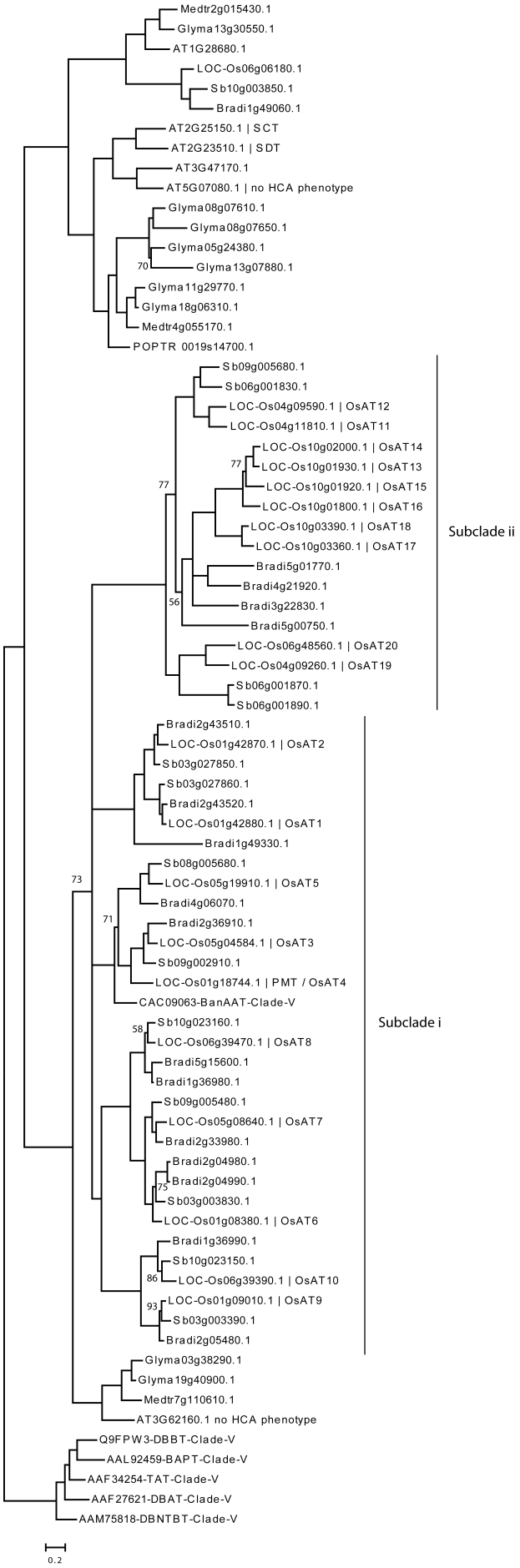
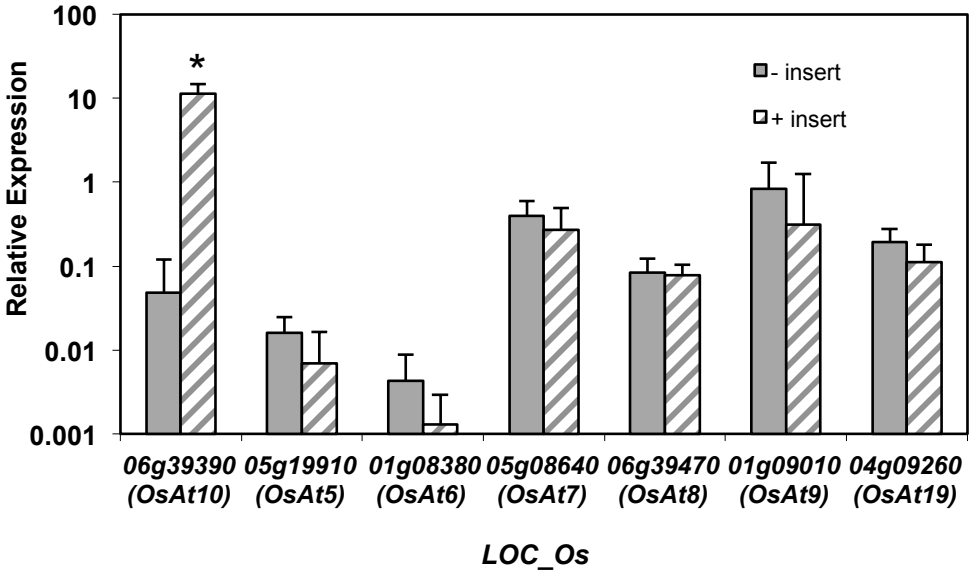
