

1 Supplementary materials

1.1 Supplementary Figures

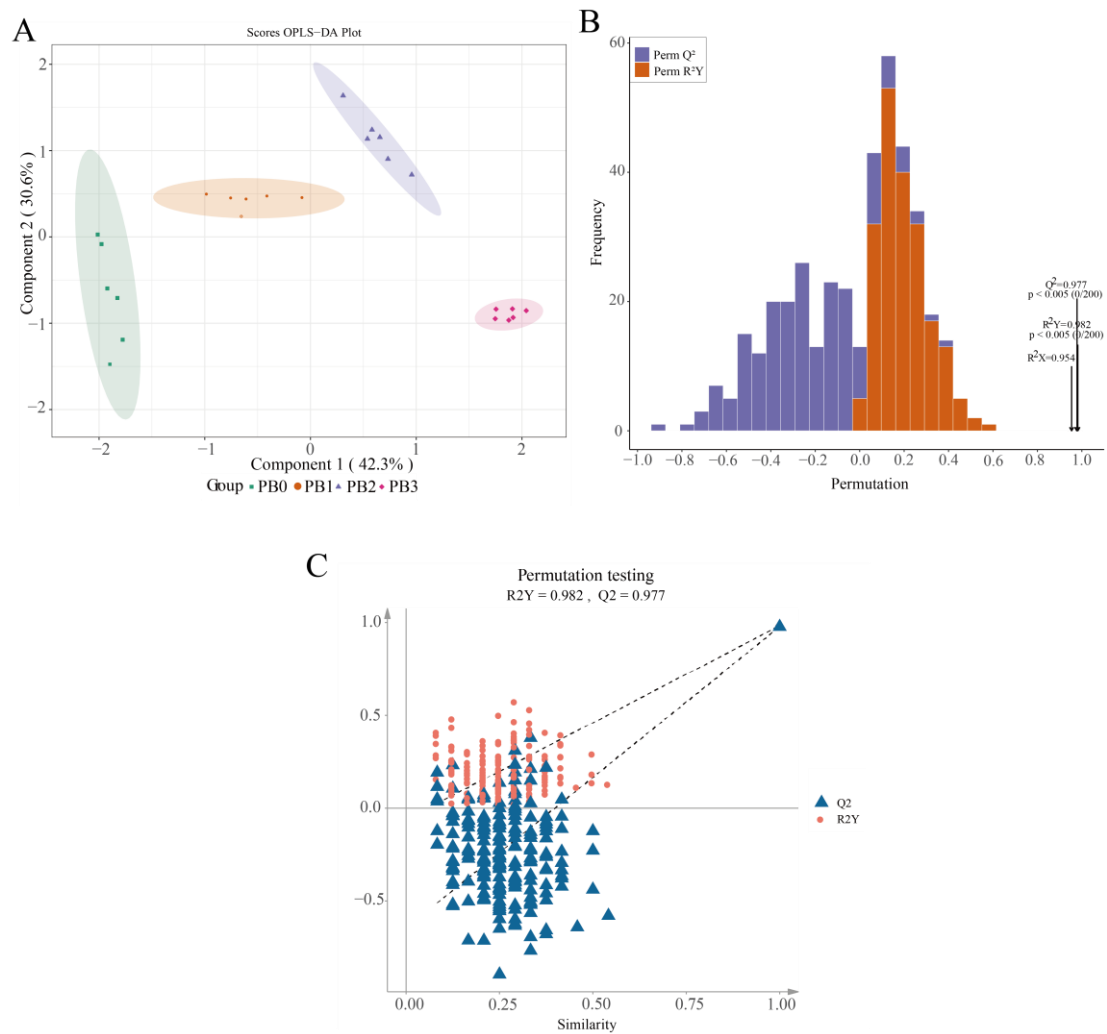


Figure S1. OPLS-DA analysis of endogenous hormone profiles at different stages of AR formation in *P. bournei* cuttings. **(A)** Score plot showing the separation of samples. **(B)** Loading plot for model diagnostics. **(C)** Permutation test plot (n = 200) validating the robustness of the OPLS-DA model. PB0, PB1, PB2, and PB3 represent 0, 15, 30, and 50 days after cutting, respectively.

