**Exome-seq read alignment and SNP analysis**

SNPs were mined in each sample using the reference with 14,706 unigene sequences in read mapping. This reference file was formatted using Picard-tools 2.3.0, rebuilt using Bowtie2 version 2.2.9 (Langmead and Salzberg, 2012).  A fai file was generated for read mapping using SAMtools version 1.3.1 (Li et al. 2009). The paired raw reads of each sample in the input data fasta files were aligned with the generated reference using Bowtie2 version 2.2.9 with arguments --local and --very-sensitive-local. The generated SAM files were converted to BAM files, sorted and indexed using SAMtools version 1.3.1. The BAM files were then analyzed for sequence variant detection and genotype calling using Freebayes version 1.0.2-16-gd466dde using default parameters with haploid mode by setting ploidy = 1, outputting VCF files (Garrison and Marth, 2012). Finally, SNP data were processed in the VCF files using VCFtools version 0.1.12b (Danecek et al. 2011). Short indel, MNV and presence/absence variants (PAV) were not included in the present study.  All extracted SNP data in tab format files were merged and analysed using in house R scripts.

**Genetic Map construction**

Genetic maps were constructed for each see family using software suite LepMAP2 (Rastas et al. 2015). The SeparateChromosomes module was used to assign SNP markers into linkage groups (LGs) at lodLimit=10, and other remaining SNP markers were added by the JoinSingles module to existing LGs at lodLimit=6. Finally the OrderMarkers module was used to calculate relative positions of SNP loci within each LG by maximizing the likelihood of the data given the order using input parameters alpha=0.1, polishWindow=100, filterWindow=10, sexAveraged=1, chromosome=X (for each chromosome X). Based on constructed maps, marker assignment to LGs and marker positions on each LG were checked. Those genes and their SNP data were removed in final map construction if multiple SNP markers of the same genes were assigned to different LGs in the same mapping population. LepMAP2 was run for the second time using SNP data with one SNP marker per gene, and the representative SNP markers for each of polymorphic genes were selected with the lowest missing data in the mapping population, the lowest error estimate, and closest position to the median position if multiple SNP markers of the same genes were mapped on the same LG in the first map construction.

The Genetic maps from seed families, r38 and r45, were integrated using LPmerge (Endelman and Plomion 2014) by ten trial runs using the maximum interval size between bins from 1 to 10. Equal weights were assigned to mapping populations due to similar sizes of these two mapping populations. For each LG, the best consensus map was chosen according to software developers’ recommendation by minimizing the average root mean-squared error (RMSE) and achieving a total map length comparable to the mean of the LG maps. Marker and gene density along LGs was estimated using the Gaussian Kernel method and the bandwidth was selected using pilot estimation of derivatives (Sheather and Jones 1991).

Framework markers on the resulting consensus linkage map were used to estimate the size (Chakravarti et al. 1991) and coverage (Lange and Boehnke 1982) of the foxtail pine genome.

We followed the approach of McDaniel et al. (2007) in calculating map lengths using two methods: that of Fishman et al. (2001) in which total map length L = Σ[(linkage group length) + 2(linkage group length/no. markers)] and Chakravarti et al. (1991), in which L = Σ[(linkage group length) × (no. markers + 1)/(no. markers − 1)]. Similarly, genome coverage (c) was calculated as c = 1 − exp(2dn/L) where d is distance in cM, n is the number of markers and L is map length. *c* =1 – *e*-2*dn*/*L* (Fishman et al. 2001)

**Synteny analysis with Pinus and Picea species**

        According to  data sets available, total of 3,856, 5,194, and 8,793 genes were mapped in P. taeda (Westbrook et al. 2015), P. pinaster (de Miguel et al. 2015; <http://w3.pierroton.inra.fr/cgi-bin/cmap_pinus>), and Picea glauca (Pavy et al. 2017), respectively. These data were downloaded to explore inter-genome syntenic relationship. BLASTn analysis was performed to determine sequence homologies between mapped limber pine genes and gene sequences mapped in above three conifer species. An E-value threshold of 1e-100 was used to retain sequence pairs with identical hits in BLASTn searches. The resulting synteny in paired inter-genome comparison was visualized using CIRCOS software (Krzywinski et al. 2009).