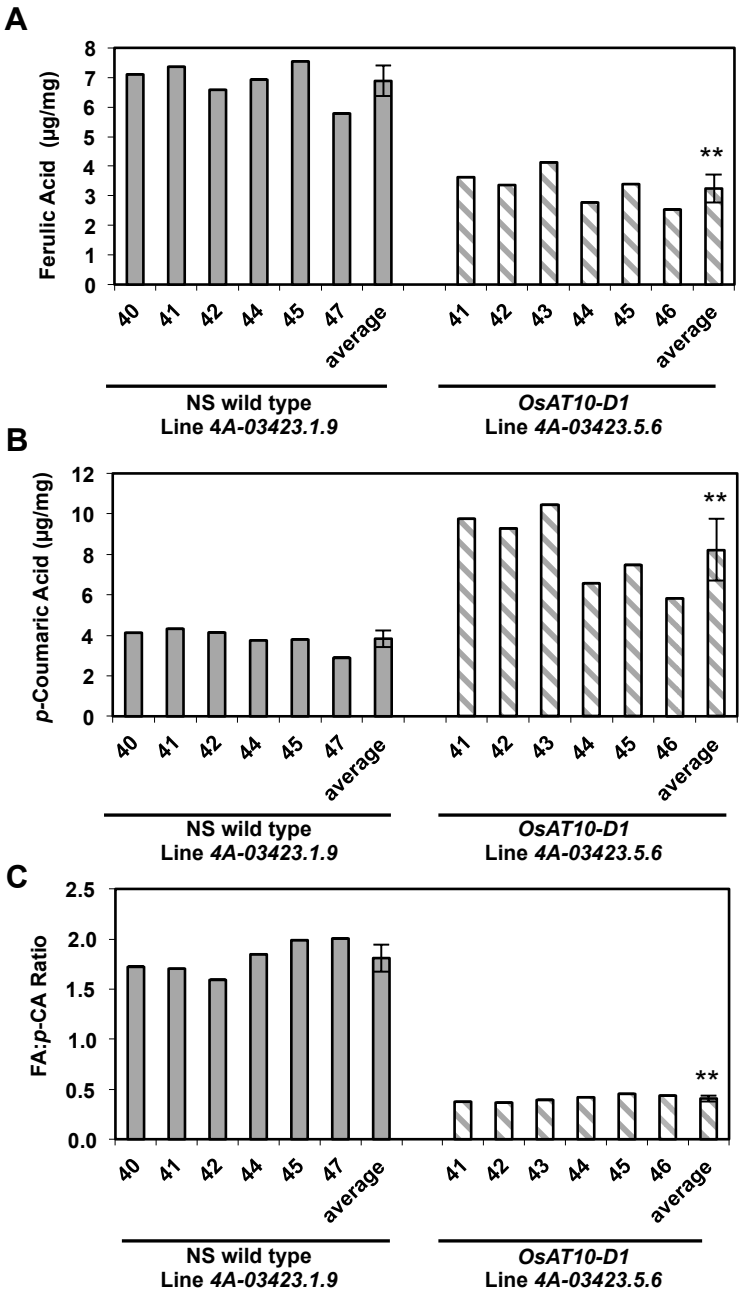


