

**Additional file 7. Pyrolysis GC-MS analysis of wood of transgenic (lines 8, 4, and 17) and wild type (WT) trees.**

<b>Line</b>	<b>C</b>	<b>G</b>	<b>S</b>	<b>H</b>	<b>P</b>	<b>L</b>	<b>S/G</b>
WT	63.08 ± 0.52	<b>11.04 ±</b> <b>0.16**</b>	<b>18.10 ±</b> <b>0.24***</b>	1.89 ± 0.05	0.30 ± 0.01	31.33 ± 0.37	<b>1.64 ±</b> <b>0.02***</b>
8	63.38 ± 0.46	11.41 ± 0.28	17.39 ± 0.35	1.83 ± 0.08	0.28 ± 0.01	30.90 ± 0.65	1.53 ± 0.02**
4	63.51 ± 0.61	12.13 ± 0.19**	16.35 ± 0.4**	1.80 ± 0.09	0.28 ± 0.01	30.56 ± 0.45	1.35 ± 0.04**
17	63.88 ± 0.38	11.09 ± 0.27	17.36 ± 0.19	1.81 ± 0.11	0.27 ± 0.01	30.54 ± 0.40	1.52 ± 0.04*

C-Carbohydrates, G - Guaiacyl lignin, S - Syringyl lignin, H - *p*-hydroxyphenyl, P - phenolics, L - G+S+H+P, S/G - Syringyl to guaiacyl ratio. All values are relative to the sum of detected identified signals. Mean ± *SE*, *n* = (8-18) biological replicates. Asterisks next to individual lines correspond to means significantly different from wild type (WT) according to the Student's *t*-test. Asterisks next to WT values in bold type denote significance of contrast between WT and transgenic lines (\* - *P* ≤ 0.1, \*\* - *P* ≤ 0.05, \*\*\* - *P* ≤ 0.01).