

1 **Supplemental Table S1.** Expression level changes of maize lignin pathway genes comparing  
 2 isolines differing for the presence/absence of the *RpI-D21* gene.

| Gene name        | Accession number             | Chromosomal position          | Fold change in B73 x H95 | Fold change in Mo17 x H95 |
|------------------|------------------------------|-------------------------------|--------------------------|---------------------------|
| HCT homologs     | HCT1806                      | Chr1:17,782,919-17,784,536    | 296.1                    | 223.7                     |
|                  | HCT 4918                     | Chr1:17,843,398-17,845,121    | 1115.0                   | 568.5                     |
|                  | HCT 0436                     | Chr1: 140,319,872-140,321,824 | 23.1                     | 46.0                      |
|                  | HCT 7251                     | Chr6:106,835,033-106,836,712  | 178.0                    | 158.8                     |
|                  | HCT 5584                     | Chr5:183,607,887-183,612,875  | 6.1                      | 4.5                       |
|                  | HCT 8083                     | Chr2:31,824,177-31,830,267    | 4.4                      | 2.8                       |
|                  | AC215260.3_FGT003            | Chr3: 17,019,972-17,021,399   | 0.3                      | 0.3                       |
|                  | GRMZM2G178769                | Chr3: 21,144,442-21,146,412   | 0.3                      | 0.3                       |
|                  | GRMZM2G131165                | Chr1: 211,437,827-211,443,198 | 0.2                      | 0.4                       |
|                  | GRMZM2G156816                | Chr3:17,001,811-17,003,958    | no difference            | no difference             |
|                  | GRMZM2G089698                | Chr4: 86,282,879-86,284,714   | mapped to 2 genes        | mapped to 2 genes         |
|                  | GRMZM2G051005                | Chr5: 213,399,607-213,401,366 | no read                  | no read                   |
|                  | GRMZM2G107211                | Chr3: 21,083,018-21,090,109   | no read                  | no read                   |
|                  | GRMZM2G125448                | Chr7:144,027,423-144,028,948  | low read                 | low read                  |
|                  | GRMZM2G095327                | Chr2:196,738,659-196,740,132  | low read                 | low read                  |
|                  | GRMZM2G034360                | Chr8:166,481,614-166,484,307  | low read                 | low read                  |
|                  | GRMZM2G013530                | Chr7:144,096,592-144,098,353  | no read                  | no read                   |
|                  | GRMZM2G307437                | Chr7:174,995,238-174,996,574  | no read                  | no read                   |
|                  | GRMZM2G175082                | Chr2:229,118,891-229,120,444  | no read                  | no read                   |
|                  | GRMZM2G025971                | Chr2:196,646,620-196,647,926  | no read                  | no read                   |
| GRMZM2G057483    | Chr4:186,826,020-186,827,545 | no read                       | no read                  |                           |
| GRMZM2G166212    | Chr4:5,989,260-5,990,669     | no read                       | no read                  |                           |
| GRMZM2G166203    | Chr4:5,979,614-5,980,990     | no read                       | no read                  |                           |
| GRMZM2G166208    | Chr4: 5,985,018-5,986,424    | no read                       | no read                  |                           |
| CCoAOMT homologs | GRMZM2G099363                | Chr9: 16,318,197-16,320,573   | 2.2                      | 1.7                       |
|                  | GRMZM2G332522                | Chr4: 198,078,696-198,080,533 | 4.3                      | 3.7                       |
|                  | GRMZM2G127948                | Chr6: 79,193,305-79,195,490   | 1.0                      | 0.7                       |
|                  | GRMZM2G004138                | Chr2:189,276,282-189,278,019  | 0.5                      | 0.3                       |
|                  | GRMZM2G470651                | Chr1:271,063,770-271,064,211  | no read                  | no read                   |
| CCR homolog      | GRMZM2G131205                | Chr1: 211,520,099-211,526,173 | 10.9                     | 5.3                       |
| CAD homologs     | GRMZM2G090980                | Chr9: 11,502,987-11,506,773   | 3.6                      | 5.3                       |

|              |                   |                               |       |        |    |
|--------------|-------------------|-------------------------------|-------|--------|----|
|              | AC234163.1_fgt002 | Chr7: 108,253,198-108,254,882 | 16.8  | 4.6    | 3  |
|              | GRMZM5G844562     | Chr5: 98,993,016-98,997,371   | 7.6   | 3.4    | 4  |
|              | GRMZM2G443445     | Chr2: 8,780,369-8,782,588     | 0.5   | 4.4    | 5  |
| PAL homologs | GRMZM2G118345     | Chr2: 28,048,958-28,052,061   | 4.3   | 13.5   | 6  |
|              | GRMZM2G063917     | Chr4: 143,512,171-143,515,157 | 85.7  | 48.1   | 7  |
|              | GRMZM2G334660     | Chr5: 186,732,964-186,735,665 | 10.8  | 13.9   | 8  |
|              | GRMZM2G081582     | Chr4: 143,464,625-143,469,700 | 17.6  | 10.4   | 9  |
|              | GRMZM2G160541     | Chr4:143,376,935-143,381,141  | 8.0   | 1.7    | 10 |
| C4H homologs | GRMZM2G147245     | Chr6: 135,535,544-135,538,221 | 12.3  | 12.4   | 11 |
|              | GRMZM2G139874     | Chr8: 83,792,802-83,796,118   | 6.1   | 6.2    | 12 |
| 4CL homologs | GRMZM2G075333     | Chr5: 89,152,269-89,156,855   | 8.6   | 5.6    | 13 |
|              | GRMZM2G048522     | Chr1: 210,095,858-210,098,161 | 13.1  | 10.5   | 14 |
|              | GRMZM2G096020     | Chr1: 7,341,979-7,348,599     | 4.0   | 2.9    | 15 |
| F5H homolog  | AC210173.4_FGT005 | Chr1: 224,037,328-224,040,990 | 4.8   | 0.4    | 16 |
| COMT homolog | GRMZM2G423331     | Chr9: 146,890,292-146,891,477 | 96.2  | 1397.5 | 17 |
| C3H homolog  | GRMZM2G140817     | Chr6: 155,651,955-155,656,419 | 16.4  | 6.9    | 18 |
| AAS homologs | AAS6469           | Chr1:17,829,269-17,830,963    | 445.5 | 140.1  | 19 |
|              | AAS3125           | Chr1:17,855,665-17,857,563    | 124.8 | 149.9  | 20 |
|              |                   |                               |       |        | 21 |
|              |                   |                               |       |        | 22 |
|              |                   |                               |       |        | 23 |
|              |                   |                               |       |        | 24 |
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|              |                   |                               |       |        | 30 |
|              |                   |                               |       |        | 31 |

