

Table S5. Validation of the expressed change ratio [Log₂FoldChange, relative to *Alternaria tenuissima* strain TJ-NH-51S-4-VF] obtained in the RNA sequencing (RNA-seq) data using reverse transcription-quantitative polymerase chain reaction (RT-qPCR). Listed genes are differentially expressed genes (DEGs) related to cytochrome P450, drug resistance, ATP-binding cassette transporter (ABC), and major facilitator superfamily (MFS) in *A. tenuissima* strain TJ-NH-51S-4 as annotated in RefSeq non-redundant proteins (NR) and protein family (Pfam) databases. Eleven DEGs were selected for the RT-qPCR validation of the RNA-seq data.

| Gene_ID | NR description | Pfam description | Regulation model | RNA-seq (Log ₂ Fold Change) ^a | qRT-PCR (2 ^{-ΔΔct}) | |
|-----------|--|------------------|------------------|---|-------------------------------|-------------|
| | | | | | TJ-NH-51S-4-VF | TJ-NH-51S-4 |
| At-g911 | Cytochrome | Cytochrome P450 | up | 1.7289 | 1.6420 | 4.9130 |
| At-g11265 | Cytochrome P450 sterol 14α-demethylase (CYP51) | Cytochrome P450 | up | 1.5392 | 1.0913 | 2.7809 |
| At-g8804 | Cytochrome P450 family protein | Cytochrome P450 | up | 1.2978 | 1.0390 | 2.5480 |
| At-g7231 | Cytochrome P450 family protein | Cytochrome P450 | down | -2.1232 | — ^b | — |
| At-g1833 | Cytochrome P450 family protein | Cytochrome P450 | down | -1.9325 | — | — |
| At-g1560 | Cytochrome P450 52A12 | Cytochrome P450 | down | -1.8548 | — | — |
| At-g5685 | Cytochrome P450 family protein | Cytochrome P450 | down | -1.6715 | — | — |
| At-g1880 | Cytochrome P450 family protein | Cytochrome P450 | down | -1.6154 | — | — |

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|-----------|---|---|------|---------|--------|--------|
| At-g10737 | Cytochrome P450 family protein | Cytochrome P450 | down | -1.5629 | — | — |
| At-g610 | Cytochrome P450 phenylacetate hydroxylase-like protein | Cytochrome P450 | down | -1.3853 | — | — |
| At-g3369 | Cytochrome P450 3A17 | Cytochrome P450 | down | -1.3084 | — | — |
| At-g3404 | Cytochrome P450 76C3 | Cytochrome P450 | down | -1.0458 | — | — |
| At-g9548 | Azole resistance protein | Major facilitator superfamily | down | -4.4061 | — | — |
| At-g9347 | Aminotriazole resistance protein | Major facilitator superfamily | down | -2.9289 | — | — |
| At-g5065 | Multidrug resistance protein | ABC transporter transmembrane region | down | -1.7886 | — | — |
| At-g1754 | ATP-binding cassette transporter | ABC-2 type transporter | down | -1.9174 | 1.0125 | 0.2708 |
| At-g6376 | Putative transporter | Major facilitator superfamily | up | 1.5736 | — | — |
| At-g2640 | MFS general substrate transporter | Major facilitator superfamily | up | 1.2894 | — | — |
| At-g8103 | Membrane transporter | Major facilitator superfamily | down | -3.3514 | 1.0144 | 0.0645 |
| At-g11728 | Putative transporter | Major facilitator superfamily | down | -2.9717 | — | — |
| At-g3039 | MFS general substrate transporter | Major facilitator superfamily | down | -2.6997 | 1.0726 | 0.0753 |
| At-g4660 | MFS general substrate transporter | Major facilitator superfamily | down | -2.6934 | 1.0074 | 0.2227 |
| At-g9794 | MFS general substrate transporter | Major facilitator superfamily | down | -1.9477 | — | — |

| | | | | | | |
|-----------|-----------------------------------|-------------------------------|------|---------|--------|--------|
| At-g10416 | MFS general substrate transporter | Major facilitator superfamily | down | -1.8821 | — | — |
| At-g5043 | MFS general substrate transporter | Major facilitator superfamily | down | -1.4775 | — | — |
| At-g2973 | Putative transporter | Major facilitator superfamily | down | -1.1134 | — | — |
| At-g2452 | Siderophore iron transporter | -- | up | 3.4328 | — | — |
| At-g1250 | Siderophore iron transporter | Major facilitator superfamily | up | 2.1654 | 1.0136 | 4.1880 |
| At-g7202 | Siderophore iron transporter | Major facilitator superfamily | up | 2.0584 | — | — |
| At-g4632 | Siderophore iron transporter 1 | Major facilitator superfamily | up | 1.6176 | 1.1762 | 2.8569 |
| At-g7816 | Phosphate permease | Phosphate transporter family | up | 3.3835 | 1.0514 | 3.5930 |
| At-g4584 | Thioredoxin-like protein | AhpC/TSA family | up | 2.0237 | 1.0064 | 6.4723 |

^a The fold change values were originated from the data of RNA-seq which were evaluated using false discovery rate $P < 0.05$ and from the data of RT- qPCR.

^b The symbol ‘—’ showed that the DEGs were not chosen for validation of the data of RNA-seq.

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