

## Supporting Tables

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**Table S1** Oligonucleotide primers used in this study

| Usage                                  | Primers        | Sequences (5' to 3')   |
|--|----------------|--|
| PCR of genomic DNA sequences           | MrNsdD-F       | TGCCATCCTCGCCAACATTGAACGC  |
|  | MrNsdD-R       | CCAGATAGATAGCCTGTATTTTCCTT   |
| Construction of gene disruption vector | NsLF           | cg <u>GAATTC</u> ATCTTAGTTCTCACGCATACGCCGC<br><i>EcoRI</i> site is underlined    |
|  | NsLR           | ccg <u>CTCGAGCGTGAAGTTGGAGCGGAATGGGCGA</u><br><i>XhoI</i> site is underlined     |
|  | NsRF           | gc <u>TCTAGATGTGCCTCTTAGCCTAATCTTTGAG</u><br><i>XbaI</i> site is underlined      |
|  | NsRR           | ccc <u>AAGCTTACA</u> ACTATTCGGAATCGGAGCAAGC<br><i>HindIII</i> site is underlined |
| Construction of gene complementation   | NsHF           | ccg <u>CTCGAGGATTGAGCACCTACACCTGTAAGCA</u><br><i>XhoI</i> site is underlined     |
|  | NsHR           | <u>aaCTGCAGGCTGTACGTTGTTAGTTTACTGAGG</u><br><i>PstI</i> site is underlined       |
| PCR verification                       | MrNsdDF        | GGAGGCAGCAGCCCAAGTCAATCAA  |
|  | MrNsdDR        | TCAGAAAGGGAGGGGCATTTCGGGAT   |
|  | MrNsdDOF       | ATCCCGCCCAAGGTGCGTTTTTACAA   |
|  | MrNsdDOR       | TCCCTTGATTTTGGTGCCTTCCCTA  |
|  | hph-F          | GCTCTCGCTAAACTCCCAATGTCA   |
|  | hph-R          | CATTGACTGGAGCGAGGCGATGTTC  |
| For analysis                           | qPCR MrNsdD-qF | CAACGGAGCATATGGTCATC   |
|  | MrNsdD-qR      | CATGCCTAGGTGAGACTGGA   |
|  | Mrtub-qF       | GGCAAGGTCGCTATGAAG   |
|  | Mrtub-qR       | CTGGATGGAGGTAGAGTTAC   |
|  | Mrtef-qF       | GTCATCGTCCTCAACCATC  |
|  | Mrtef-qR       | CAGTCTCAACAGCCTTACC  |
|  | MrFlbC-qF      | CTCGACCGAGCTCATTACAA   |
|  | MrFlbC-qR      | TCTGCGTAAATTGGAAACGA   |
|  | MrHyd1-qF      | CATCATCGGTGTTGGTGTTT   |
|  | MrHyd1-qR      | AGGCGAGGTTGAGGAGAC   |
|  | MrCsp-qF       | GCCGACAATATGAAGCAGCA   |
|  | MrCsp-qR       | TTGCGACTGGAGGATGAAGT   |

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|            |                      |
|------------|----------------------|
| Mrap1-qF   | ACATACGCCAGAAAGAACC  |
| Mrap1-qR   | AGTTGGTTGCAGCTCAAATG |
| MrSt-qF    | TCACTACGCTGGGTTCGATA |
| MrSt-qR    | TTCGACCTGAAAGCACAGAC |
| MrCp450-qF | CTATATGGCACGTCCACGAC |
| MrCp450-qR | GCTACGATTCCTTGGTTGGT |
| MrCat-qF   | GAGCCAGCCTCGTCTGTTCT |
| MrCat-qR   | CTGGGCGAGGACGTTCTTCT |
| Mrgst-F    | GGAGGTACTTGGACCGGATA |
| Mrgst-R    | TACGGTTTCCTTTCCGTCTC |
| MrSod-qF   | TGCCTGCTTTATCAATCGAC |
| MrSod-qR   | TCAAGAATGAGTGTGCGTCA |
| MrCcp-qF   | GTCCTTGGTAGGGTTGACGA |
| MrCcp-qR   | ATGGTACTCTGAGCCTGCTG |
| MrDh-qF    | CTTGTGGACGAGCATCTTGG |
| MrDh-qR    | AGCGGAATCATCGAGTCCTT |
| MrH101-qF  | TGGAGAAGCGTTTGGAGGAT |
| MrH101-qR  | GCCACCAGAAGCATTGAGAG |
| MrLaeA-qF  | TATTGACTGGGCCGACACTT |
| MrLaeA-qR  | TGTCTCCTGACGGTCATCTG |
| MrNao-qF   | CTCTTGAAGGAGTCGATGCG |
| MrNao-qR   | TCTCCCTTCTCGACAGATGC |
| MrPkd-qF   | GAAGTGAAGACGGACGTGTG |
| MrPkd-qR   | CAGCCAAGAAACACCTCTGG |
| MrGliT-qF  | CGGCGTGATAGACATTCCAC |
| MrGliT-qR  | ATCTCAGCCGTCGTCATCAT |
| MrUce-qF   | TAGGCAGCCGTCCACTTATC |
| MrUce-qR   | GCTCCTCCAAGTGTCTCTT  |
| MrApses-qF | TCACTACGCTGGGTTCGATA |
| MrApses-qR | TTCGACCTGAAAGCACAGAC |
| MrArdp-qF  | CCACCCAGATTCTCAAGGTT |
| MrArdp-qR  | TGCTCGCCTGTTTGTATCTC |
| MrPp-qF    | GCCGAGACCATCAAAGAACC |
| MrPp-qR    | TGTCGAATACCGTCGCATTG |
| MrPpt-qF   | GGCCGTGGAAGGTGATTAC  |

