

Supplemental Figures

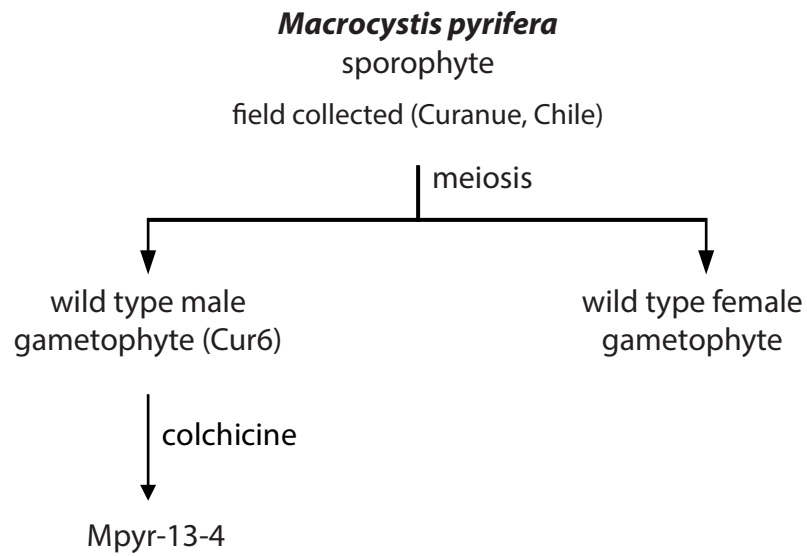


Figure S1. Pedigree of the *M. pyrifera* strains used in this study.

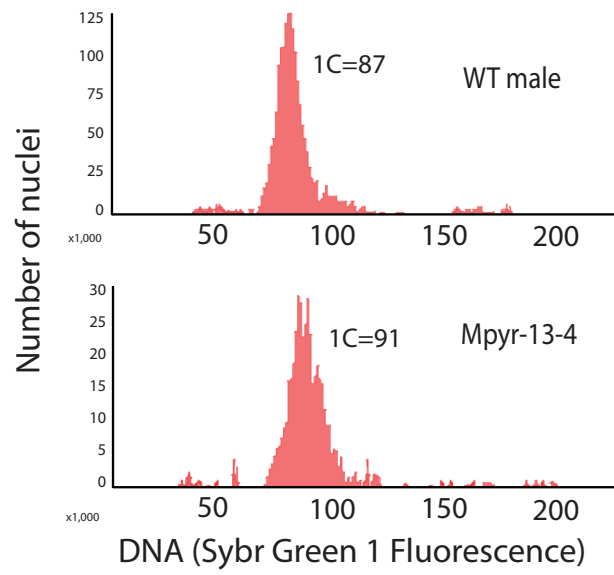


Figure S2. Flow cytometry analysis of a wild-type male line (top) and the Mpyr-13-4 line (bottom) of *M. pyrifera*.

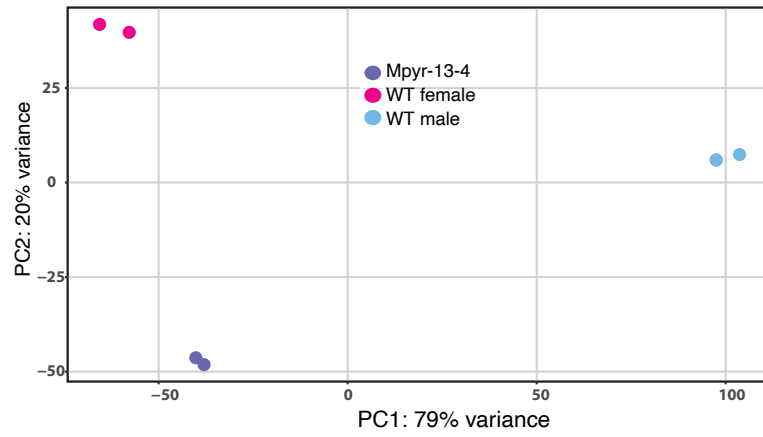


Figure S3. PCA was used to compare transcript abundance patterns across samples. The two dimensions represent 79% and 20% of the variance.

