

Table S1. Primers used in this study.

| Primer name | Sequencing (5'-3') | Relevant characteristics |
|----------------|---|--|
| pFC1 | TACTGGGCCCCGGAAGATCTGCGTAAGCTCCCTAATTGGC | gRNA construction |
| pCF2 | ACAGCTATGACCATGAGATCTGAGCCAAGAGCGGATTCCTC | |
| pFC1-g3571-R | AGCTTACTCGTTTCGTCCTCACGGACTCATCAGGTTGGCCGGTGATGTCTGCTCAAGC G | gRNA construction |
| pCF2-g3571-F | AGTAAGCTCGTCGTTGGCCGGCAGTGCTCCCCCGTTTTAGAGCTAGAAATAGCAAGT TAAA | |
| pFC1-g3762-R | AGCTTACTCGTTTCGTCCTCACGGACTCATCAGGTTTGGCCGGTGATGTCTGCTCAAGC G | gRNA construction |
| pCF2-g3762 - F | AGTAAGCTCGTCGTTTGGTATGCTTACGCTAAGTTTTAGAGCTAGAAATAGCAAGTT AAA | |
| pFC1-g2654-R | AGCTTACTCGTTTCGTCCTCACGGACTCATCAGgCCCAACGGTGATGTCTGCTCAAGC G | gRNA construction |
| pCF2-g2654 - F | AGTAAGCTCGTCgCCCAACCTGTCAGCCCCGGGGTTTTAGAGCTAGAAATAGCAAGT TAAA | |
| g3571-JD-F | TCGGCTGATTCCTACGGT | transformants identification |
| g3571-JD-R | CAAGGCACAGGGAGAACG | |
| g3762-JD-F | TCCAACGACTGCGGACTT | transformants identification |
| g3762-JD-R | TGGCGGCTCACGAGATAG | |
| g2654-JD-F | GAGTAGTGAAACCGGAAACG | transformants identification |
| g2654-JD-R | GCACCATCTGCGACTGAC | |
| 3530-Q-F: | TGTTAGCACATCGCTTCCTG | Amplify the <i>Pdw03_3530</i> gene in qRT-PCR assays |
| 3530-Q-R: | GCCATACTCATACTCGCATCAC | |
| 3762-Q-F: | CAGGATGAGAAACGGAACA | Amplify the <i>Pdw03_3762</i> gene in qRT-PCR assays |

| | |
|-----------|-------------------------|
| 3571-Q-F | CCAACACCCAGAAGAAGCACA |
| 3571-Q-R | TCGTCATCGTCACCAGAGCC |
| 3636-Q-F | CTCGCTTCCTCCCTACAA |
| 3636-Q-R | AGGTCGGCTACAGTCTCG |
| 2655-Q-F | CTTGAGGCAAATCTCCCA |
| 2655-Q-R | TGCTTTCATCGGTCCACT |
| 2654-Q-F | ATCATCAAATCAACCACCAA |
| 2654-Q-R | CCACTATTAGGCTCGTAAGG |
| 7336-Q-F | ATTCAGCATTCGCTCTGTAGTCT |
| 7336-Q-R | CCATTTCGGTTTCATCCATC |
| 2323-Q-F | GGAGGGTGGTGGATGTGA |
| 2323-Q-R | CGGGACTGTGGGAGTTGT |
| 2460-Q-F: | TCTTCCTCTTCGCCTTCTCC |
| 2460-Q-R: | GCCTTGTTGTAATAGCCGTTGT |
| CYP51A-F | GTCGTCATACCTCGAACTCCC |
| CYP51B-R | CGGATTGGCCTTTGAAGCTG |
| CYP51B-F | CACAGAAGAAGTTGACCGAGAC |
| CYP51B-R | GGATGACGACGAGTGATGG |
| Actin-F | TCCACTACTGCCGAGCGTGAAAT |
| Actin-R | CCGCCAGACTCAAGACCAAGAAC |
| 4069-F: | ACGTATGGCTACATCACTGACTC |
| 4069-R: | CAAACCTACATCGCCGAAAGA |
| 7095-F: | AGTCCTTCGCCGATGCTC |
| 7095-R: | ATGCCTCCACCCGTGAGA |
| 386-F: | AGGCTGTTTGGTCTGTTTGT |
| 386-R: | GTGTCGTAGAGTTTGGCGTAT |

