

Wagner *et al.* 10.1073/pnas.0701428104.

Supporting Information

Files in this Data Supplement:

[SI Figure 5](#)

[SI Figure 6](#)

[SI Figure 7](#)

[SI Figure 8](#)

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1  MLITVKN SQMVRPAAP TPQRDLWNSNVDLVVPR IHTASVYFYRPTGSPDFFSMN ILRDAL PrHCT
1  MKIEVKEST MVKPAAE TPQORLWNSNVDLVVNFHTPSVYFYRPTGSPNFFDGKVLKEAL NtHCT

61  SKLLVPFYPMAGRLK RDPDGRIEINCNGE GVLVEAITDSVI DDFGDFAPT MELKQLIPK PrHCT
61  SKALVPFYPMAGRLC RDEEDGRIEIDCKGQGVLFVEAESDGVV DDFGDFAPTLELRQLIPA NtHCT

121 VNYSEDISSYP LLV LQVTF FFKCGG VSLGVGMQH HVADGYAGI HFINTWSDVARGLDITLP PrHCT
121 VDYSQGIQSYA LLV LQIT HFKCGG VSLGVGMQH HAADGASGL HFINTWSDMARGLDLITLP NtHCT

181 PFIDRTLLRARNPPTPKFQHIEYQOPPPLKDTSG--IMNGEKTDISVAIFKLTKEQLEIL PrHCT
181 PFIDRTLLRARDPPQPFPHVEYQPPPTLKVTPENTPISEAVPETSVSIFKLTRDQINTL NtHCT

239 KGKARENGNNIAYSSYEMLSGHIWRCACKARNLAEDQETKLYIATDGRNRLRPSIPPGYF PrHCT
241 KAKSKEDGNTVNYSSYEMLAGHVWRSTCMARGLAHDQETKLYIATDGRSRLRPSLPPGYF NtHCT

299 GNVIFTTTPMAVTGDIISKPTYAASVIHEALGRMDDEYLRSALDYLELQPDLTALVRGA PrHCT
301 GNVIFTTTPIAVAGDIQSKPIWYAASKLHDALARMNDYLRSA LDYLELQPDLKALVRGA NtHCT

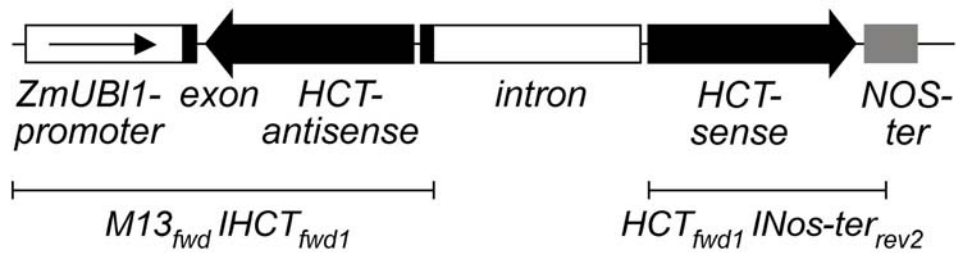
359 HTFRCPNIGITSW SRLPIHDADFGWGRPIFMGPGGIAYEGLAFVLPSVNDGSLSVALGL PrHCT
361 HTFKCPNLGITSW SRLPIHDADFGWGRPIFMGPGGIAYEGLSEILPSP TNDGSO SVAISL NtHCT

419 QPDHMRFAKMLYEI. PrHCT
421 QAEHMKLFEKFLYDF. NtHCT

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Fig. 5. Alignment of the deduced amino acid sequence of the putative *P. radiata* *HCT* clone *PrHCT* (top strand; accession no. EF121452) and the amino acid sequence of *N. tabacum* *HCT* (bottom strand; accession no. AJ507825). Conserved amino acids have gray and identical amino acids have black background.

pHF5



pAW16

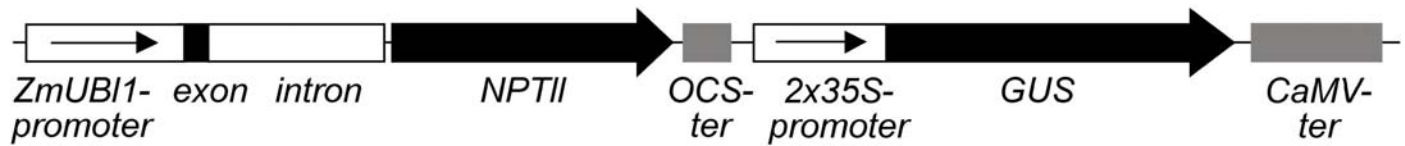


Fig. 6. Schematic diagrams of the constructs used in *HCT* gene-silencing experiments in *P. radiata* callus cultures. *pAW16* contains the *NPT II* resistance gene controlled by the *Z. mays* *UBI1* promoter and the *GUS* reporter gene driven by the double $35S$ *CaMV* promoter; *pHF5* contains an inverted repeat of the *P. radiata* *HCT* coding region separated by the *Z. mays* *UBI1* intron and controlled by the *Z. mays* *UBI1* promoter. The position of genomic PCR fragments generated to investigate the integration of construct is indicated.

