

**Table S2.** Relative transcript levels of candidate lignin biosynthesis genes in different tissues of wheat<sup>w</sup>

Gene	FB	FS	PE	IN-1	IN-2&3	IN-4
<i>PAL1</i>	0.34 ±0.08 <sup>xy</sup>	0.02 ±0.00c	0.01 ±0.00d	0.25 ±0.06b	2.18 ±0.25a	2.40 ±0.29a
<i>PAL2</i>	0.26 ±0.05cd	0.16 ±0.02d	0.36 ±0.10c	0.75 ±0.13b	2.76 ±0.22a	3.22 ±0.23a
<i>PAL3</i>	0.26 ±0.03c	0.12 ±0.01d	0.16 ±0.03d	0.32 ±0.05c	1.48 ±0.16b	2.35 ±0.30a
<i>PAL4</i>	0.54 ±0.03d	1.58 ±0.16c	7.92 ±0.60a	6.51 ±0.70b	6.95 ±1.07ab	7.28 ±0.76a
<i>PAL5</i>	0.32 ±0.03e	0.28 ±0.01e	0.49 ±0.08d	0.89 ±0.04c	3.80 ±0.44b	5.71 ±0.65a
<i>PAL6</i>	0.83 ±0.07d	9.05 ±0.80c	89.25 ±19.53a	54.50 ±6.76b	54.57 ±11.98b	33.66 ±6.98b
<i>C4H1</i>	0.38 ±0.03d	0.91 ±0.04c	2.68 ±0.40b	3.67 ±0.61b	9.57 ±1.20a	11.22 ±3.71a
<i>4CL1</i>	1.00 ±0.09d	2.04 ±0.08c	7.61 ±1.10b	7.13 ±0.57b	12.51 ±2.02a	16.84 ±2.83a
<i>HCT1</i>	0.58 ±0.03d	0.70 ±0.06d	2.53 ±0.54b	1.54 ±0.20c	3.09 ±0.40b	5.42 ±0.60a
<i>HCT2</i>	0.19 ±0.02d	0.31 ±0.02d	2.77 ±0.72a	0.85 ±0.09c	1.35 ±0.10b	2.18 ±0.40ab
<i>C3H1</i>	0.12 ±0.03e	0.21 ±0.03de	1.24 ±0.06a	0.87 ±0.12b	0.55 ±0.13c	0.46 ±0.03cd
<i>C3H2</i>	nd <sup>z</sup>	nd	nd	0.01 ±0.00	nd	nd
<i>C3H3</i>	0.06 ±0.01d	0.35 ±0.16b	0.92 ±0.26a	0.31 ±0.01b	0.24 ±0.09bc	0.15 ±0.02c
<i>CCoAOMT1</i>	1.52 ±0.17e	3.32 ±0.58d	32.73 ±5.28a	11.98 ±2.51c	19.56 ±3.50bc	21.89 ±4.77b
<i>CCoAOMT2</i>	0.02 ±0.00c	0.05 ±0.00c	0.03 ±0.00a	0.02 ±0.00ab	0.02 ±0.00c	0.02 ±0.00bc
<i>CCoAOMT3</i>	0.72 ±0.04d	0.94 ±0.07cd	6.35 ±1.81a	1.24 ±0.13c	3.15 ±0.56b	5.04 ±1.47ab
<i>CCR1</i>	11.11 ±0.21a	6.64 ±0.36b	0.29 ±0.03f	1.59 ±0.31c	0.78 ±0.02d	0.45 ±0.07e
<i>CCR2</i>	0.17 ±0.02e	1.56 ±0.07d	3.77 ±0.78c	5.93 ±0.29b	8.44 ±0.85a	7.82 ±1.09a
<i>CCR3</i>	0.03 ±0.00cd	0.01 ±0.00e	0.02 ±0.00de	0.06 ±0.00bc	0.22 ±0.08ab	0.56 ±0.01a
<i>CCR4</i>	0.02 ±0.01b	0.01 ±0.01b	0.01 ±0.00b	0.03 ±0.02b	0.03 ±0.01b	0.12 ±0.00a
<i>CCR5</i>	13.49 ±1.10a	9.33 ±0.21b	0.93 ±0.09d	2.76 ±0.66cd	2.85 ±0.36cd	3.54 ±0.63c
<i>CCR6</i>	nd	0.01 ±0.00d	0.03 ±0.00c	0.08 ±0.02ab	0.06 ±0.00b	0.11 ±0.01a
<i>F5H1</i>	0.44 ±0.13c	0.37 ±0.07cd	4.56 ±0.80a	0.80 ±0.09b	0.20 ±0.03d	0.55 ±0.09bc
<i>F5H2</i>	0.84 ±0.04e	1.39 ±0.04d	9.20 ±1.67a	6.09 ±0.97ab	3.38 ±1.05c	4.23 ±0.84bc
<i>COMT1</i>	0.01 ±0.00f	1.28 ±0.27c	6.06 ±1.16a	2.82 ±0.32b	0.34 ±0.09d	0.16 ±0.02e
<i>COMT2</i>	15.51 ±1.13b	36.04 ±4.20a	16.09 ±2.86b	31.56 ±4.40a	14.18 ±1.64b	12.63 ±0.67b
<i>COMT3</i>	0.14 ±0.02c	0.21 ±0.02c	1.97 ±0.24a	0.90 ±0.23b	0.87 ±0.10b	0.64 ±0.21b
<i>CAD1</i>	1.40 ±0.01ab	1.00 ±0.03bc	0.38 ±0.09c	0.61 ±0.12c	1.81 ±0.23a	1.61 ±0.34a
<i>CAD2</i>	1.32 ±0.07b	2.05 ±0.08a	0.16 ±0.00c	0.95 ±0.22b	2.02 ±0.17a	2.55 ±0.29a
<i>CAD3</i>	0.84 ±0.10abc	1.15 ±0.10ab	1.36 ±0.37a	1.10 ±0.25ab	0.70 ±0.04bc	0.42 ±0.05c

<sup>w</sup>Transcript levels in different tissues of cv. Harvest were expressed relative to that of *4CL1* in flag leaf, which was arbitrarily set to value of 1.

<sup>x</sup>Data are means of 2 to 3 independent biological replicates ± SE.

<sup>y</sup>Means followed by different letters within each gene show statistically significant difference at  $P < 0.05$ .

<sup>z</sup>nd, not detected

FB, flag leaf blade; FS, flag leaf sheath; PE, peduncle; IN-1, the first internode; IN-2&3, the second and third internode; IN-4, the fourth internode (see the materials and methods section for numerical designation of internodes).