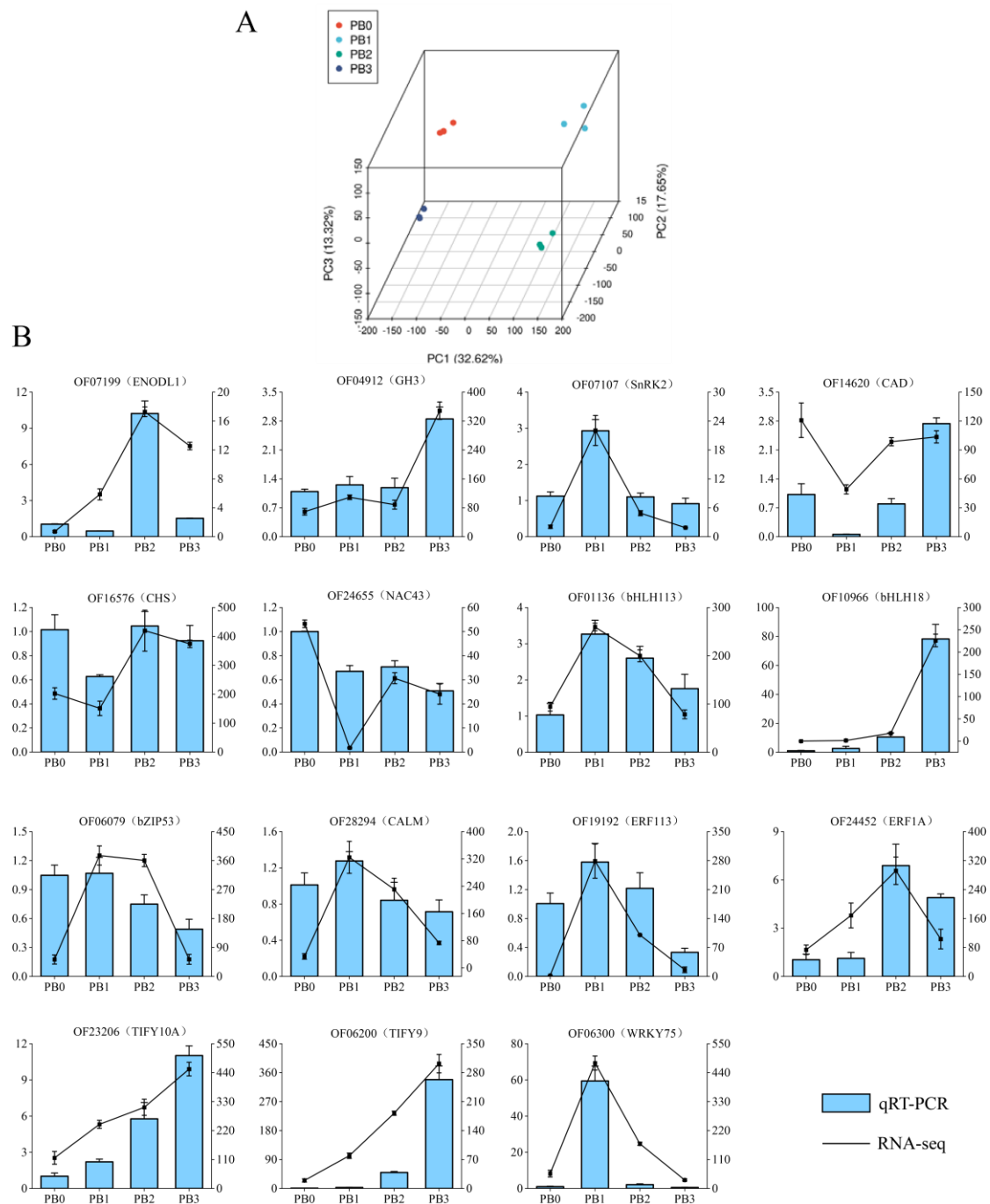


Figure S2. PCA and qRT-PCR Validation. **(A)** Principal component analysis (PCA) plot of gene expression profiles for PB0, PB1, PB2, and PB3 samples. **(B)** Comparison analysis of qRT-PCR and RNA-seq results. The black line represents the RNA-seq FPKM, and the blue bars represent the relative expression levels from qRT-PCR. PB0, PB1, PB2, and PB3 represent 0, 15, 30, and 50 days after cutting, respectively.

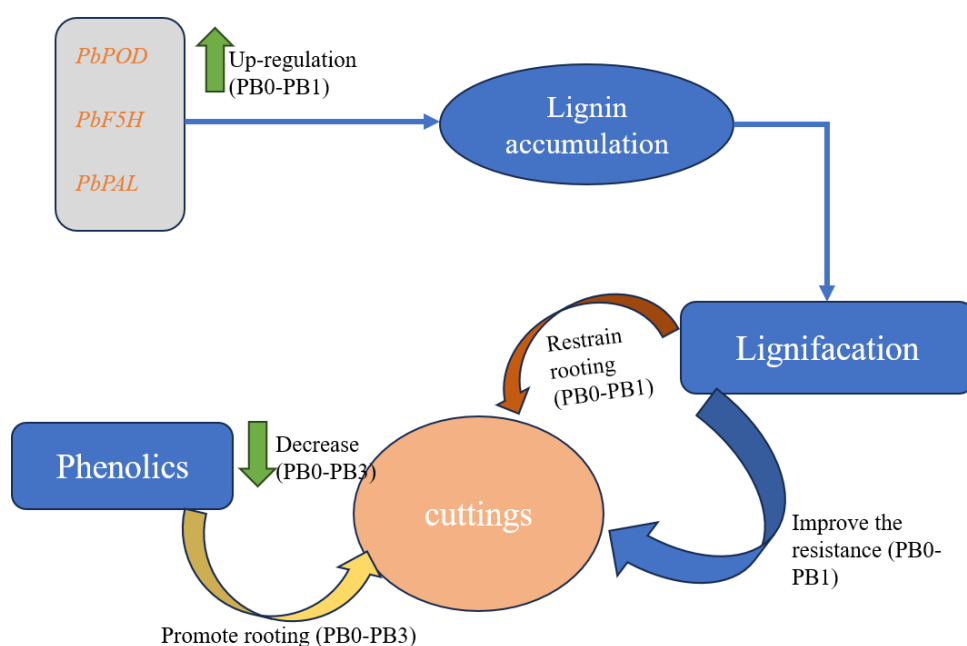


Figure S3. Simplified schematic model of lignin and phenolic regulation during AR formation in *P. bournei*