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|           |                      |
|-----------|----------------------|
| MrPpt-qR  | CTTGATCTCGTCCTCGGTGA |
| MrHe1-qF  | TTGAGGCCGATATGCAGCTA |
| MrHe1-qR  | GGTAAGCTCCTGCTCTCGAT |
| MrDpd1-qF | TTTGTCACGCTTCACGTACC |
| MrDpd1-qR | GCAATCTTTCCAGACCGCAT |
| MrOas-qF  | AGGCAGCCAGACTATTTGGT |
| MrOas-qR  | CCATGCGCTTCTCAAAGACA |
| MrSa-qF   | AGCTTTGGAGAGGACAGCAT |
| MrSa-qR   | ACCCACTGTTGGGTGAAGA  |
| MrOtp-qF  | TGCTCCTGCTCTCAACTCAA |
| MrOtp-qR  | ACGAGGAGTGCTCTGTTCAA |
| MrCatf-qF | CTGTGTCTCGACTACACGGA |
| MrCatf-qR | ATCTGCACGCCATTCTTCAC |
| MrFaao-qF | TGGCCATGGGTACAAGTTCT |
| MrFaao-qR | TCGTCATCGATGCTCTTCCA |
| MrPbf2-qF | GCCGAGATTCTACTGGCTCT |
| MrPbf2-qR | GCATACTTGCCAAAGACGGT |

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**Table S2** Unique genes expressed only in WT or  $\Delta MrNsdD$  mutant during dimorphic transition

| Annotation                               | GW1_FPKM | GW2_FPKM | GW3_FPKM | GN1_FPKM | GN2_FPKM | GN3_FPKM | log2FC | up/down | FDR      |
|--|----------|----------|----------|----------|----------|----------|--------|---------|----------|
| Hypothetical protein MAM_03824           | 0.537749 | 0.541193 | 0.533825 | 0        | 0        | 0        | -Inf   | down    | 3.19E-05 |
| Nuclease                                 | 0.314154 | 0.266167 | 0.541029 | 0        | 0        | 0        | -Inf   | down    | 6.95E-12 |
| Hypothetical protein NOR_01340           | 1.730075 | 1.012586 | 0.513961 | 0        | 0        | 0        | -Inf   | down    | 2.54E-05 |
| Protein kinase domain containing protein | 0        | 0        | 0        | 1.466    | 1.096    | 0.872    | Inf    | up      | 1.70E-14 |
| Hypothetical protein VFPPC_02352         | 0        | 0        | 0        | 3.007    | 5.598    | 4.178    | Inf    | up      | 1.22E-19 |
| Hypothetical protein NOR_07528           | 0        | 0        | 0        | 2.167    | 2.471    | 1.719    | Inf    | up      | 1.66E-13 |
| Hypothetical protein NOR_06355           | 0        | 0        | 0        | 2.488    | 1.866    | 1.912    | Inf    | up      | 1.98E-14 |

Abbreviation used: RPKM: fragments per kilobase million; FDR: false discovery rate; Inf:  $\infty$ ; FC: fold change; Up/Down: up-/down-regulated. GW1, GW2, and GW3 were three replicates of the wild-type (WT) strain. GN1, GN2, and GN3 were three replicates of the  $\Delta MrNsdD$  mutant during dimorphic transition.

**Table S3** Unique genes expressed only in WT or  $\Delta MrNsdD$  mutant during microsclerotium development

| Annotation                             | W1_FPKM | W2_FPKM | W3_FPKM | N1_FPKM | N2_FPKM | N3_FPKM | log2FC | up/down | FDR      |
|--|---------|---------|---------|---------|---------|---------|--------|---------|----------|
| Hypothetical protein NOR_04043         | 1.469   | 0.912   | 1.386   | 0       | 0       | 0       | -Inf   | down    | 3.19E-05 |
| AMP-dependent synthetase/ligase        | 100.777 | 161.240 | 83.140  | 0       | 0       | 0       | -Inf   | down    | 6.95E-12 |
| Zinc knuckle domain-containing protein | 0       | 0       | 0       | 9.481   | 6.599   | 9.022   | Inf    | up      | 9.44E-15 |
| Hypothetical protein X797_000653       | 0       | 0       | 0       | 0.785   | 2.438   | 1.730   | Inf    | up      | 2.37E-08 |
| Drug/metabolite transporter            | 0       | 0       | 0       | 5.143   | 3.740   | 4.024   | Inf    | up      | 6.64E-12 |
| Cytochrome P450                        | 0       | 0       | 0       | 0.664   | 0.664   | 0.839   | Inf    | up      | 6.65E-12 |
| Hypothetical protein NOR_08109         | 0       | 0       | 0       | 2.194   | 2.128   | 1.682   | Inf    | up      | 1.08E-08 |

