Table S1. Akaike information criterion (AIC) for diameter at breast height (**DBH30**), total height (**HT30**) at age 30 years, and western gall rust normal score at age 36 years (**NSWGR36**) across the four RES-FOR progeny test sites (JUDY, VIRG, SWAN, and TIME). See the text for a detailed description of the *a priori* design (**Design**) and *a posteriori* first-order autoregressive (**AR1×AR1**) models. The lowest AIC values and, therefore, the model used to obtain the spatially adjusted phenotype for each combination of trait and site are shown in bold. The AIC values were not estimated due to a lack of convergence for WGR36 in JUDY and SWAN.

Site/Trait[a]	**DBH30**		**HT30**		**NSWGR36**	
	Design	**AR1×AR1**	**Design**	**AR1×AR1**	**Design**	**AR1×AR1**
JUDY	18571	**18542**	13991	**13816**	11485	[b]
VIRG	15802	**15793**	12862	**12706**	10857	**10855**
SWAN	21458	**21449**	13316	**13243**	12445	[b]
TIME	21425	**21424**	14084	**13995**	12482	**12475**

NOTE: [a] **DBH30**: diameter at breast height at age 30 years
HT30: total height at age 30 years
NSWGR36: west gall rust normal score at age 36 years
[b] AIC values were not estimated due to convergence problems

Table S2. Genetic correlation (and approximated standard errors) between traits within sites based on ABLUP and ssGBLUP for the full SNP set (ssGBLUP$_{25K}$) and the highest ancestry-informative SNP subset (ssGBLUP$_{8K}$) using the design (above diagonal) and spatial (below diagonal) phenotype adjustments. See text for traits´ abbreviations, Table 1 for sites´ abbreviations, and Table 3 for models´ abbreviations.

Model	Site	Trait	DBH30	HT30	NSWGR36
ABLUP	JUDY	DBH30	-	0.60 (0.04)	-0.40 (0.05)
		HT30	0.65 (0.04)	-	-0.40 (0.05)
		NSWGR36	-0.38 (0.05)	-0.37 (0.05)	-
	VIRG	DBH30	-	0.48 (0.05)	-0.27 (0.05)
		HT30	0.48 (0.05)	-	-0.01 (0.06)
		NSWGR36	-0.30 (0.05)	-0.03 (0.06)	-
	SWAN	DBH30	-	0.60 (0.04)	-0.38 (0.04)
		HT30	0.61 (0.03)	-	-0.35 (0.04)
		NSWGR36	-0.38 (0.04)	-0.35 (0.04)	-
	TIME	DBH30	-	0.52 (0.04)	-0.36 (0.05)
		HT30	0.53 (0.04)	-	-0.47 (0.05)
		NSWGR36	-0.37 (0.05)	-0.48 (0.05)	-
ssGBLUP_25K	JUDY	DBH30	-	0.68 (0.03)	-0.42 (0.05)
		HT30	0.70 (0.07)	-	-0.38 (0.05)
		NSWGR36	-0.40 (0.11)	-0.37 (0.11)	-
	VIRG	DBH30	-	0.44 (0.05)	-0.33 (0.05)
		HT30	0.45 (0.11)	-	0.02 (0.06)
		NSWGR36	-0.34 (0.09)	-0.01 (0.12)	-
	SWAN	DBH30	-	0.57 (0.04)	-0.42 (0.04)
		HT30	0.59 (0.06)	-	-0.33 (0.04)
		NSWGR36	-0.42 (0.06)	-0.32 (0.07)	-
	TIME	DBH30	-	0.51 (0.04)	-0.38 (0.04)
		HT30	0.51 (0.08)	-	-0.48 (0.05)
		NSWGR36	-0.39 (0.1)	-0.48 (0.08)	-
ssGBLUP_8K	JUDY	DBH30	-	0.68 (0.04)	-0.46 (0.05)
		HT30	0.72 (0.06)	-	-0.38 (0.06)
		NSWGR36	-0.41 (0.10)	-0.38 (0.11)	-
	VIRG	DBH30	-	0.45 (0.05)	-0.26 (0.05)
		HT30	0.46 (0.11)	-	0.02 (0.06)
		NSWGR36	-0.33 (0.09)	-0.01 (0.12)	-
	SWAN	DBH30	-	0.58 (0.04)	-0.42 (0.04)
		HT30	0.59 (0.06)	-	-0.34 (0.04)
		NSWGR36	-0.42 (0.06)	-0.32 (0.07)	-
	TIME	DBH30	-	0.51 (0.04)	-0.40 (0.04)
		HT30	0.52 (0.08)	-	-0.47 (0.05)
		NSWGR36	-0.39 (0.09)	-0.48 (0.09)	-

Table S3. Genetic correlation (and approximated standard errors) between sites based on ABLUP and ssGBLUP for the full SNP set (ssGBLUP$_{25K}$) and the highest ancestry-informative SNP subset (ssGBLUP$_{8K}$) using the design (above diagonal) and spatial (below diagonal) phenotype adjustments. See text for traits′ abbreviations, Table 1 for sites′ abbreviations, and Table 3 for models′ abbreviations.