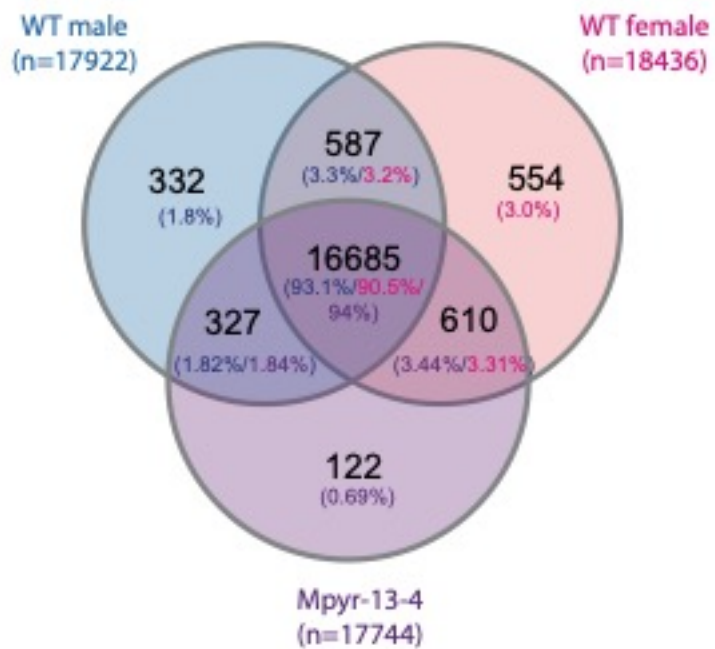


Figure S4. Venn diagram showing the sets of expressed genes (TPM>5th percentile) in wild-type male, wild-type female and variant Mpyr-13-4 lines and the overlap between the three sets.

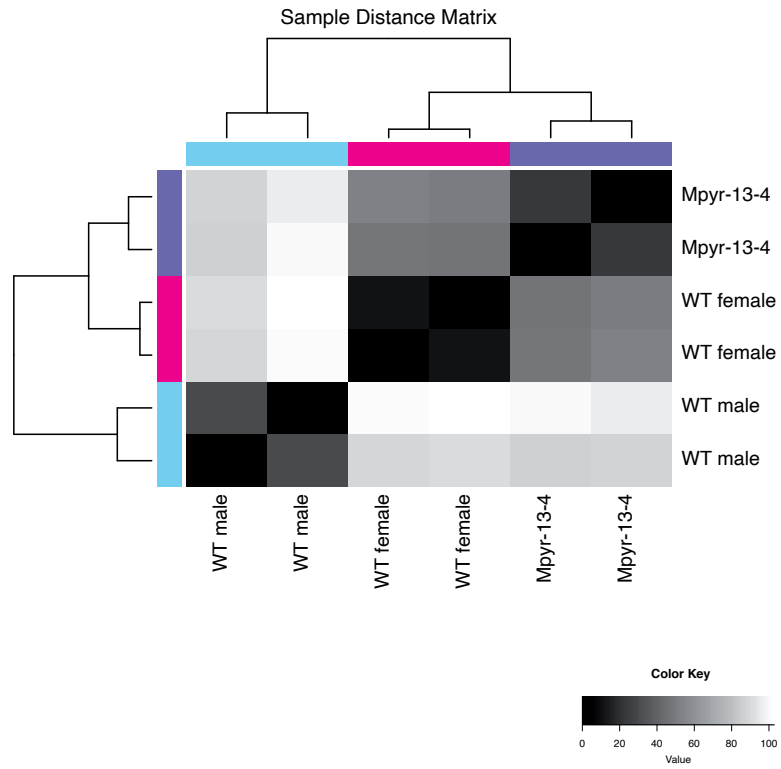


Figure S5. Expression heatmap of sample-to-sample distances on the matrix of variance-stabilized data for overall gene expression. Darker colors indicate more similar expression (color key is in arbitrary units). Clustering (top) demonstrates that the variant and female samples are very similar to each other but show complete separation from the male samples.