Abbreviation used: W1, W2, and W3 were three replicates of the WT strain. N1, N2, and N3 were three replicates of the  $\Delta MrNsdD$  mutant during microsclerotium development.

**Table S4** Gene expression in the  $\Delta MrNsdD$  mutant relative to WT during dimorphic transition

| Annotation   |  |  | Gene         |          |          |          |          |          |          |        | Up/Down | FDR      |
|--|--|--|--------------|----------|----------|----------|----------|----------|----------|--------|---------|----------|
|  |  |  | Name         | GW1_FPKM | GW2_FPKM | GW3_FPKM | GN1_FPKM | GN2_FPKM | GN3_FPKM | log2FC |         |          |
| Protein kinase domain containing protein                 |  |  | <i>Pkd</i>   | 0        | 0        | 0        | 1.466    | 1.096    | 0.872    | ∞      | Up      | 1.70E-14 |
| Glutathione S-transferase II                             |  |  | <i>Gst</i>   | 459.336  | 461.663  | 487.714  | 188.596  | 190.044  | 203.619  | -1.168 | Down    | 1.66E-64 |
| Cytochrome P450  |  |  | <i>Cp450</i> | 55.208   | 71.895   | 94.818   | 5.132    | 6.058    | 5.607    | -3.626 | Down    | 1.31E-15 |
| C <sub>2</sub> H <sub>2</sub> finger domain protein FlbC |  |  | <i>FlbC</i>  | 7.781    | 9.640    | 11.403   | 26.652   | 30.336   | 28.136   | 1.6301 | Up      | 2.80E-07 |
| Catalase   |  |  | <i>Cat</i>   | 83.164   | 102.472  | 106.883  | 222.180  | 340.178  | 277.785  | 1.568  | Up      | 1.42E-17 |
| Heat shock protein 101                                   |  |  | <i>H101</i>  | 90.944   | 107.584  | 84.997   | 459.228  | 388.246  | 436.369  | 2.249  | Up      | 6.90E-28 |
| bZIP transcription factor                                |  |  | <i>Ap1</i>   | 72.343   | 77.130   | 75.824   | 72.314   | 73.991   | 77.028   | 0.0819 | Normal  | 0.883    |
| APSES-type DNA-binding domain protein                    |  |  | <i>Apses</i> | 3.470    | 3.508    | 3.591    | 2.855    | 2.812    | 3.3600   | -0.132 | Normal  | 0.410    |
| Cytochrome c peroxidase                                  |  |  | <i>Ccp</i>   | 58.498   | 88.807   | 61.365   | 146.474  | 124.676  | 143.215  | 1.034  | Up      | 1.32E-34 |
| Ubiquitin-conjugating enzyme                             |  |  | <i>Uce</i>   | 40.875   | 37.356   | 34.386   | 24.012   | 36.971   | 29.675   | -0.317 | Normal  | 0.555    |
| Thioredoxin reductase GliT                               |  |  | <i>GliT</i>  | 31.148   | 36.369   | 29.078   | 6.101    | 4.541    | 7.979    | -2.303 | Down    | 1.95E-11 |
| Cu/Zn superoxide dismutase                               |  |  | <i>Sod</i>   | 79.295   | 71.054   | 66.574   | 33.627   | 44.313   | 44.303   | -0.758 | Normal  | 0.021    |
| NADH:ubiquinone  |  |  | <i>Nao</i>   | 328.826  | 341.058  | 316.477  | 261.556  | 252.094  | 255.611  | -0.288 | Normal  | 0.352    |

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oxidoreductase

|                        |             |        |        |        |        |        |        |        |        |       |
|------------------------|-------------|--------|--------|--------|--------|--------|--------|--------|--------|-------|
| Methyltransferase LaeA | <i>LaeA</i> | 8.688  | 7.455  | 8.874  | 7.6544 | 9.071  | 8.801  | 0.108  | Normal | 0.898 |
| Dienelactone hydrolase | <i>Dh</i>   | 22.361 | 17.834 | 24.661 | 15.823 | 14.850 | 14.815 | -0.165 | Normal | 0.730 |

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Abbreviation used: GW1, GW2, and GW3 were three replicates of the WT strain. GN1, GN2, and GN3 were three replicates of the  $\Delta MrNsdD$  mutant during dimorphic transition.