Model	Trait	Site	JUDY	VIRG	SWAN	TIME
ABLUP	DBH30	JUDY	-	0.64 (0.04)	0.71 (0.04)	0.76 (0.03)
		VIRG	0.61 (0.05)	-	0.82 (0.02)	0.73 (0.03)
		SWAN	0.69 (0.04)	0.82 (0.02)	-	0.84 (0.02)
		TIME	0.74 (0.03)	0.74 (0.03)	0.83 (0.02)	-
	HT30	JUDY	-	0.60 (0.05)	0.66 (0.04)	0.66 (0.04)
		VIRG	0.65 (0.04)	-	0.72 (0.03)	0.57 (0.05)
		SWAN	0.64 (0.04)	0.72 (0.03)	-	0.78 (0.03)
		TIME	0.65 (0.04)	0.61 (0.04)	0.75 (0.03)	-
	NSWGR36	JUDY	-	0.85 (0.02)	0.92 (0.01)	0.88 (0.02)
		VIRG	0.86 (0.02)	-	0.91 (0.01)	0.93 (0.01)
		SWAN	0.93 (0.01)	0.91 (0.01)	-	0.95 (0.01)
		TIME	0.89 (0.01)	0.92 (0.01)	0.95 (0.01)	-
ssGBLUP$_{25K}$	DBH30	JUDY	-	0.72 (0.04)	0.78 (0.03)	0.76 (0.03)
		VIRG	0.68 (0.13)	-	0.86 (0.02)	0.81 (0.02)
		SWAN	0.75 (0.10)	0.86 (0.10)	-	0.89 (0.01)
		TIME	0.75 (0.10)	0.81 (0.11)	0.88 (0.06)	-
	HT30	JUDY	-	0.62 (0.05)	0.67 (0.04)	0.64 (0.04)
		VIRG	0.68 (0.13)	-	0.75 (0.03)	0.56 (0.05)
		SWAN	0.65 (0.10)	0.75 (0.10)	-	0.79 (0.03)
		TIME	0.63 (0.12)	0.60 (0.12)	0.76 (0.07)	--
	NSWGR36	JUDY	-	0.86 (0.02)	0.91 (0.01)	0.85 (0.02)
		VIRG	0.86 (0.05)	-	0.92 (0.01)	0.91 (0.01)
		SWAN	0.91 (0.05)	0.91 (0.04)	-	0.95 (0.01)
		TIME	0.86 (0.06)	0.91 (0.04)	0.95 (0.03)	-
ssGBLUP$_{8K}$	DBH30	JUDY	-	0.72 (0.04)	0.79 (0.03)	0.77 (0.03)
		VIRG	0.68 (0.13)	-	0.86 (0.02)	0.81 (0.02)
		SWAN	0.75 (0.08)	0.85 (0.10)	-	0.89 (0.01)
		TIME	0.76 (0.08)	0.80 (0.10)	0.88 (0.05)	-
	HT30	JUDY	-	0.63 (0.05)	0.68 (0.04)	0.65 (0.04)
		VIRG	0.67 (0.14)	-	0.76 (0.03)	0.59 (0.05)
		SWAN	0.65 (0.10)	0.76 (0.10)	-	0.79 (0.03)
		TIME	0.63 (0.12)	0.61 (0.12)	0.75 (0.07)	-
	NSWGR36	JUDY	-	0.81 (0.02)	0.88 (0.02)	0.84 (0.02)
		VIRG	0.86 (0.05)	-	0.88 (0.02)	0.86 (0.02)
		SWAN	0.92 (0.05)	0.92 (0.03)	-	0.92 (0.01)
		TIME	0.89 (0.06)	0.92 (0.03)	0.95 (0.03)	-

Table S4. Across sites predictive ability (PA) average for each studied trait (DBH30, HT30, and NSWGR36) in the lodgepole pine population by increasing the number of markers from 0.5K to 8K SNPs (out of 25K) selected using the largest population statistic F_{st} scores (Fst), the largest absolute estimated effects (Marker_effect), and the lowest association statistic *p*-values (p_value). See text for traits´ abbreviations.