Amplify the *Pdw03_3571* gene in qRT-PCR assays

Amplify the *Pdw03_3636* gene in qRT-PCR assays

Amplify the *Pdw03_2655* gene in qRT-PCR assays

Amplify the *Pdw03_2654* gene in qRT-PCR assays

Amplify the *Pdw03_7336* gene in qRT-PCR assays

Amplify the *Pdw03_2323* gene in qRT-PCR assays

Amplify the *Pdw03_2460* gene in qRT-PCR assays

Amplify the *CYP51A* gene in qRT-PCR assays

Amplify the *CYP51B* gene in qRT-PCR assays

Amplify the Actin gene in qRT-PCR assays

Amplify the ERG24 gene in qRT-PCR assays

Amplify the ERG1 gene in qRT-PCR assays

Amplify the ERG3A gene in qRT-PCR assays

| | | |
|---------|-----------------------|--|
| 2864-F: | TACCTGGCATTACTTCTCCC | Amplify the ERG25 gene in qRT-PCR assays |
| 2864-R: | GAAGCCCAAGATCATCACTT | |
| 3754-F: | TCGTGAGGTATGGCAAAGCG | Amplify the ERG6 gene in qRT-PCR assays |
| 3754-R: | AGCGGCAGAAATGGAAGGAG | |
| 2561-F: | GAACCTGAAAGTCCGCAACG | Amplify the ERG5 gene in qRT-PCR assays |
| 2561-R: | GGGTAAGCCTCCTCATCGTG | |
| 6706-F: | AGGGTGAGGAGTGCATTGTT | Amplify the ERG4A gene in qRT-PCR assays |
| 6706-R: | TACTCAGCAGGGTCGTGGTT | |
| 2117-F: | TGGTGTCCCTATGTCTTACTG | Amplify the ERG4B gene in qRT-PCR assays |
| 2117-R: | CTTCTGGCTGTTTGCTGTG | |
| 7067-F: | TTCACAGATAGCGGGATTTA | Amplify the ERG3B gene in qRT-PCR assays |
| 7067-R: | GGTAGACATGGTAGGGCAGA | |

Table S2. Statistics of sequencing data.

| SampleID | Total Reads | BaseSum | GC(%) | Q20(%) | Q30(%) | Mapped Reads | Uniq Mapped Reads | Multiple Map Reads |
|----------|-------------|------------|-------|--------|--------|---------------------|---------------------|--------------------|
| CK-1 | 53616314 | 8024495430 | 53.84 | 97.77 | 89.25 | 46,590,024 (86.90%) | 46,332,920 (86.42%) | 257,104 (0.48%) |
| CK-2 | 57572066 | 8616132164 | 53.84 | 98.08 | 90.64 | 50,621,319 (87.93%) | 50,372,154 (87.49%) | 249,165 (0.43%) |
| CK-3 | 59750474 | 8940526268 | 53.71 | 98.09 | 90.72 | 52,605,895 (88.04%) | 52,300,386 (87.53%) | 305,509 (0.51%) |
| IMZ12h-1 | 41677974 | 6237134752 | 53.63 | 98.78 | 93.08 | 39,124,888 (93.87%) | 38,953,257 (93.46%) | 171,631 (0.41%) |
| IMZ12h-2 | 47531050 | 7112072644 | 53.64 | 98 | 90.3 | 41,953,633 (88.27%) | 41,709,160 (87.75%) | 244,473 (0.51%) |
| IMZ12h-3 | 52769732 | 7897659212 | 53.8 | 98.04 | 90.51 | 46,537,883 (88.19%) | 46,324,455 (87.79%) | 213,428 (0.40%) |
| IMZ2h-1 | 49636364 | 7426564082 | 53.56 | 98.17 | 91.03 | 44,481,475 (89.61%) | 44,305,115 (89.26%) | 176,360 (0.36%) |

| | | | | | | | | |
|---------|----------|------------|-------|-------|-------|---------------------|---------------------|-----------------|
| IMZ2h-2 | 58121086 | 8698518980 | 53.58 | 98.02 | 90.4 | 51,612,383 (88.80%) | 51,380,291 (88.40%) | 232,092 (0.40%) |
| IMZ2h-3 | 51602940 | 7724795970 | 53.9 | 97.92 | 89.92 | 46,099,477 (89.33%) | 45,921,451 (88.99%) | 178,026 (0.34%) |