**Table S5** Gene expression in the  $\Delta MrNsdD$  mutant relative to WT during microsclerotium development

| Annotation   | Gene Name    | W1_FPKM | W2_FPKM | W3_FPKM | N1_FPKM | N2_FPKM  | N3_FPKM  | log2FC | Up/Down | FDR      |
|--|--------------|---------|---------|---------|---------|----------|----------|--------|---------|----------|
| Dienelactone hydrolase                                   | <i>Dh</i>    | 2.679   | 1.137   | 2.703   | 17.839  | 9.924    | 16.373   | 2.255  | Up      | 0.0003   |
| Methyltransferase LaeA                                   | <i>LaeA</i>  | 3.884   | 4.920   | 5.204   | 18.886  | 16.660   | 21.060   | 1.585  | Up      | 0.0139   |
| Cytochrome P450  | <i>Cp450</i> | 0.456   | 1.885   | 0.922   | 8.374   | 13.663   | 5.574    | 2.761  | Up      | 0.00929  |
| NADH:ubiquinone oxidoreductase                           | <i>Nao</i>   | 404.651 | 337.089 | 390.943 | 62.826  | 65.136   | 71.161   | -1.824 | Down    | 4.80E-06 |
| Cu/Zn superoxide dismutase                               | <i>Sod</i>   | 29.357  | 65.068  | 25.335  | 269.373 | 459.048  | 192.231  | 2.645  | Up      | 0.0094   |
| Ankyrin repeat-containing domain protein Swi6            | <i>Swi6</i>  | 36.937  | 52.827  | 31.701  | 16.717  | 18.29    | 19.87    | -1.373 | Down    | 0.00045  |
| Heat shock protein 101                                   | <i>H101</i>  | 298.837 | 123.399 | 390.334 | 3063.3  | 1394.507 | 3522.477 | 2.914  | Up      | 0.00498  |
| bZIP transcription factor                                | <i>Ap1</i>   | 2.617   | 3.633   | 4.3989  | 27.588  | 14.839   | 24.163   | 2.301  | Up      | 0.00518  |
| APSES-type DNA-binding domain protein                    | <i>Apses</i> | 2.127   | 2.367   | 1.959   | 11.338  | 7.827    | 10.161   | 1.826  | Up      | 0.00524  |
| Ubiquitin-conjugating enzyme                             | <i>Uce</i>   | 105.892 | 86.619  | 52.5359 | 24.615  | 9.165    | 10.965   | -2.020 | Down    | 2.92E-06 |
| C <sub>2</sub> H <sub>2</sub> finger domain protein FlbC | <i>FlbC</i>  | 1.268   | 1.097   | 1.102   | 2.392   | 4.360    | 2.041    | 0.437  | Normal  | 0.666    |
| Protein kinase domain containing protein                 | <i>Pkd</i>   | 0.977   | 1.321   | 0.677   | 0.386   | 0.824    | 0.630    | 0.815  | Normal  | 0.570    |
| Glutathione S-transferase II                             | <i>Gst</i>   | 5.371   | 4.530   | 8.220   | 11.231  | 8.216    | 11.314   | 0.563  | Normal  | 0.540    |

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|                         |            |         |         |         |        |        |        |        |        |          |
|-------------------------|------------|---------|---------|---------|--------|--------|--------|--------|--------|----------|
| Catalase                | <i>Cat</i> | 32.861  | 55.597  | 38.678  | 24.375 | 24.109 | 21.799 | -0.971 | Normal | 0.0342   |
| Cytochrome c peroxidase | <i>Ccp</i> | 193.788 | 133.213 | 165.189 | 82.132 | 70.201 | 67.496 | -1.828 | Down   | 0.000103 |

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Abbreviation used: W1, W2, and W3 were three replicates of the WT strain. N1, N2, and N3 were three replicates of the  $\Delta MrNsdD$  mutant during microsclerotium development.