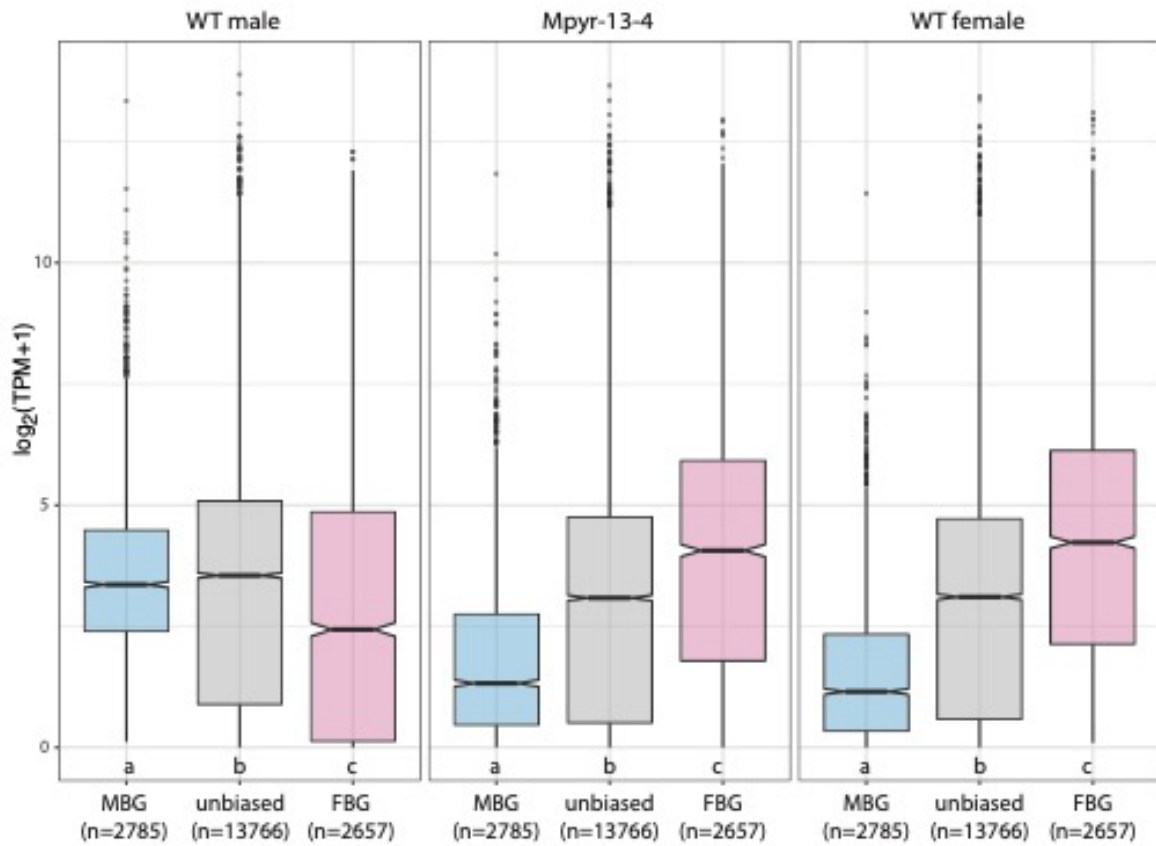


Figure S6. Box-plots representing the levels of expression ($\log_2\text{TPM}+1$) of sex-biased genes in wild-type males, Mpyr-13-4 and wild-type females of *M. pyrifera*. MBG: male-biased genes; FBG: female-biased genes. Significant differences (Wilcoxon test, $p < 0.01$) are indicated with different letters below the plots.