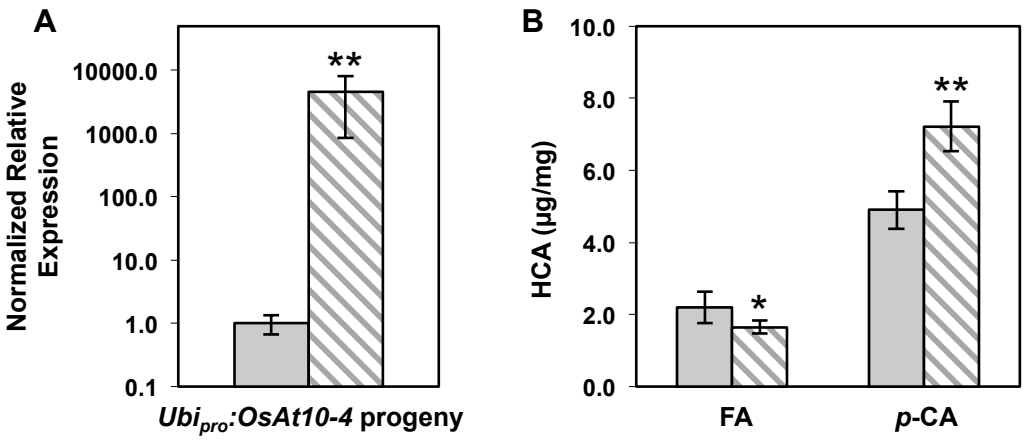

**Supplemental Figure 1.** Inferred Bayesian phylogeny for BAHD CoA acyltransferases identified from diverse species based on grouping closely with the biochemically characterized proteins that are similar to the “Mitchell clade” of BAHD proteins, namely BanAAT, and the taxol biosynthesis genes. Branch likelihood scores are >95% if not specified. Subclades i and ii, described in the text and Figure 1B, are marked. SCT and SDT are the most closely related Arabidopsis proteins for which functions have been identified (Luo et al. 2009). The note “no HCA phenotype” is based on Rautengarten et al. (2012). HCA is hydroxycinnamate.



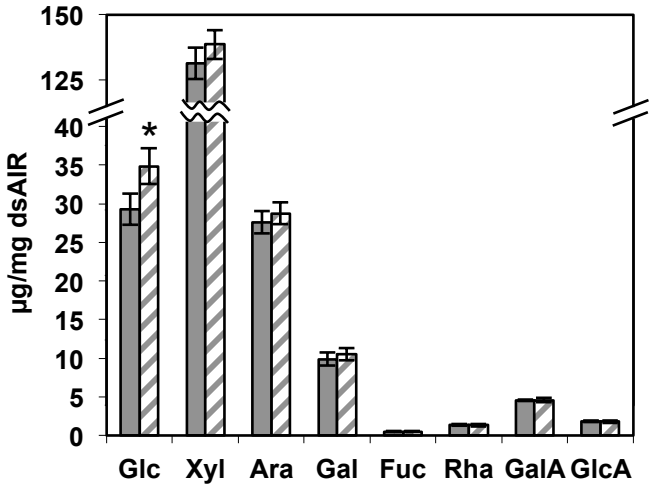

**Supplemental Figure 2.** Quantitative gene expression analysis suggests no change in the expression of other closely related acyltransferases in *OsAT10-D1* (*4A-03423.5*, + insert, cross-hatched bars) and negative segregant lines (*4A-03423.1*, - insert, solid bars). Shown are the average relative expression data for each target gene and related BAHD acyltransferases in young leaves. Error bars are 2*SEM of three to four biological replicates. '*' indicates significance via Student's t-test at $p < 0.05$.