Statistics/Trait	DBH30	HT30	NSWGR36
Fst			
0.5K	0.444 (0.024)	0.487 (0.043)	0.617 (0.043)
2K	0.424 (0.030)	0.466 (0.043)	0.554 (0.052)
4K	0.414 (0.031)	0.457 (0.042)	0.540 (0.044)
6K	0.415 (0.033)	0.458 (0.042)	0.517 (0.055)
8K	0.416 (0.031)	0.456 (0.041)	0.502 (0.060)
Marker_effect			
0.5K	0.472 (0.019)	0.506 (0.046)	0.659 (0.035)
2K	0.449 (0.023)	0.461 (0.040)	0.551 (0.048)
4K	0.435 (0.024)	0.464 (0.039)	0.507 (0.052)
6K	0.433 (0.023)	0.456 (0.032)	0.484 (0.066)
8K	0.431 (0.024)	0.458 (0.044)	0.468 (0.059)
p_value			
0.5K	0.433 (0.031)	0.478 (0.042)	0.584 (0.041)
2K	0.400 (0.030)	0.444 (0.033)	0.479 (0.093)
4K	0.398 (0.033)	0.452 (0.034)	0.509 (0.071)
6K	0.392 (0.040)	0.450 (0.039)	0.485 (0.071)
8K	0.388 (0.043)	0.442 (0.036)	0.473 (0.072)

Fig. S1: Plot of age 30 tree height breeding value (%) family rankings for Alberta's Region C lodgepole pine tree improvement population. The colours represent the 40 original families chosen for genotyping in this study: Low (green), Medium (blue), High (orange).

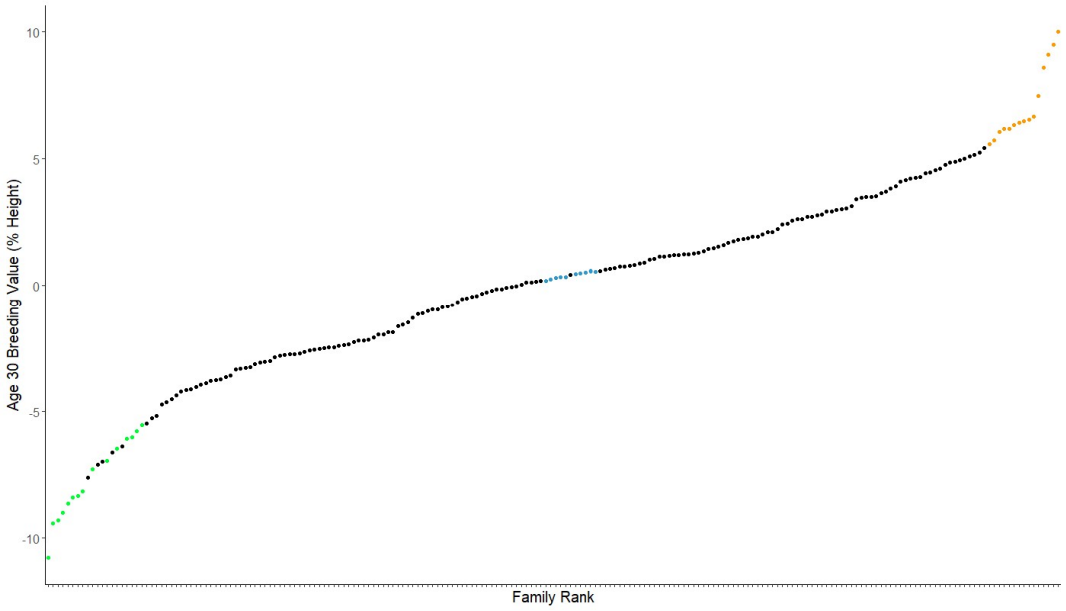


Fig. S2: Comparison of observed pairwise relationship coefficients for half-siblings according to the uncorrected (***left panel***) and corrected (***right panel***) pedigree for the two SNP subsets (25K and 8K).

