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Correction: The oleaginous yeast *Cutaneotrichosporon oleaginosum* modifies corn stover alkali lignin

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The original version of this Article contained an error in the legends of Figure 4, 5 and 6, in which the legend of Figure 4 was given as the legend of Figure 6, the legend of Figure 5 was given as the legend of Figure 4, and the legend of Figure 6 was given as the legend of Figure 5. This error was introduced by the Scientific Reports typesetting team.

For Figure 4, the legend now reads:

"High-resolution microscopy reveals lignin-dependent yeast cell fluorescence and morphological differences. (A) Fluorescence microscopy results showing lignin autofluorescence and subtle differences between lignin and benzoate cultures. (B) Fluorescence intensity distributions for cell populations recorded over time. (C) Airyscan images show difference in fluorescence of the cellular envelope and putative mitochondrial clusters. (D) Airyscan images of yeast labeled with MitoTracker Red CMXRos Dye. 5 μm scale bars are shown in the bottom right corners for Panel D. Differences in yeast fluorescence intensities may be attributed to mitochondrial autofluorescence, lignin interactions, and/or carbon-limited oxidative stress[47]. For panel B, cell population fluorescence intensities for three images were averaged then these three mean values were used for t-tests. Significance levels from two-sample t-tests are included as asterisks in the box plots. One asterisk is a p-value of 0.05. No significant difference is "ns".

For Figure 5, the legend now reads:

"Distinct protein expression patterns in lignin and glucose conditions uncovered by secretomics and proteomics. (A) Venn diagrams indicating overlap of unique, quantifiable protein IDs. Only one missing LFQ intensity value was permitted among the replicates of each condition. Secretomics results were filtered using a cutoff of 0.85 according to SignalP 6.0[45]. (B) Correlogram of Pearson correlations for overlapping LFQ results from secretomics data. (C) Correlogram of Pearson correlations for proteomics data. (D) Donut charts of CUPP-annotated CAZymes found in our secretomics and proteomics data[46]. "Observed" refers to all unique identifications. "DE-filtered" refers to IDs for which two LFQ values were present to conduct differential expression analysis. (E) Volcano plots summarizing FCs from separate differential expression analyses of secretomics and proteomics data. The vertical purple lines designate FCs of −1 and +1, whereas the dashed black line designates an adjusted p-value of 0.05. (F) Summarized dot plot results from KEGG pathway enrichment analysis[198,199] using protein IDs with significant differences (adjusted p-value ≤ 0.05) in expression: "Down" refers to those with FC ≤ −1, and "Up" refers to FC ≥ 1."

For Figure 6, the legend now reads:

"Proposed pathways for lignin modification and catabolism of lignin-derived aromatics. According to our NMR results, extensive homology searches, and literature review, pathways are only shown for H- and G-lignin-derived aromatics. Additional details regarding ROS-mediated mechanisms for lignin modification are provided in the *SI Appendix*, Fig. S4. The predicted pathways for G-lignin derivatives are discussed in *SI Appendix*, Supporting Text. JGI protein IDs are included within boxes that are colored according to the average FC for lignin vs. glucose. Note that boldface green lettering corresponds to proteins only observed in the lignin condition. Boldface blue lettering corresponds to proteins that were observed, but for which no differential expression analysis could be conducted due to missing intensity values. Boldface purple lettering corresponds to IDs for which raw intensity values were used in DEP differential expression analysis due to missing LFQ intensity values. Question marks and dotted arrows represent uncertain annotations. The numbers in circles designate the following putative enzyme annotations: 1. Laccases, 2. Peroxidases, 3. Phenol 2-monooxygenase,

4. Catechol 1,2-dioxygenase, 5. Muconate cycloisomerase, 6. Muconolactone isomerase, 7. β-ketoadipate enol-lactone hydrolase, 8. β-ketoadipate-succinyl-CoA transferase, 9. β-ketoadipyl-CoA thiolase, 10. Benzoate 4-monooxygenase (Cytochrome P450), 11. *p*-Coumarate-CoA ligase, 12. Cinnamoyl-CoA hydratase/dehydrogenase (first arrow = IDs on the left) and 3-ketoacyl CoA thiolase (second arrow = IDs on the right), 13. Thioesterase, 14. Hydroxylase, 15. Protocatechuate 3,4-dioxygenase, 16. β-carboxymuconate lactonizing enzyme, 17. γ-carboxymuconolactone decarboxylase, 18. Monooxygenase/decarboxylase, 19. Hydroxyquinol 1,2-dioxygenase, 20. Maleylacetate reductase, 21. Cinnamoyl-CoA reductase, 22. Aldehyde dehydrogenase/cytochrome P450 (see IDs below coniferyl aldehyde structure), 23. Feruloyl-CoA synthetase, 24. Cinnamoyl-CoA hydratase/dehydrogenase (first arrow = IDs on the left) and 3-ketoacyl CoA thiolase (second arrow = IDs on the right), 25. Thioesterase, 26. Vanillin dehydrogenase, 27. Vanillyl alcohol oxidase, 28. Vanillate hydroxylase, 29. O-demethylase, 30. (Di)methoxyhydroquinone 1,2-dioxygenase, 31. *p*-Hydroxybenzoate decarboxylase, 32. GMC oxidoreductase, 33. Gluconate kinase."

The original Article has been corrected.