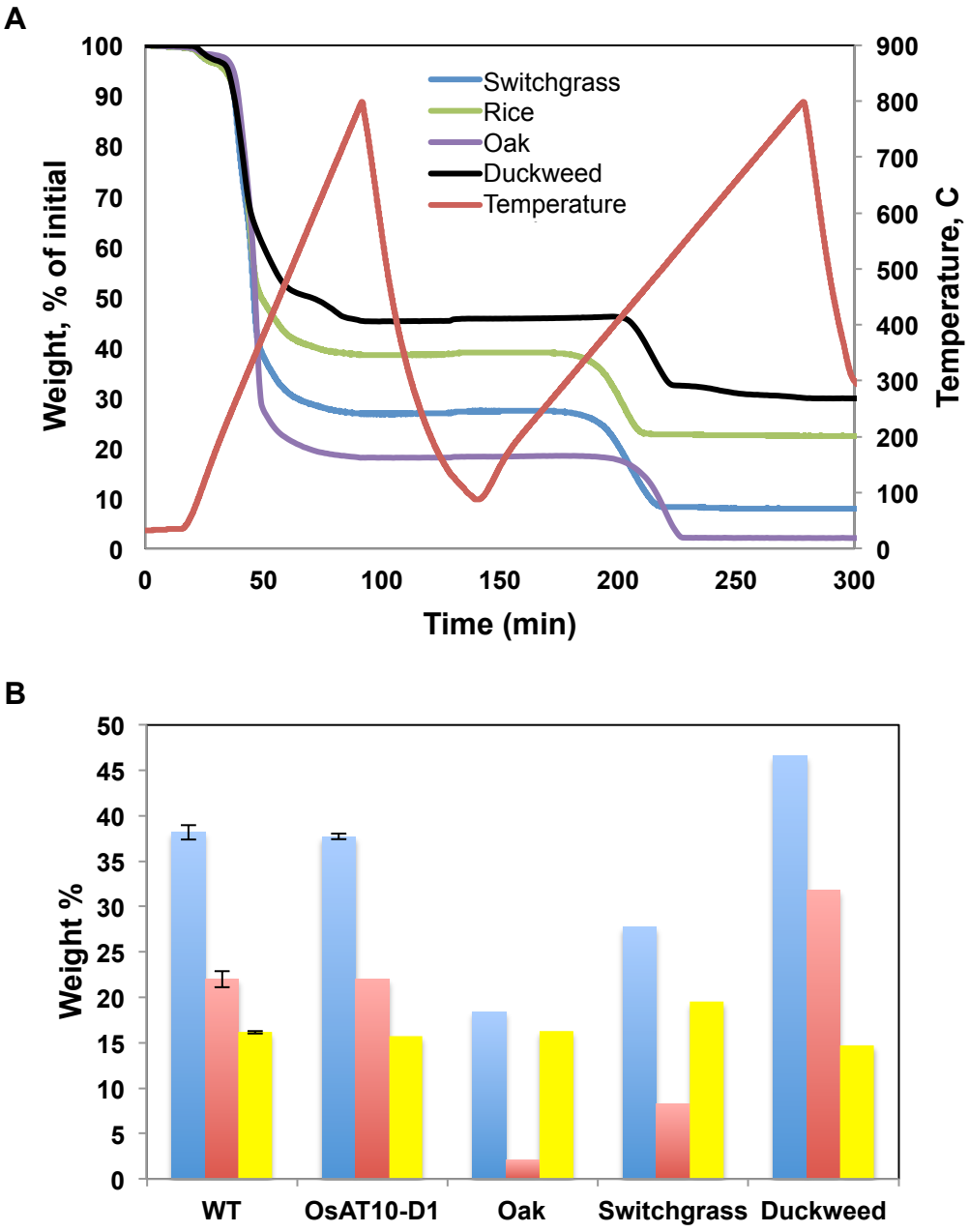

**Supplemental Figure 3.** *OsAT10-D1* shows consistent alterations in cell wall hydroxycinnamic acids. Data are for young leaves from a third generation of progeny of negative segregant (NS) wild-type line (*4A-03423.1.9*, grey bars) and of a mutant line homozygous for the insert (*4A-03423.5.6*, crosshatched bars). **(A)** Ferulic acid content in an alcohol insoluble residue (AIR) preparation. **(B)** *p*-Coumaric acid content from AIR. **(C)** The ratio of ferulic acid (FA) to *p*-coumaric acid (*p*-CA). The average and error bars indicate 2*SEM for the shown biological young leaf replicates. * indicates significance via Student's t-test at $p < 0.05$ and ** indicates significance at $p < 0.01$.