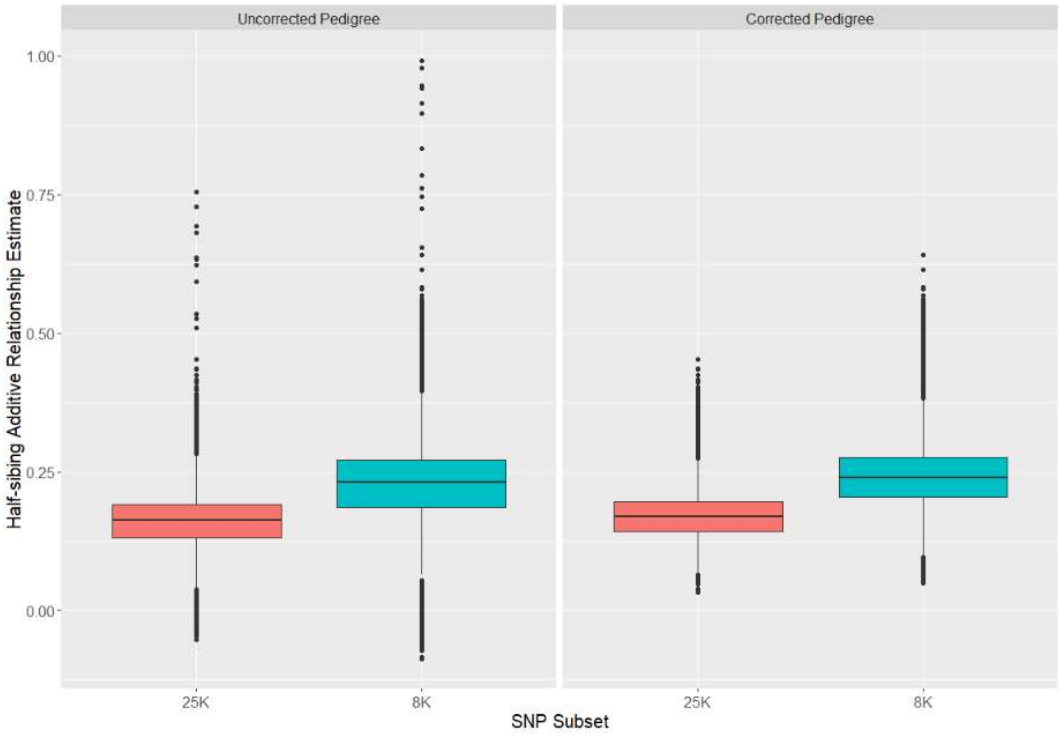


Fig. S3: Sensitivity analysis plot showing the mean half-sibling relationship of the realized relationship matrix (***G***-matrix) and the theoretical expected half-sibling relationship coefficient (horizontal black bar). A subset of 8,000 SNPs (vertical black line) was selected based on the ancestry informativeness marker coefficient.