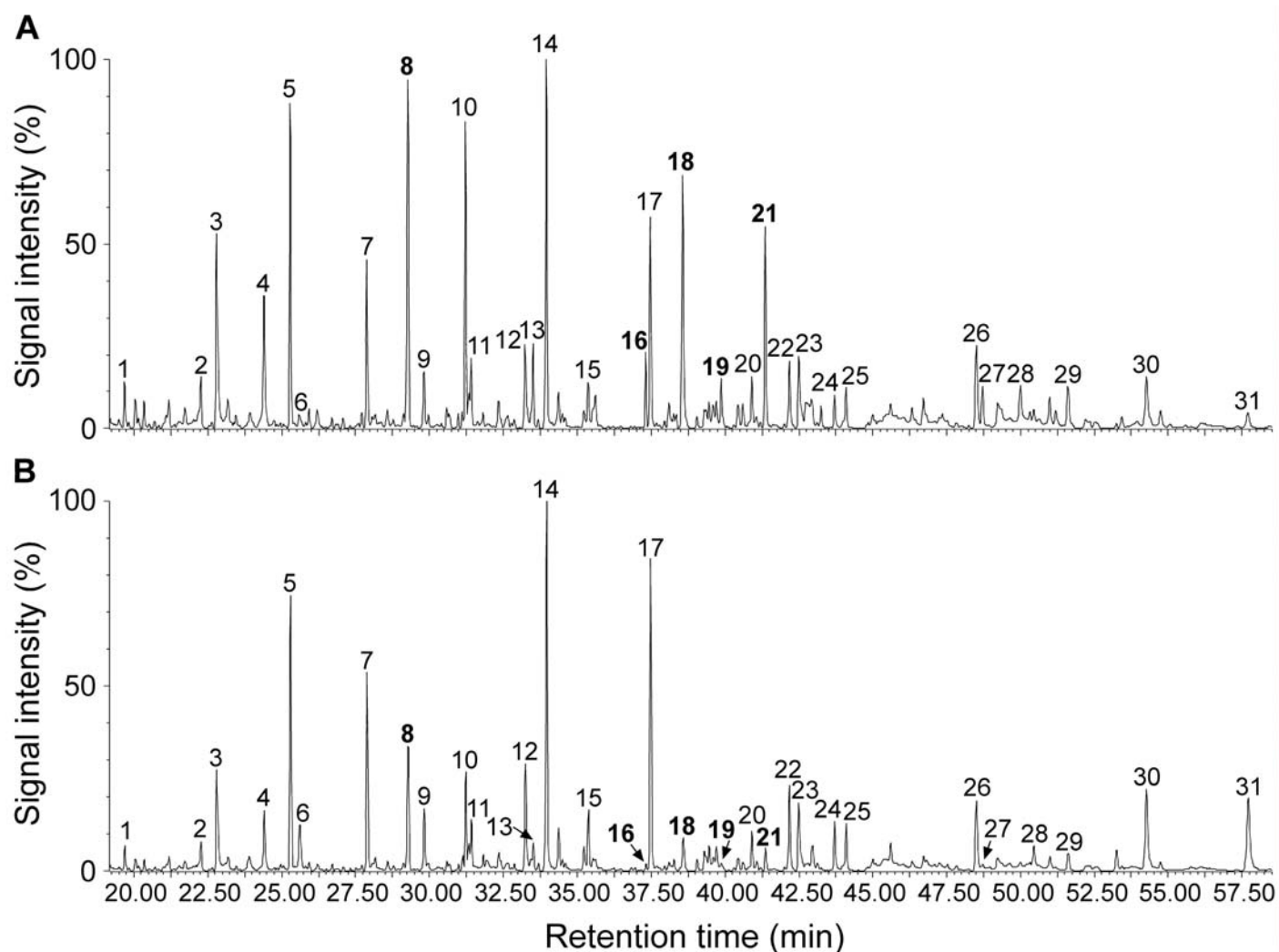


Fig. 7. Pyrogram (total ion chromatogram) of transgenic line pHF5-18 (*A*) compared with a WT control (*B*). Numbers 1-31 refer to the following major thermal breakdown products: 1, 2-furfuryl alcohol; 2, (3*H*) furan-2-one; 3, dihydro-methyl-furanone; 4, 2-hydroxy-1-methyl-1-cyclopentene-3-one; 5, guaiacol; 6, 4-hydroxy-5,6-dihydro-(2*H*)-pyran-2-one; 7, 4-methyl-guaiacol; 8, phenol; 9, 4-ethyl-guaiacol; 10, dimethyl-phenol; 11, 4-methyl-phenol; 12, eugenol; 13, 4-ethyl-phenol; 14, 4-vinyl-guaiacol; 15, *cis*-isoeugenol; 16, 4-allyl-phenol; 17, *trans*-isoeugenol; 18, 4-vinyl-phenol; 19, *cis*-4-propenyl-phenol; 20, 5-hydroxymethyl-2-furaldehyde; 