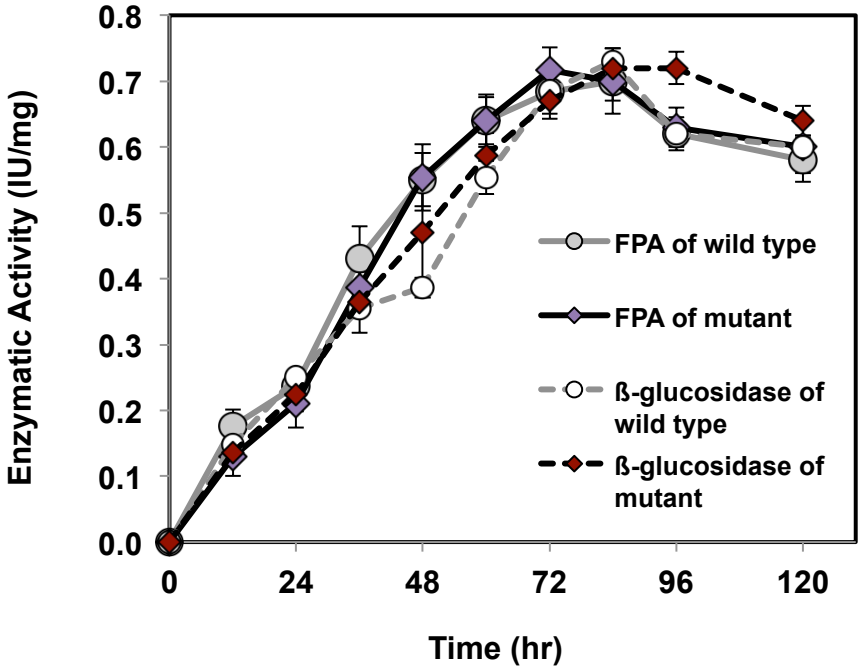

**Supplemental Figure 4.** Gene expression and hydroxycinnamate content of the second generation of *Ubi$_{pro}$:OsAt10-4* plants reveals a similar phenotype to the *OsAT10-D1* line. The wild type is shown in grey and the mutant in crosshatch. **(A)** qRT-PCR analysis of RNA isolated from the flag leaf of a tiller from the 4-5 leaf stage shows increased expression of *OsAt10* in the mutant relative to the wild type. **(B)** Hydroxycinnamic acids (HCA), i.e., ferulic acid (FA), *p*-coumaric acid (pCA), released from AIR from mature straw from wild-type and mutant plants by saponification. N = 3 for the wild type and N = 7 for the mutant. Error bars indicate 2*SEM for the average of the replicates. '*' indicates significance via Student's t-test at $p < 0.05$ and '**' indicates significance at $p < 0.01$.




**Supplemental Figure 5.** Destarched AIR from OsAT10-D1 mature straw has increased glucose (Glc) content relative to that of the wild type, but no other significant changes by mass in xylose (Xyl) and arabinose (Ara), galactose (Gal), fucose (Fuc), rhammnose (Rha), galacturonic acid (GalA), or glucuronic acid (GlcA). Wild-type (4A-03423.1 progeny) samples are solid and mutant (4A-03423.5 progeny) samples are hatched. Error bars show 2*SEM of three replicates. '*' indicates a difference at $p < 0.05$ via unpaired, two-tailed Student's t-test.




**Supplemental Figure 6.** Thermogravimetric analysis detects no mass difference upon heating between wild-type and mutant mature straw. **(A)** Example gravimetric traces throughout heating. The first heating phase (red line, right axis) represents heating in the absence of oxygen and the second represents heating in the presence of oxygen (combustion). Data are normalized to values at 30 minutes (177 °C), which represent the initial dry weights. **(B)** Selected times report on biomass composition. WT and *OsAT10-D1* are indistinguishable in terms of the mass of char (blue bars) remaining after pyrolysis at 800 °C (blue bars, t = 112 minutes), the ash content after combustion (red bars, t=250 minutes), and, by extension, the fraction of the char that is combustible (yellow bars, difference between char and ash). This provides further evidence that there is no difference in the lignin composition or content between the two genotypes. Switchgrass, oak, and duckweed samples are shown for comparison. Values are the % of the dry weight. When error bars are shown, values are averages and the error bars are 2*SEM of 2-4 technical replicates.




**Supplemental Figure 7.** Enzymatic activity in media during *Penicillium sp.* YT02 incubation with straw from the wild type (circles) and *OsAT10-D1* (diamonds). FPA (dashed lines) is the activity on cellulose filter paper. ß-glucosidase activity (solid lines) uses cellobiose as a substrate. IU is nmoles of sugar per minute per mL. Data are normalized for mg of total protein. Error bars show 2*SEM of five replicate cultures.