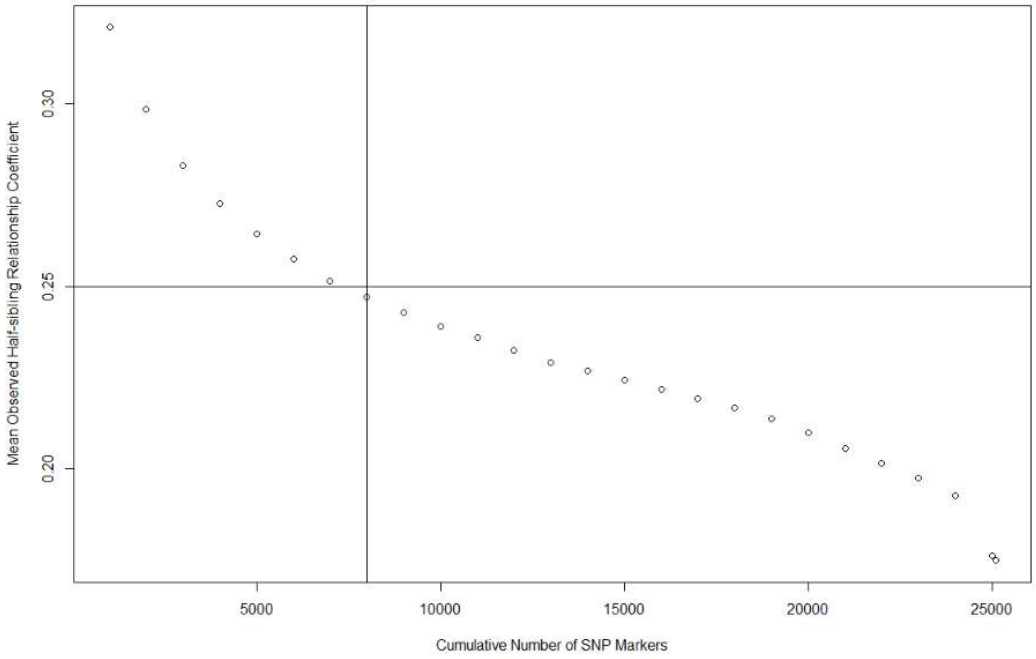


Fig. S4: Spatial pattern estimates using the design (left) and autoregressive spatial (right) models showing the different short and long spatial ranges for the four progeny test sites and traits studied in the Region C lodgepole pine population. The spatial effects were not estimated due to a lack of convergence for NSWGR36 in JUDY and SWAN. See text for traits´ abbreviations, and Table 1 for sites´ abbreviations.

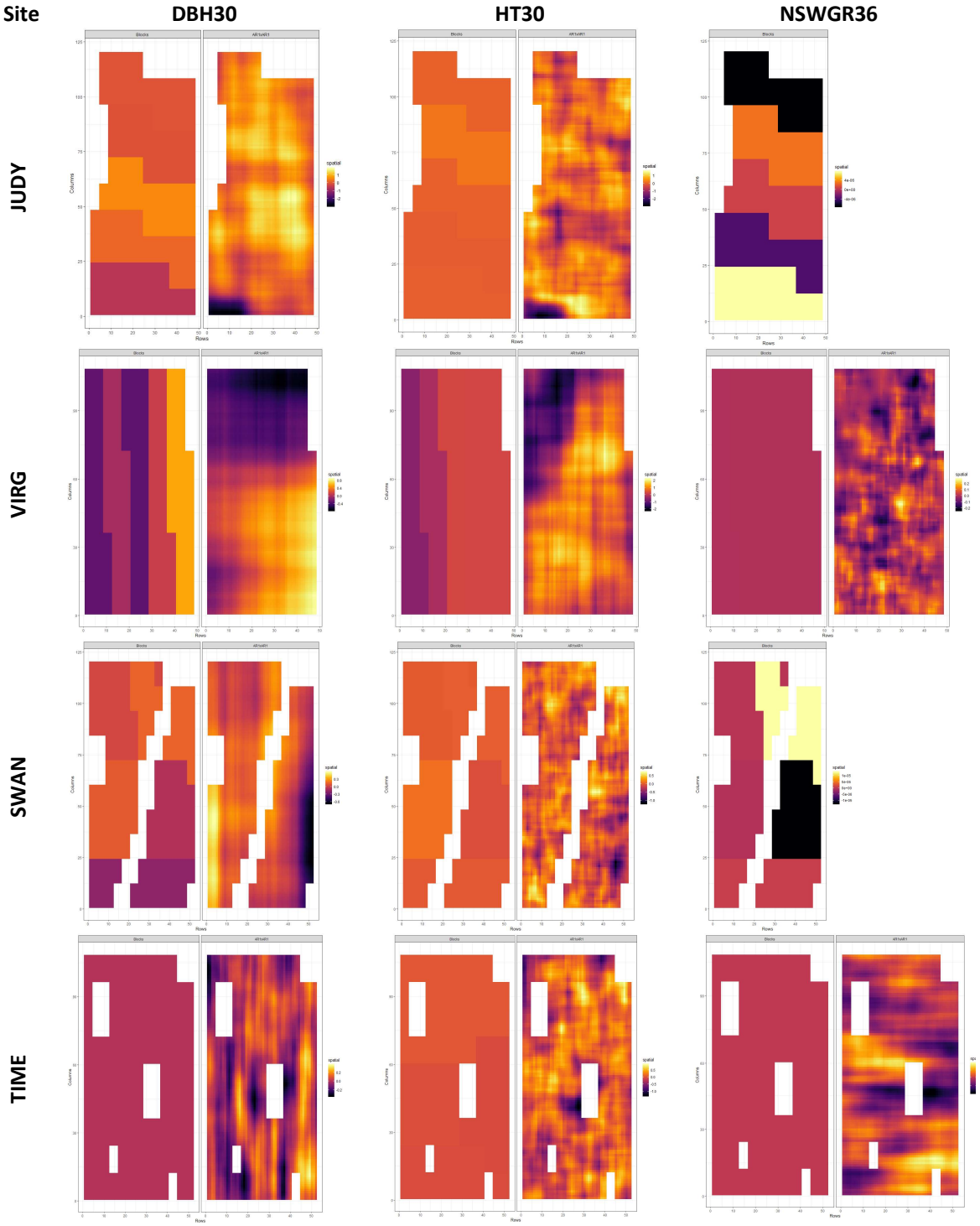
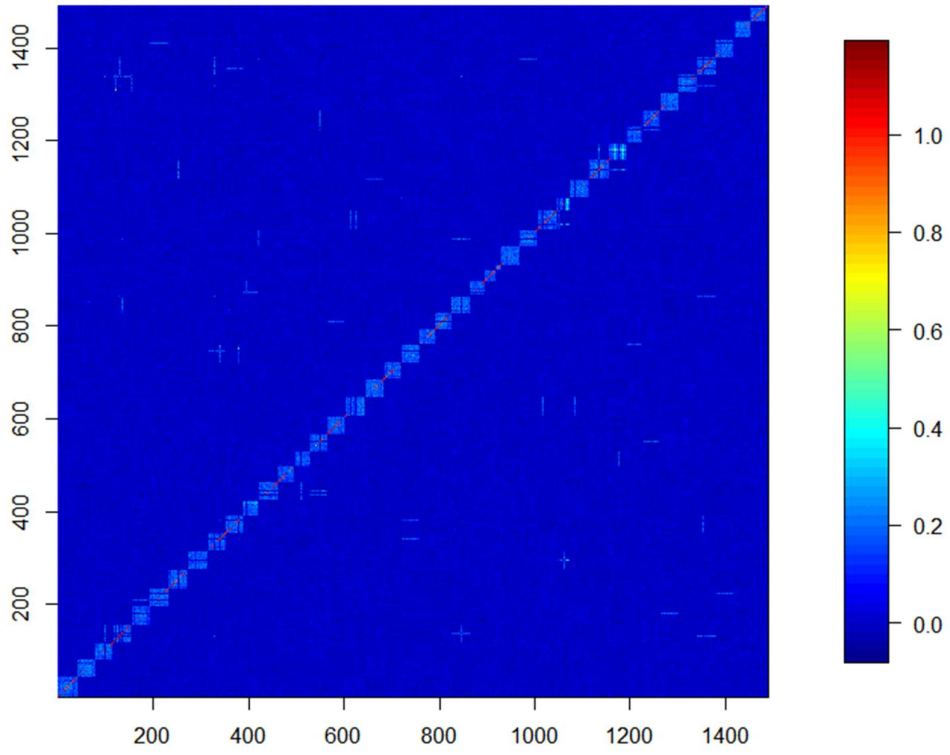