1.2 Supplementary tables

Table S1 Primers used in qRT-PCR in this study

Gene name	primers for qPCR (F5'-3')	primers for qPCR (R5'-3')
<i>PbENODL1</i>	AAAGGGTCGCTGTGAGAAGG	GACACACCCCATGCAAAACC
<i>PbNAC43</i>	GGTCTGTGCGCTCTTCAAGA	CTTGACATCCTCCCCATGT
<i>PbERF1A</i>	GAATCCGCTCCGTCTCCG	TCGAACGTTCCCAGCCAC
<i>PbSnRK2</i>	TCAACGGTAGGAACACCAGC	ACACCCTCACGTAGTCTGGA
<i>PbbHLH113</i>	ACCTCCAGAGTGAGCCCT	CATGACGGGCGCCCATAT
<i>PbbHLH18</i>	CGCCAGCCAGGGATCAAA	AGCAATGAACCGCTGGCT
<i>PbbZIP53</i>	TGAGGACGCAGGTGATGG	AGCTGCCATGGCCTAAGC
<i>PbCAD</i>	CACCCTACCAATTCAGCCGT	CGACAATCTCATGCCCAGGT
<i>PbCHS</i>	TGTCCCAGGCCTCATATCCA	ACTGAGAACATGCCTGGTGG
<i>PbCALM</i>	TGCGCCATGTGATGACCA	GGCCATCACCGTCGACAT
<i>PbERF113</i>	ATGCACAGCTGCTACGCA	TGCAAGCGATGATGGCGA
<i>PbGH3</i>	GATGCTCTGTGGCCTCTACC	CGGATTCTCGGACTGATGGG
<i>PbTIFY10A</i>	CATCCATGGCCGCCTCTT	CTCGCTCGGAGTCGACAC
<i>PbWRKY75</i>	TGGGCAGAAGGCTGTGAAG	GGCGCTGAACCTTGCTTCT
<i>PbEF1α</i>	CATTCAAGTATGCGTGGGT	ACGGTGACCAGGAGCA

Table S2. VIP values of endogenous hormone contents during AR formation in *P. bournei*

Comparable group	Var ID	VIP
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PB0 vs. PB1	ABA	1.069951229
	GA	0.998343471
	IAA	1.229221807
	IBA	0.419829474
	ZR	1.082253041
PB1 vs. PB2	ABA	1.083709125
	GA	1.069800482
	IAA	1.082453681
	IBA	1.055862733
	ZR	0.628131655
PB2 vs. PB3	ABA	1.072364671
	GA	1.040332222
	IAA	1.070786291
	IBA	1.061868622
	ZR	0.687209763

Table S3. Statistical summary of sequencing data volume.

Sample	Raw reads	Raw bases	Clean reads	Clean bases	Q_20 rate	Q_30 rate	GC_content
PB0_1	43,368,530	6,505,279,500	43,368,530	6,464,403,432	98.651%	95.562%	45.668%
PB0_2	43,386,174	6,507,926,100	43,386,174	6,489,383,196	98.456%	94.842%	45.593%
PB0_3	43,338,394	6,500,759,100	43,338,394	6,472,927,004	98.371%	94.583%	45.589%
PB1_1	43,346,432	6,501,964,800	43,346,432	6,481,971,940	98.793%	95.611%	45.827%
PB1_2	43,393,028	6,508,954,200	43,393,028	6,482,224,410	98.824%	95.722%	45.788%
PB1_3	43,375,670	6,506,350,500	43,375,670	6,481,777,130	98.804%	95.637%	45.965%
PB2_1	43,350,160	6,502,524,000	43,350,160	6,476,101,836	98.804%	95.649%	45.985%
PB2_2	43,393,464	6,509,019,600	43,393,464	6,486,199,562	98.702%	95.273%	46.072%
PB2_3	43,351,290	6,502,693,500	43,351,290	6,482,113,132	98.692%	95.239%	46.128%
PB3_1	43,357,528	6,503,629,200	43,357,528	6,484,038,226	98.553%	95.143%	45.788%
PB3_2	43,365,806	6,504,870,900	43,365,806	6,484,866,702	98.610%	95.361%	45.518%
PB3_3	43,357,888	6,503,683,200	43,357,888	6,486,456,540	98.571%	95.227%	45.717%