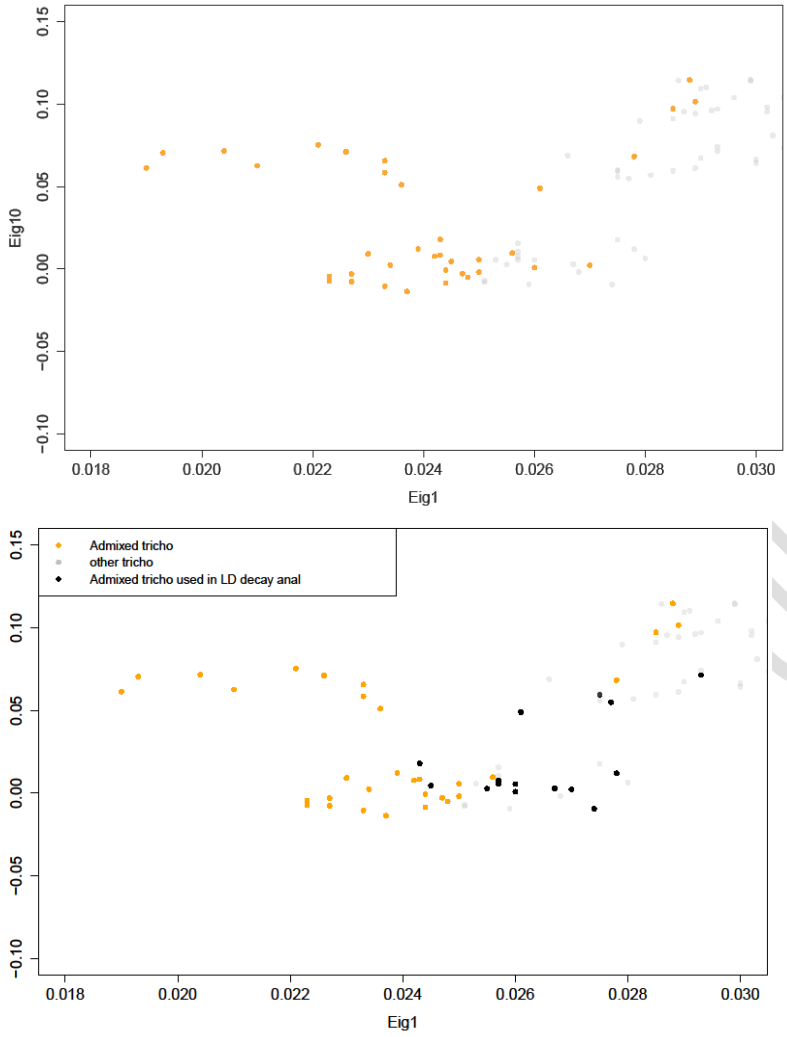

Figure 2. Detail of the PCA plot in Figure 1 of SNPs from admixed *P. trichocarpa* accessions. Left: Admixed *P. trichocarpa* accessions selected for RASPberry analysis (orange), and those selected for LD decay estimates (black).