S6 Table Current status of major international conifer genome sequencing projects.

Species	Genome size	Type of material used for sequencing	Sequencing and assembly strategy	Number of scaffolds & N50	Number of gene models predicted
Pinus pinaster	51-60 pg / 2C [1]	DNA from a single haploid line generated by *in vitro* culture of a megagametophyte	Short reads sequencing (Illumina) + mate pair sequencing 454. Assembly: MaSuRCA + SOAPdenovo2.	Scaffolds >500 bp: 4.4 millions N50: ~920 bp Assembly version 0.8.	-
Picea abies	40 pg / 2C [2]	DNA from haploid and diploid tissues of the same genotype	Haploid WGS combined with diploid fosmid pools and diploid WGS. Short reads sequencing (Illumina) Assembly: GAM-NGS, BESST	Scaffolds >500 bp: 10.2 millions N50: ~600bp Assembly version 1.0	28,354
Pinus taeda	44 pg / 2C [3,4]	DNA from haploid and filtered diploid tissue of the same genotype.	Haploid WGS combined with filtered diploid WGS + short read sequencing PE and MP (Illumina) Assembly: MaSuRCA	Scaffolds >500bp: 2.2 millions N50: 76 Kbp Assembly version 1.01	9,024 (full-length) 32,432 (partial/ low quality
Picea glauca	42 Gb / 2C [5,6]	DNA from diploid tissues	WGS + short read sequencing PE and MP (Illumina) Assembly: ABySS	Scaffolds >500bp: 4.9 millions N50: 20.4 Kbp	23,589 (full-length)
Pinus sylvestris	50-54pg / 2C	DNA from haploid and diploid tissues from the same individual	Haploid combined with diploid WGS Short read sequencing (Illumina) Assembly: CLC	Scaffolds >500bp: 6.5 millions N50: 2245 bp	-
Pinus sibirica	60 pg / 2C [7]	DNA from haploid megagametophytes and diploid needle tissues of the same genotype	Short read sequencing PE and MP 2× 100 sequencing (Illumina) Assembly: CLC Assembly Cell, ABySS and MaSuRCA	Scaffolds: in progress Contigs >500 bp: 9.9 millions N50: ~3200 bp Assembly version 0.9	-

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