Table S3. Differentially expressed transcription factors after IMZ treatment.

| geneID | Annotation | 2h-Log2FC | 12h-Log2FC | TF |
|------------|---|--------------|--------------|--------------|
| Pdw03_2654 | Basic-leucine zipper (bZIP) transcription factor | -5.277533055 | -3.222305046 | bZIP_1 |
| Pdw03_7664 | C6 transcription factor, putative | -3.954842386 | -2.989891018 | Zn_clus |
| Pdw03_7446 | PHD transcription factor (Rum1), putative | -3.290720486 | -3.151349521 | ARID |
| Pdw03_5422 | Fungal transcriptional regulatory protein, N-terminal | -4.537605924 | -1.496805996 | Zn_clus |
| Pdw03_1620 | Pyruvate/Phosphoenolpyruvate kinase | -2.314303153 | -3.683901617 | Fungal_trans |
| Pdw03_4243 | Winged helix-turn-helix transcription repressor DNA-binding | -3.072669681 | -2.491612848 | Fork_head |
| Pdw03_4194 | Zinc finger, C2H2 | -2.051737923 | -3.328531995 | zf-C2H2 |
| Pdw03_3762 | Fungal transcriptional regulatory protein, N-terminal | -3.082146853 | -2.285568712 | Zn_clus |
| Pdw03_3206 | Aflatoxin biosynthesis regulatory protein | -2.863532581 | -2.131716068 | Zn_clus |
| Pdw03_5090 | Protease inhibitor I4, serpin | -2.24718469 | -2.55681538 | Zn_clus |
| Pdw03_4703 | C2H2 transcription factor (Rpn4), putative | -2.924428711 | -1.521661744 | zf-C2H2 |
| Pdw03_8176 | GATA factor SREP | -2.05753796 | -2.032890953 | GATA |
| Pdw03_2365 | Zn(2)-C6 fungal-type DNA-binding domain | -2.331173497 | -1.752696665 | Zn_clus |
| Pdw03_3389 | Basic-leucine zipper (bZIP) transcription factor | -1.862816276 | -2.094483706 | bZIP_1 |
| Pdw03_7768 | Uracil-DNA glycosylase | -1.760556056 | -1.921033059 | Fungal_trans |
| Pdw03_3922 | pH-response transcription factor pacC/RIM101 | -1.281121113 | -2.317608671 | zf-C2H2 |
| Pdw03_8795 | Fungal transcriptional regulatory protein, N-terminal | -1.289465478 | -2.0743941 | Zn_clus |
| Pdw03_6801 | Homeobox transcription factor (RfeB), putative | -1.082151854 | -2.255542957 | Homeobox |
| Pdw03_1622 | Pyruvate/Phosphoenolpyruvate kinase | -1.304302023 | -1.989166656 | Zn_clus |
| Pdw03_4334 | Fungal specific transcription factor, putative | -1.674763231 | -1.568344224 | Zn_clus |
| Pdw03_8415 | Transcriptional regulator | -2.122343752 | -1.058645786 | zf-C2H2 |

