

**Additional file 1 - Sequences of the cpDNA fragments in Norway spruce (*Picea abies*) with information on the region name, applied primer pairs, name of the fossil and extant samples and length of the sequence**

Bold and underlined bases refer to variable positions or blocks.

CK; ndhK-for1, ndhC\_ndhK-rev; all samples (non-variable); 136 bases  
CACTTCAGTTCTTGTGTTCCCTGATGTTGGAACAGTCTCCCTTTATCTATGGGCTATGAG  
TTCTAGTATACAGGGTATATCTGTATTTATAAGAGCTTCAATTCTCGTGCTTATTTTCAT  
CGTTGGTTCTGTGGCG

MD; psbM\_trnD-f1, psbM\_trnD-rev1; all samples (non-variable); 200 bases  
GTTTCGAGTAACGGAATCTAACTAACGGATTGAATGAATTCCTCGATGAAAATAGTATAAC  
ATAATATGATCACTTTTGATAACTAGTAAGAAAACTTACGTGCATCAGAAAACGTTTC  
CGATCAACACATGTCTGTATCATTTCGAAAGAATAGGATTCGTACGAATAATAACCTTCT  
GCTACTCCAGAAGACGTTCC

B (Pt3024); B-for, B-rev; C+12A+5G (haplotype 1, 6, 8); 213 bases  
GCTTATGGCATTGTTGATGTCTAGCGGAAGTTGATCTCATATCGGAAGATCCTCTTTT  
TAATTGATTTTTATAATGAAGTGTAACTGATCTCTCTTTTCTT**AAAAAAAAAAAAAGG**  
**GGG**AAAGGGAAAGTGATTCATTTCAATAAACCTTATATGGTTAGGATCAATCCGAACCA  
GTTGATTCCGCATACAATACAGCTAGAATGCC

B (Pt3024); B-for, B-rev; C+11A+6G (haplotype 2,3); 213 bases  
GCTTATGGCATTGTTGATGTCTAGCGGAAGTTGATCTCATATCGGAAGATCCTCTTTT  
TAATTGATTTTTATAATGAAGTGTAACTGATCTCTCTTTTCTT**AAAAAAAAAAAAAGG**  
**GGG**AAAGGGAAAGTGATTCATTTCAATAAACCTTATATGGTTAGGATCAATCCGAACCA  
GTTGATTCCGCATACAATACAGCTAGAATGCC

B (Pt3024); B-for, B-rev; C+10A+6G (haplotype 4,7 and P1) 212 bases  
GCTTATGGCATTGTTGATGTCTAGCGGAAGTTGATCTCATATCGGAAGATCCTCTTTT  
TAATTGATTTTTATAATGAAGTGTAACTGATCTCTCTTTTCTT**AAAAAAAAAAAAAGGG**  
**GG**AAAGGGAAAGTGATTCATTTCAATAAACCTTATATGGTTAGGATCAATCCGAACCA  
TTGATTCCGCATACAATACAGCTAGAATGCC

B (Pt3024); B-for, B-rev; C+13A+5G (haplotype 5); 214 bases  
GCTTATGGCATTGTTGATGTCTAGCGGAAGTTGATCTCATATCGGAAGATCCTCTTTT  
TAATTGATTTTTATAATGAAGTGTAACTGATCTCTCTTTTCTT**AAAAAAAAAAAAAGG**  
**GGG**AAAGGGAAAGTGATTCATTTCAATAAACCTTATATGGTTAGGATCAATCCGAACCA  
GTTGATTCCGCATACAATACAGCTAGAATGCC

B (Pt3024); B-for, B-rev; T+12A+4G+3A+G (haplotype 9); 216 bases  
GCTTATGGCATTGTTGATGTCTAGCGGAAGTTGATCTCATATCGGAAGATCCTCTTTT  
TAATTGATTTTTATAATGAAGTGTAACTGATCTCTCTTTTCTT**AAAAAAAAAAAAAGG**  
**GGAAAG**AAAGGGAAAGTGATTCATTTCAATAAACCTTATATGGTTAGGATCAATCCGAA  
CCAGTTGATTCCGCATACAATACAGCTAGAATGCC