32 Fold change in isoline pairs (the isoline carrying Rp1-D21 divided by the wild type isoline) in B73 x H95 and Mo17 x H95  
33 background is shown. The relative expression of all the HCT homologs identified in maize is listed. For the other phenylpropanoid  
34 pathway genes only differentially expressed genes are shown.

35 **Supplemental Table S2.** The primers used in this study

| Primer name     | Sequence  | Usage  |
|-----------------|---|--|
| HCT1806-attB1   | GGGGACAAGTTTGTACAAAAAAGCAGGCTCCAT<br>GGAGACCATGAAGGCAA        | Amplifying <i>HCT1806</i> full-length and cloning it into entry vector pDONR207                              |
| HCT1806-attB2   | GGGGACCACTTTGTACAAGAAAGCTGGGTGATC<br>GATCGAGTGGCAGATC         |  |
| HCT4918-attB1   | GGGGACAAGTTTGTACAAAAAAGCAGGCTCCAT<br>GGAGATTATCACGACGGC       | Amplifying <i>HCT1806</i> full-length sequence and cloning it into entry vector pDONR207                     |
| HCT4918-attB2   | GGGGACCACTTTGTACAAGAAAGCTGGGTGATC<br>GATGGAGTGGCAGATCT        |  |
| AAS-attB1       | GGGGACAAGTTTGTACAAAAAAGCAGGCTCCAT<br>GGCCCCGCCATCACAC         | Amplifying <i>AAS6469</i> and <i>AAS3125</i> full-length sequences and cloning it into entry vector pDONR207 |
| AAS-attB2       | GGGGACCACTTTGTACAAGAAAGCTGGGTGATA<br>ATCTTCATGCATCTCCATTTTAGC |  |
| HCT0436-attB1   | GGGGACAAGTTTGTACAAAAAAGCAGGCTCCAT<br>GACGACCACGTTAGTGAC       | Amplifying <i>HCT0436</i> full-length sequence and cloning it into entry vector pDONR207                     |
| HCT0436-attB2   | GGGGACCACTTTGTACAAGAAAGCTGGGTGATC<br>CATGGAGTAGCAGATGTG       |  |
| HCT7251-attB1   | GGGGACAAGTTTGTACAAAAAAGCAGGCTCCAT<br>GGCGCCGACGGTGGAG         | Amplifying <i>HCT7251</i> full-length sequence and cloning it into entry vector pDONR207                     |
| HCT7251-attB2   | GGGGACCACTTTGTACAAGAAAGCTGGGTGCAT<br>GACCTCCAGGCTCGCGA        |  |
| HCT8083-attB1   | GGGGACAAGTTTGTACAAAAAAGCAGGCTCCAT<br>GGCGATTACTGTGAGGCG       | Amplifying <i>HCT8083</i> full-length sequence and cloning it into entry vector pDONR207                     |
| HCT8083-attB2   | GGGGACCACTTTGTACAAGAAAGCTGGGTGAGC<br>TTCGCCGATTAGCTTCC        |  |
| HCT5584-attB1   | GGGGACAAGTTTGTACAAAAAAGCAGGCTCCAT<br>GAAGATCACGGTGC GG        | Amplifying <i>HCT5584</i> full-length sequence and cloning it into entry vector pDONR207                     |
| HCT5584-attB2   | GGGGACCACTTTGTACAAGAAAGCTGGGTGGAA<br>GTCGTAGATGAGCTTCCG       |  |
| AtHCT-attB1     | GGGGACAAGTTTGTACAAAAAAGCAGGCTCCAT<br>GAAAATTAACATCAGAGATT     | Amplifying <i>AtHCT</i> full-length sequence and cloning it into entry vector pDONR207                       |
| AtHCT-attB2     | GGGGACCACTTTGTACAAGAAAGCTGGGTGTAT<br>CTCAAACAAAACTTCTCA       |  |
| HCT1806-3H-F    | GCATCATCTGCGCCGCCGCGTCCGACGG                                  | Overlapping primers used for generate site-directed mutant HCT1806-H153A/H154A/H155A                         |
| HCT1806-3H-R    | CCGTCGGCGACGGCGGGCGCAGATGATGC                                 |  |
| HCT4918-H152A-F | ATCACCAGCCACGCCAAGTCGCCGAC                                    | Overlapping primers used for generate site-directed mutant HCT4918-H152A                                     |
| HCT4918-H152A-R | CTTGGGCGTGGCTGGTGATGCCGATCAC                                  |  |