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|------------|---|--------------|--------------|--------------|
| Pdw03_4859 | C6 transcription factor, putative | -1.739536797 | -1.36586337 | Zn_clus |
| Pdw03_2353 | Fungal transcriptional regulatory protein, N-terminal | -1.656515291 | -1.435342234 | Zn_clus |
| Pdw03_5802 | Zinc finger, C2H2-like | -1.76768398 | -1.095455284 | zf-C2H2 |
| Pdw03_5521 | Fungal transcriptional regulatory protein, N-terminal | -1.472516178 | -1.371394588 | Zn_clus |
| Pdw03_1773 | Non-histone chromosomal protein 6 | -1.160980152 | -1.597176957 | HMG_box |
| Pdw03_7815 | Nitrogen assimilation transcription factor nit-4 | -1.370932517 | -1.316195242 | Zn_clus |
| Pdw03_7397 | C6 transcription factor, putative | -1.410439571 | -1.001334238 | Zn_clus |
| Pdw03_7117 | Helix-loop-helix DNA-binding | -1.084308743 | -1.1776687 | HLH |
| Pdw03_3834 | C6 transcription factor OefC | -1.099214596 | -1.006203653 | Zn_clus |
| Pdw03_1121 | Fungal transcriptional regulatory protein, N-terminal | 1.006093879 | 1.081296982 | Zn_clus |
| Pdw03_6778 | Fungal transcriptional regulatory protein, N-terminal | 1.240236789 | 1.01559008 | Zn_clus |
| Pdw03_4388 | BZIP transcription factor, putative | 1.06478547 | 1.199523445 | bZIP_1 |
| Pdw03_4216 | C6 transcription factor, putative | 1.187094091 | 1.22706668 | Zn_clus |
| Pdw03_1937 | Winged helix-turn-helix transcription repressor DNA-binding | 1.115770981 | 1.299985248 | Fork_head |
| Pdw03_4483 | Fungal transcriptional regulatory protein, N-terminal | 1.324844271 | 1.15056483 | Zn_clus |
| Pdw03_2083 | Zn(2)-C6 fungal-type DNA-binding domain protein | 1.089311174 | 1.408277236 | Zn_clus |
| Pdw03_8240 | MADS box transcription factor Mcm1 | 1.517325935 | 1.050142498 | SRF-TF |
| Pdw03_5998 | putative transcriptional regulatory protein | 1.106514825 | 1.527346247 | Zn_clus |
| Pdw03_4875 | C6 transcription factor RosA-like, putative | 1.346633966 | 1.32768232 | Zn_clus |
| Pdw03_3221 | Fungal transcriptional regulatory protein, N-terminal | 1.569397568 | 1.257424451 | Zn_clus |
| Pdw03_8372 | Crotonase, core | 1.655157074 | 1.179922712 | Zn_clus |
| Pdw03_3819 | C2H2 transcription factor, putative | 1.133373819 | 1.800863227 | zf-C2H2 |
| Pdw03_3511 | C6 transcription factor, putative | 1.071951431 | 1.904047227 | Fungal_trans |
| Pdw03_2703 | Zn(2)-C6 fungal-type DNA-binding domain | 1.601193745 | 1.436383037 | Zn_clus |
| Pdw03_2910 | Zn(II)2Cys6 transcription factor | 1.405417185 | 1.65099444 | Zn_clus |
| Pdw03_5143 | Fungal transcriptional regulatory protein, N-terminal | 1.079126964 | 2.041288803 | Zn_clus |