B (Pt3024); B-for, B-rev; C+10A+7G (S9); 213 bases  
GCTTATGGCATTGTTGATGTCTAGCGGAAGTTGATCTCATATCGGAAGATCCTCTTTT  
TAATTGATTTTTATAATGAAGTGTAACTGATCTCTCTTTTCTT**AAAAAAAAAAAAAGGG**  
**GGG**AAAGGGAAAGTGATTCATTTCAATAAACCTTATATGGTTAGGATCAATCCGAACCA  
GTTGATTCCGCATACAATACAGCTAGAATGCC

D (Pt15169); D-for, D-rev; A+A+C (haplotype 1, 2, 4, 5, 7, 8 and S3, S10); 124 bases  
CTGGATGGAATAGCAGCCAACCTCAGTAAATCTTCAGGTCCCTTTCTTTTTCTATTTTC  
TTATTACTAATTT**AA**TAT**C**TATTAGCCCTTCATATAGCTATAATGACCTTAATGCGC

TTCC

D (Pt15169); D-for, D-rev; C+A+C (haplotype 3, and cone, S8, P2, P3); 124 bases  
CTTGGATGGAATAGCAGCCAACCTCAGTAAATCTTCAGGTCCCTTTCTTTTTCTATTTTC  
TTATTACTAATTTCATATCTATTAGCCCTTCATATAGCTATAATGACCTTAATGCGC  
TTCC

D (Pt15169); D-for, D-rev; A+C+T (haplotype 9); 124 bases  
CTTGGATGGAATAGCAGCCAACCTCAGTAAATCTTCAGGTCCCTTTCTTTTTCTATTTTC  
TTATTACTAATTTACTATTTATTAGCCCTTCATATAGCTATAATGACCTTAATGCGC  
TTCC

TL; trnT\_trnL-sp-f1, trnT\_trnL-sp-brev; G+T+C+G (haplotypes 1-8, and cone, S8, S9, P4-P11); 251 bases  
CTGAGCTAAGCAGGCTCAATGGAATATAACTCCTCATTTCATTGGTGTGAGATCCATAGA  
TTCTTTTGGAAATCCTAACGATTATAGCGCGAATCAGATTCAATGACGCAATCCAGATTAC  
AATTACAACGGAACATTGTTTGAATGTAGATTGTAGATTCCCTTCAAGGGAAAGAAAAGGG  
AAGTAAGGATGAATTTTCTATCGATCGTTTTACTCACTCTTCCAAATCGACTAGGGGAGGA  
TAATAACATGC

TL; trnT\_trnL-sp-f1, trnT\_trnL-sp-brev; G+T+A+G (haplotype 9 and P12); 251 bases  
CTGAGCTAAGCAGGCTCAATGGAATATAACTCCTCATTTCATTGGTGTGAGATCCATAGA  
TTCTTTTGGAAATCCTAACGATTATAGCGCGAATCAGATTCAATGACGCAATCCAGATTAC  
AATTACAACGGAACATTGTTTGAATGTAGATTGTAGATTCCCTTCAAGGGAAAGAAAAGGG  
AAGTAAGGATGAATTTTATATCGATCGTTTTACTCACTCTTCCAAATCGACTAGGGGAGGA  
TAATAACATGC

TL; trnT\_trnL-sp-f1, trnT\_trnL-sp-brev; A+G+A+A (P13); 251 bases  
CTGAGCTAAGCAGGCTCAATGGAATATAACTCCTCATTTCATTGGTGTGAGATCCATAGA  
TTCTTTTGGAAATCCTAACGATTATAGCGCGAATCAGATTCAATGACGCAATCCAGATTAC  
AATTACAACGGAACATTGTTTGAATGTAGATTGTAGATTCCCTTCAAGAGAAAGAAAAGGG  
AAGTAAGGATGAATTTGATATCGATCATTTTACTCACTCTTCCAAATCGACTAGGGGAGGA  
TAATAACATGC

Li; trnL-intron-f2, trnL-intron-rev; T+C (haplotypes 1-3, 5-8, and S10); 237 bases  
GAACGCTCTATTTACACCTAAAAAGTGGGAATGTGATATAACATCAGACAAAACCTCGCGA  
TCAGAACTTGAATCGTTCCAAGCATCTATTCGTAAGATAGATGCCAGATTCCGAGTTGAAG  
TACTGATTTTACATTAAGTAATCCAATTATGAATTTCTCTACTTTAGATAGAGAATTGAA  
TCAGTTTTTGGAAATAAATGGTTGGACGAGAATAAAGATAGAGTCCAATTCTACGTGT