**Table S6** Unique genes expressed only in microsclerotium development and dimorphic transition

| Annotation                            | GN1_FPKM | GN2_FPKM | GN3_FPKM | N1_FPKM | N2_FPKM | N3_FPKM | log2FC | up/down | FDR      |
|---------------------------------------|----------|----------|----------|---------|---------|---------|--------|---------|----------|
| Hypothetical protein HIM_10759        | 1149.867 | 952.831  | 1021.620 | 0       | 0       | 0       | -Inf   | down    | 3.19E-05 |
| Hypothetical protein NOR_07528        | 1962.821 | 1665.370 | 1746.956 | 0       | 0       | 0       | -Inf   | down    | 6.95E-12 |
| Subtilisin-like protease              | 2157.614 | 1837.403 | 1970.264 | 0       | 0       | 0       | -Inf   | down    | 2.54E-05 |
| Hypothetical protein NOR_04263        | 2157.931 | 1849.956 | 2085.348 | 0       | 0       | 0       | -Inf   | down    | 1.26E-05 |
| Hypothetical protein NOR_08395        | 2825.316 | 2310.678 | 2686.503 | 0       | 0       | 0       | -Inf   | down    | 5.30E-15 |
| Hypothetical protein VFPPC_02352      | 2966.663 | 2974.025 | 2757.046 | 0       | 0       | 0       | -Inf   | down    | 2.47E-12 |
| Hypothetical protein X797_005699      | 5313.584 | 3371.721 | 5834.958 | 0       | 0       | 0       | -Inf   | down    | 4.15E-46 |
| Hypothetical protein NOR_02109        | 2089.942 | 1741.069 | 1763.632 | 0       | 0       | 0       | -Inf   | down    | 1.06E-05 |
| Sugar transporter family protein      | 2150.327 | 1803.89  | 1766.464 | 0       | 0       | 0       | -Inf   | down    | 4.81E-07 |
| Cell wall galactomannoprotein         | 1564.026 | 1355.543 | 1416.758 | 0       | 0       | 0       | -Inf   | down    | 0.005201 |
| Deuterolysin metalloprotease          | 1495.990 | 1308.908 | 1339.283 | 0       | 0       | 0       | -Inf   | down    | 4.73E-09 |
| 60S ribosomal protein L37             | 0        | 0        | 0        | 122.657 | 122.584 | 118.637 | Inf    | up      | 1.98E-11 |
| Transcription initiation factor TFIID | 0        | 0        | 0        | 164.125 | 162.790 | 161.027 | Inf    | up      | 1.70E-10 |
| CFEM domain protein                   | 0        | 0        | 0        | 236.703 | 234.417 | 229.607 | Inf    | up      | 3.30E-13 |
| Peptidyl-arginine deiminase           | 0        | 0        | 0        | 151.880 | 151.981 | 146.520 | Inf    | up      | 1.06E-05 |
| Hypothetical protein NOR_00485        | 0        | 0        | 0        | 101.609 | 103.342 | 99.851  | Inf    | up      | 7.43E-09 |
| UDP-glucose 4-epimerase               | 0        | 0        | 0        | 109.246 | 110.536 | 106.583 | Inf    | up      | 1.80E-16 |
| RTA-like protein                      | 0        | 0        | 0        | 624.761 | 644.328 | 625.530 | Inf    | up      | 2.32E-12 |

|  |   |   |   |          |          |          |     |    |          |
|--|---|---|---|----------|----------|----------|-----|----|----------|
| Hypothetical protein NOR_02709                                 | 0 | 0 | 0 | 834.643  | 819.231  | 807.902  | Inf | up | 1.92E-12 |
| Oxidoreductase, 2OG-Fe(II) oxygenase family                    | 0 | 0 | 0 | 403.733  | 411.446  | 398.397  | Inf | up | 2.37E-07 |
| Hexokinase XprF  | 0 | 0 | 0 | 121.622  | 121.522  | 118.235  | Inf | up | 1.03E-48 |
| Ketol-acid reductoisomerase                                    | 0 | 0 | 0 | 107.598  | 108.619  | 105.132  | Inf | up | 0.002459 |
| Methyltransferase type 11                                      | 0 | 0 | 0 | 193.430  | 196.519  | 187.507  | Inf | up | 0.002795 |
| Alanyl-tRNA synthetase   | 0 | 0 | 0 | 142.236  | 141.559  | 136.805  | Inf | up | 0.000394 |
| Serine/threonine protein kinase Hsk1                           | 0 | 0 | 0 | 165.067  | 163.970  | 161.896  | Inf | up | 0.000464 |
| Small GTPase superfamily                                       | 0 | 0 | 0 | 333.772  | 338.666  | 326.076  | Inf | up | 0.000563 |
| Hypothetical protein NOR_05265                                 | 0 | 0 | 0 | 154.090  | 155.570  | 148.757  | Inf | up | 0.001638 |
| Major facilitator superfamily domain                           | 0 | 0 | 0 | 183.658  | 183.570  | 178.055  | Inf | up | 0.000557 |
| NADH:ubiquinone oxidoreductase 11.6kD subunit                  | 0 | 0 | 0 | 149.338  | 147.364  | 143.774  | Inf | up | 0.000652 |
| Ubiquinol-cytochrome-C oxidoreductase complex III subunit VIII | 0 | 0 | 0 | 1266.988 | 1264.988 | 1241.058 | Inf | up | 0.005686 |
| DNase1 protein   | 0 | 0 | 0 | 477.723  | 486.753  | 454.419  | Inf | up | 0.000699 |
| Pre-mRNA branch site protein p14                               | 0 | 0 | 0 | 148.053  | 145.706  | 142.192  | Inf | up | 0.000555 |

Abbreviation used: N1, N2, and N3 were three replicates of the  $\Delta MrNsdD$  mutant during microsclerotium development. GN1, GN2, and GN3 were three replicates of the  $\Delta MrNsdD$  mutant during dimorphic transition.