21, *trans*-4-propenyl-phenol; 22, vanillin; 23, 1,5-anhydro-arabinofuranose; 24, acetoguaiacone; 25, guaiacyl acetone; 26, 1,5-anhydro-xylofuranose; 27, *p*-coumaryl alcohol; 28, 4-hydroxy-benzaldehyde; 29, resorcinol; 30, coniferaldehyde; 31, *trans*-coniferyl alcohol. Signals, which largely represent thermal breakdown products of H lignin, such as **8, 16, 18, 19, and 21** are significantly enriched in pHF5-18 compared with the WT control.

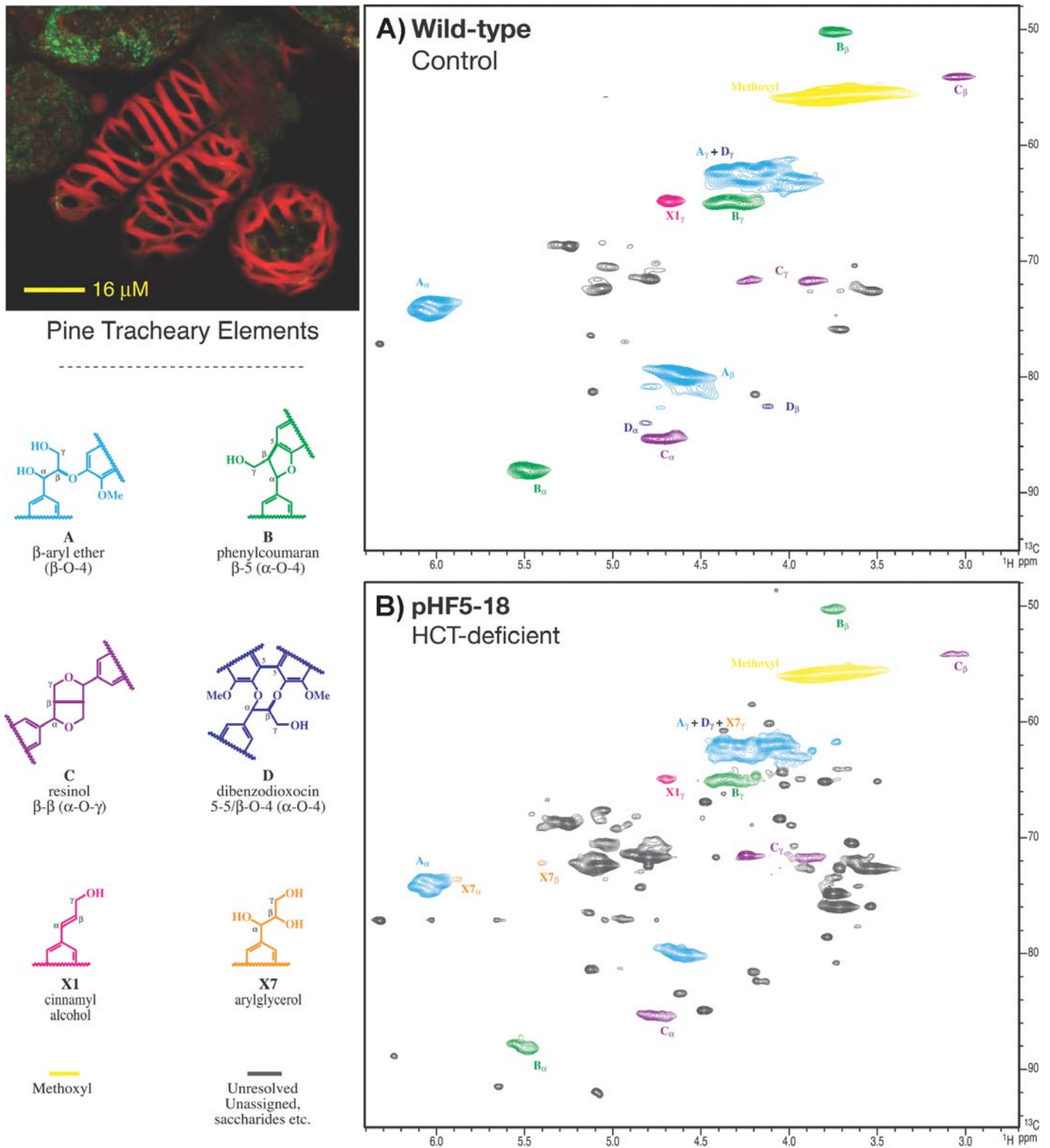


Fig. 8. Partial short-range ^{13}C - ^1H (HSQC) spectra (side-chain regions) of acetylated enzyme lignins isolated from (A) the wild-type control and (B) *HCT*-deficient line pHF5-18.