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|------------|---|-------------|-------------|----------------|
| Pdw03_2909 | Zn(II)2Cys6 transcription factor | 1.651838646 | 1.502391416 | Fungal_trans |
| Pdw03_8375 | Zn(II)2Cys6 transcription factor | 1.548544733 | 1.731357513 | Fungal_trans_2 |
| Pdw03_6876 | Fungal transcriptional regulatory protein, N-terminal | 1.676364772 | 1.665870421 | Zn_clus |
| Pdw03_2841 | Ubiquitin-conjugating enzyme E2 6 | 1.436135989 | 1.923939917 | Fungal_trans_2 |
| Pdw03_8470 | Fungal transcriptional regulatory protein, N-terminal | 1.656096208 | 1.721453297 | Zn_clus |
| Pdw03_8563 | NDT80 / PhoG like DNA-binding family protein | 1.133101834 | 2.251507565 | NDT80_PhoG |
| Pdw03_8042 | Fungal transcriptional regulatory protein, N-terminal | 1.510786239 | 1.892390311 | zf-C2H2 |
| Pdw03_6475 | C6 transcription factor (PrnA), putative | 1.879398891 | 1.546664826 | Zn_clus |
| Pdw03_8511 | Nitrogen assimilation transcription factor nirA | 2.322853838 | 1.108029983 | Zn_clus |
| Pdw03_8248 | Zinc finger, C2H2 | 1.725170568 | 1.722909652 | zf-C2H2 |
| Pdw03_4853 | Fungal transcriptional regulatory protein, N-terminal | 1.755883389 | 1.717378541 | Zn_clus |
| Pdw03_6734 | C6 transcription factor, putative | 1.625373576 | 1.86077108 | Zn_clus |
| Pdw03_8324 | Zn(2)-C6 fungal-type DNA-binding domain | 2.284554098 | 1.40701085 | Fungal_trans_2 |
| Pdw03_4958 | C6 transcription factor, putative | 1.570917316 | 2.1493182 | Fungal_trans |
| Pdw03_3512 | C6 transcription factor SndA, putative | 1.901216561 | 1.850359802 | Zn_clus |
| Pdw03_4894 | Helix-loop-helix DNA-binding | 2.299159573 | 1.483272197 | HLH |
| Pdw03_8323 | Fungal transcriptional regulatory protein, N-terminal | 2.1543773 | 1.687916376 | Zn_clus |
| Pdw03_8357 | C6 transcription factor, putative | 2.383815359 | 1.492877734 | Zn_clus |
| Pdw03_5577 | Fungal transcriptional regulatory protein, N-terminal | 2.282020274 | 1.616108101 | Fungal_trans |
| Pdw03_2416 | Zinc finger, C2H2 | 1.50293679 | 2.515142853 | zf-C2H2 |
| Pdw03_8169 | Fungal transcriptional regulatory protein, N-terminal | 2.086893538 | 2.001197701 | Zn_clus |
| Pdw03_1634 | C6 transcription factor, putative | 2.199539519 | 1.923919637 | Zn_clus |
| Pdw03_6398 | Fungal specific transcription factor, putative | 1.785094658 | 2.351014078 | Zn_clus |
| Pdw03_7652 | Major facilitator superfamily domain, general substrate transporter | 2.219900272 | 2.17180482 | zf-C2H2 |
| Pdw03_4980 | C6 transcription factor, putative | 2.816385349 | 1.607752323 | Zn_clus |
| Pdw03_2719 | Aflatoxin biosynthesis regulatory protein | 2.179193277 | 2.245882288 | Zn_clus |

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|------------|---|-------------|-------------|----------------|
| Pdw03_2541 | Fungal transcriptional regulatory protein, N-terminal | 2.572974818 | 2.034802517 | Fungal_trans_2 |
| Pdw03_4048 | DNA binding HTH domain, Psq-type | 1.964900208 | 2.687450191 | CENP-B_N |
| Pdw03_7357 | Blue (type 1) copper domain | 2.54780061 | 2.132054444 | Fungal_trans |
| Pdw03_2337 | Fungal transcriptional regulatory protein, N-terminal | 2.632414376 | 2.076137225 | Zn_clus |
| Pdw03_7674 | C6 transcription factor, putative | 1.673862415 | 3.063508157 | Fungal_trans |
| Pdw03_4267 | C6 sexual development transcription factor NosA | 1.875303027 | 3.007631528 | Zn_clus |
| Pdw03_3530 | Zinc finger, NHR/GATA-type | 3.380534425 | 2.051652253 | GATA |
| Pdw03_6775 | Homeobox transcription factor, putative | 2.190338624 | 3.45471108 | Homeobox |
| Pdw03_7068 | Fungal transcriptional regulatory protein, N-terminal | 1.951341751 | 3.820371396 | Fungal_trans |
| Pdw03_7336 | Zinc finger, C2H2-type/integrase, DNA-binding | 3.229268341 | 2.691057417 | zf-C2H2 |
| Pdw03_3571 | C2H2 conidiation transcription factor FlbC | 3.418330825 | 2.717238277 | zf-C2H2 |