**Table S7** Differentially expressed genes in the  $\Delta MrNsdD$  mutant involved in carbon metabolism and peroxisome in two distinct development stages

| Annotation                           | Gene        | GN1_FPKM | GN2_FPKM | GN3_FPKM | N1_FPKM | N2_FPKM | N3_FPKM | log2FC | Up/Down | FDR        |
|--------------------------------------|-------------|----------|----------|----------|---------|---------|---------|--------|---------|------------|
|                                      | Name        |          |          |          |         |         |         |        |         |            |
| Phosphoserine phosphatase            | <i>Pp</i>   | 75.428   | 71.779   | 76.483   | 0.119   | 0.090   | 0.273   | -9.368 | Down    | 2.82 E-100 |
| Pyridoxal phosphate-dependent enzyme | <i>Ppt</i>  | 9.211    | 13.642   | 14.902   | 1.431   | 0.676   | 1.869   | -3.175 | Down    | 3.38E-07   |
| Hexokinase-1                         | <i>Hel</i>  | 32.646   | 33.607   | 33.199   | 7.159   | 7.285   | 4.491   | -2.171 | Down    | 4.71E-10   |
| D-3-phosphoglycerate dehydrogenase 1 | <i>Dpdl</i> | 66.028   | 63.682   | 67.063   | 142.104 | 105.583 | 134.67  | 1.025  | Up      | 0.00157    |
| O-acetylserine sulfhydrylase         | <i>Oas</i>  | 102.876  | 74.523   | 96.193   | 1491.97 | 756.503 | 1338.71 | 3.770  | Up      | 3.85E-10   |
| Catalase 1                           | <i>Cat1</i> | 2.047    | 4.099    | 2.608    | 0.622   | 0.235   | 0.209   | -2.962 | Down    | 9.36E-05   |
| Sarcosine oxidative                  | <i>So</i>   | 6.613    | 6.275    | 2.927    | 0.461   | 0.738   | 0.334   | -2.452 | Down    | 0.00015    |
| Oligopeptide transporter protein     | <i>Otp</i>  | 17.976   | 22.915   | 23.619   | 4.201   | 3.901   | 2.139   | -2.442 | Down    | 1.79E-12   |
| Carnitine acetyl transferase         | <i>Catf</i> | 78.114   | 72.885   | 80.213   | 7.145   | 4.477   | 5.386   | -3.727 | Down    | 3.05E-33   |
| Fructosyl-amino acid oxidase         | <i>Faao</i> | 4.778    | 5.359    | 5.285    | 23.345  | 12.124  | 18.063  | 1.852  | Up      | 0.00012    |
| Superoxide dismutase                 | <i>Sod</i>  | 185.782  | 396.804  | 154.091  | 20.834  | 22.236  | 28.329  | -2.737 | Down    | 3.96E-19   |
| Peroxisomal biogenesis factor 2      | <i>Pbf2</i> | 15.902   | 13.590   | 16.237   | 33.965  | 24.566  | 31.561  | 1.038  | Up      | 0.00112    |

Abbreviation used: N1, N2, and N3 were three replicates of the  $\Delta MrNsdD$  mutant during microsclerotium development. GN1, GN2, and GN3 were three replicates of the  $\Delta MrNsdD$  mutant during dimorphic transition.

## Figure legends

**Fig. S1** Phylogenetic tree of MrNsdD protein.

**Fig. S2** Confirmation of gene disruption and complementation.

**Fig. S3** Gene ontology annotation of differentially expressed genes and all genes during dimorphic transition.

**Fig. S4** Clusters of orthologous groups classifications of consensus sequence during dimorphic transition.

**Fig. S5** Kyoto Encyclopedia of Genes and Genomes enrichment pathways of differentially expressed genes during dimorphic transition.

**Fig. S6** Gene ontology annotation of differentially expressed genes and all genes during microsclerotium development.

**Fig. S7** Clusters of orthologous groups classifications of consensus sequence during microsclerotium development.

**Fig. S8** Kyoto Encyclopedia of Genes and Genomes enrichment pathways of differentially expressed genes during microsclerotium development.

**Fig. S9** Quantitative real-time-PCR (qPCR) of the WT and the  $\Delta MrNsdD$  mutants during (A) dimorphic transition and (B) microsclerotium development.