Fig. S5: Heat map of the pair-wise relationship coefficients among the 1,490 genotyped lodgepole pine trees. The heat scale represents pair-wise relationship coefficients for all pairs of individual trees. Trees below the same family are presented by the small squares around the diagonal elements.



R_code S1. R code used to generate the ancestry informative coefficients (AIM; Rosenberg et al. 2003).

```
# GEN11 is an n by p matrix of samples with genotypes coded as 0, 0.5, and 1
# fam$ID is a vector of genetic groups of length n
# AIM1 is an p x 2 matrix of SNP indices and AIM coefficients, respectively.

GEN12<-cbind(fam$ID,GEN11)  #add identifier of genetic group to genotypes

Pij<-NULL

for(j in 1:max(fam$ID)){

 print(j)

 GEN13<-GEN12[GEN12[,1]==j,]

 if(is.null(dim(GEN13))){
  CM<-GEN13
  Pij<-rbind(Pij,CM)

 }

 if(!is.null(dim(GEN13))){
  CM<-colMeans(GEN13)
  Pij<-rbind(Pij,CM)
 }
}

Pij[Pij==0]<-0.0000000001 # modify allelic frequency to be non-zero for fixed alleles at
particular genetic group
Pij[Pij==1]<-0.9999999999

AIM<-matrix(0,ncol(snp.aim1),2)
AIM[,1]<-c(1:ncol(snp.aim1))

for(k in 1:ncol(snp.aim1)){
 A1<-(-
mean(GEN12[,(k+1)])*log(mean(GEN12[,(k+1)]))+sum((Pij[,(k+1)]/max(fam$ID))*lo
g(Pij[,(k+1)]))

 A2<-(-(1-mean(GEN12[,(k+1)]))*log(1-mean(GEN12[,(k+1)]))+sum(((1-
Pij[,(k+1)])/max(fam$ID))*log(1-Pij[,(k+1)]))
 AIM[k,2]<-A1+A2
}
AIM1<-as.data.frame(AIM[order(-AIM[,2]),],stringsAsFactors = F)
```