Li; trnL-intron-f2, trnL-intron-rev; T+A (haplotype4 and S4); 237 bases  
GAACGCTCTATTTACACCTAAAAAGTGGGAATGTGATATAACATCAGACAAAACCTCGCGA  
TCAGAACTTGAATCGTTCCAAGCATCTATTCGTAAGATAGATGCCAGATTCCGAGTTGAAG  
TACTGATTTTACATTAAGTAATCCAATTATGAATTTATCTACTTTAGATAGAGAATTGAA  
TCAGTTTTTGGAAATAAATGGTTGGACGAGAATAAAGATAGAGTCCAATTCTACGTGT

Li; trnL-intron-f2, trnL-intron-rev; C+C (haplotype 9); 237 bases  
GAACGCTCTATTTACACCTAAAAAGTGGGAATGTGATATAACATCAGACAAAACCTCGCGA  
TCAGAACTTGAATCGTTCCAAGCATCTATTCGTAAGATAGATGCCAGATTCCGAGTTGAAG  
TACTGATTTTACATTAAGTAATCCAATTATGAATTTCTCTACTTTAGATAGAGAATTGAA  
TCAGTTTTTGGAAATAAATGGTTGGACGAGAATAAAGATAGAGTCCAATTCTACGTGT

LF; Aa\_trnLF-for, Aa\_trnLF-rev; T+T (haplotype 1); 186 bases  
GGTTCAAGTCCCTCTATCCCCACCTAGGTTTCGTTCCCGAACGACTGATCTATTTTCTCCA  
ATTCCATTAGTTCGAATCCATTCTCACTTCTCGATTATTTTACCTCACTATTTTTTTTCT  
TCATGAACAGAATAAATTAGAACATGAATCTGTCCATCCATCTTATGACAAGTTGAGTTG  
ATCAGT

LF; Aa\_trnLF-for, Aa\_trnLF-rev; A+T (haplotype 2-8, and cone, S9); 186 bases  
GGTTCAAGTCCCTCTATCCCCACCTAGGTTTCGTTCCCGAACGACTGATCTATTTTCTCCA  
ATTCCATTAGTTCGAATCCATTCTCACTTCTCGATTATTTTACCTCACTATTTTATTCT  
TCATGAACAGAATAAATTAGAACATGAATCTGTCCATCCATCTTATGACAAGTTGAGTTG  
ATCAGT

LF; Aa\_trnLF-for, Aa\_trnLF-rev; A+G (haplotype 9); 186 bases

GGTTCAAGTCCCTCTATCCCCACCTAGGTTTCGTTCCCGAACGACTGATCTATTTTCTCCA  
ATTCCATTAGTTCGAATCCATTCTCACTTCTCGATTATTTTACCTCACTATTTTATTCT  
TCATGAACAGAAGAAATTAGAACATGAATCTGTCCATCCATCTTATGACAAGTTGAGTTG  
ATCAGT

K2i; trnK2i-f1, trnK2i-r1; C (haplotype 1-3, 5-9, and cone, S9, S10); 204 bases

GCCCTCGTTCATGAGAATAACCTCTTAAATTCTGAGATAATACAATACATGGTGCGATCT  
AGTCGGGACAAGATAGGAAAAAGATAGATGATATAAAGATTCTATCTTCTATTCAGCAGA  
TTTACTACCCAAGGATCTCGTTCGTCATGAGGAAGAACGAAAATCTTTTATCCTGGCAAC  
CAATCGCTCTCCTGACTCATGACG

K2i; trnK2i-f1, trnK2i-r1; T (haplotype 4); 204 bases

GCCCTCGTTCATGAGAATAACCTCTTAAATTCTGAGATAATACAATACATGGTGCGATCT  
AGTCGGGACAAGATAGGAAAAAGATAGATGATATAAAGATTCTATCTTCTATTIAGCAGA  
TTTACTACCCAAGGATCTCGTTCGTCATGAGGAAGAACGAAAATCTTTTATCCTGGCAAC  
CAATCGCTCTCCTGACTC