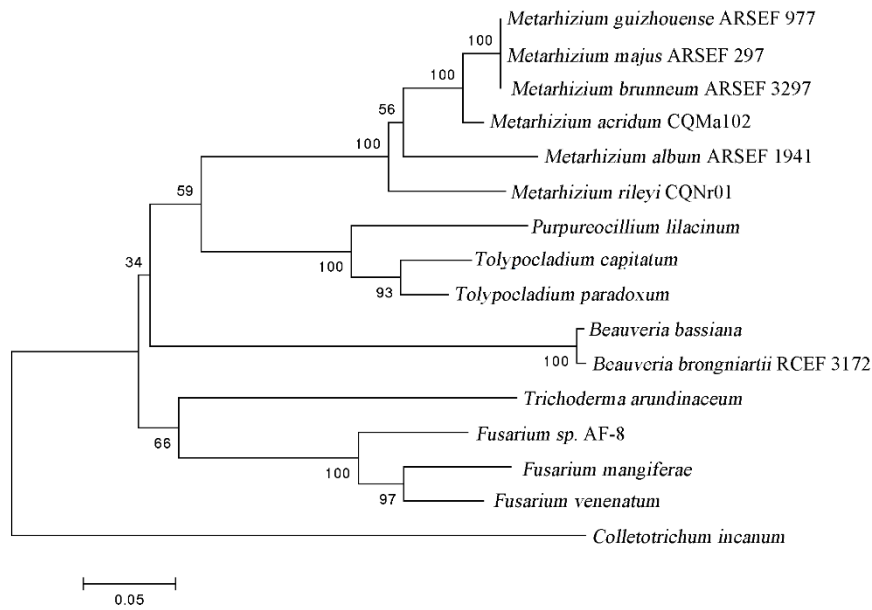
**Fig. S10** Gene ontology annotation of differentially expressed genes and all genes in two developmental stages (dimorphic transition vs microsclerotium development) in the  $\Delta MrNsdD$  mutant.

**Fig. S11** Clusters of orthologous groups classifications of consensus sequence in two developmental stages (dimorphic transition vs microsclerotium development) in the  $\Delta MrNsdD$  mutant.

**Fig. S12** Kyoto Encyclopedia of Genes and Genomes enrichment pathways of consensus sequence in two developmental stages (dimorphic transition vs microsclerotium development) in the  $\Delta MrNsdD$  mutant.

**Fig. S13** Venn diagram showing the number of shared differentially expressed genes in the three fungal transcription factors.

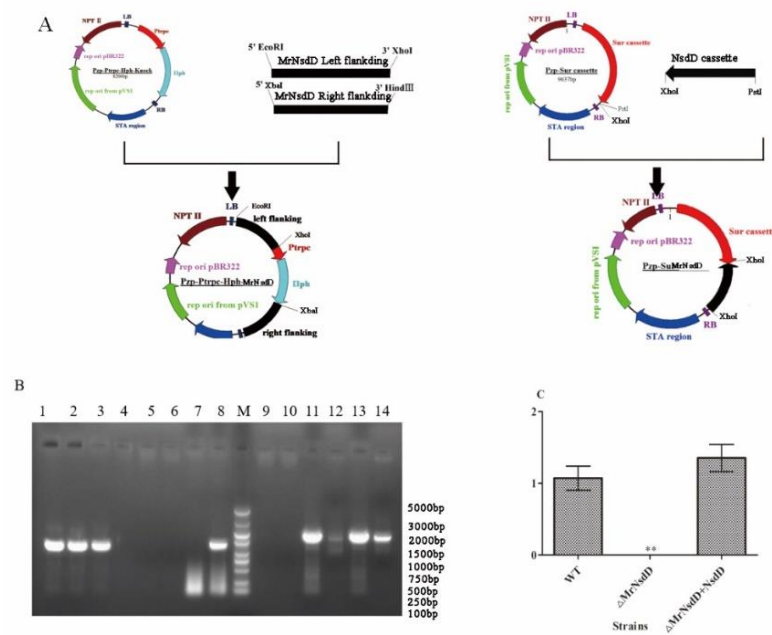
**Fig. S1** Phylogenetic tree of MrNsdD protein



The numbers at the nodes represent the results of bootstrap analyses (1000 replicates) carried out using the neighbor-joining method. The sequences aligned with the MrNsdD of *M. rileyi* are from *Metarhizium guizhouense* ARSEF 977 (KID91293.1); *Metarhizium acridum* CQMa 102 (XP\_007807473.1); *Metarhizium majus* ARSEF 297 (KID99887.1); *Metarhizium brunneum* ARSEF 3297 (XP\_014549395.1); *Metarhizium album* ARSEF 1941 (KHN94332.1); *Fusarium sp.* AF-8 (RSL70760.1); *Purpureocillium lilacinum* (PWI75759.1); *Tolypocladium paradoxum* (POR32608.1); *Tolypocladium capitatum* (PNY28176.1); *Fusarium venenatum* (XP\_025590605.1); *Fusarium mangiferae* (CVK92672.1); *Trichoderma arundinaceum* (RFU79615.1); *Beauveria brongniartii* RCEF 3172 (OAA49748.1); *Beauveria bassiana* (PMB72364.1); *Colletotrichum incanum* (KZL85235.1).



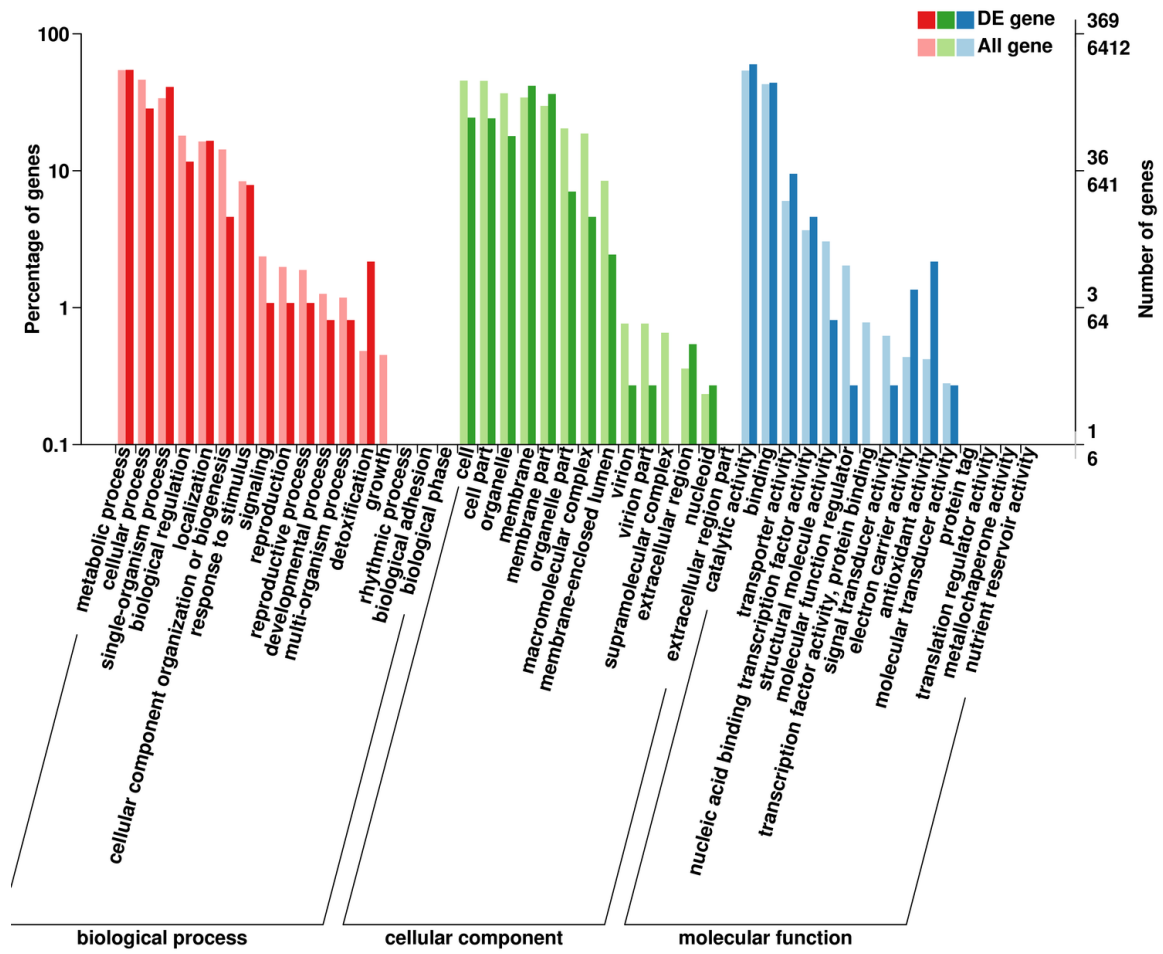
**Fig. S2** Confirmation of gene disruption and complementation strains



(A) Construction of knockout and complementation vectors. (B) PCR characterization of  $\Delta MrNsdD$  mutants, WT, and complemented (CP) strains. Generation and confirmation of open reading frame (ORF) was amplified by PCR using primers MrNsdDOF/MrNsdDOR (Lanes 1-5: 1-*MrNsdD* of WT, 2-CP1, 3-CP2, 4- $\Delta MrNsdD-1$ , 5- $\Delta MrNsdD-2$ ); The hygromycin phosphotransferase gene (*hph*) was amplified by PCR using primers hph-F/hph-R (Lanes 6-8: 6-WT, 7- $\Delta MrNsdD-1$ , 8- $\Delta MrNsdD-2$ ). The *hph* and genomic sequence outside the flank regions was amplified by PCR using primers hph-F/hph-R and MrNsdDF/MrNsdDR (Lanes 9-14: 9-Left Frame (LF)-WT, 10-Right Frame (RF)-WT, 11-LF- $\Delta MrNsdD-1$ , 12-RF- $\Delta MrNsdD-1$ , 13-LF- $\Delta MrNsdD-2$ , 14-RF- $\Delta MrNsdD-2$ ). M, DNA molecular size markers (DL 5000, Takara, Beijing). The  $\Delta MrNsdD-2$  mutants were subjected to further experiments. (C) qPCR analysis of *MrNsdD* in the tested strains. Error bars represent standard error. \*  $P < 0.05$ , \*\*  $P < 0.01$ , significantly different when compared with the results obtained for the WT in liquid amended medium (AM) cultures.

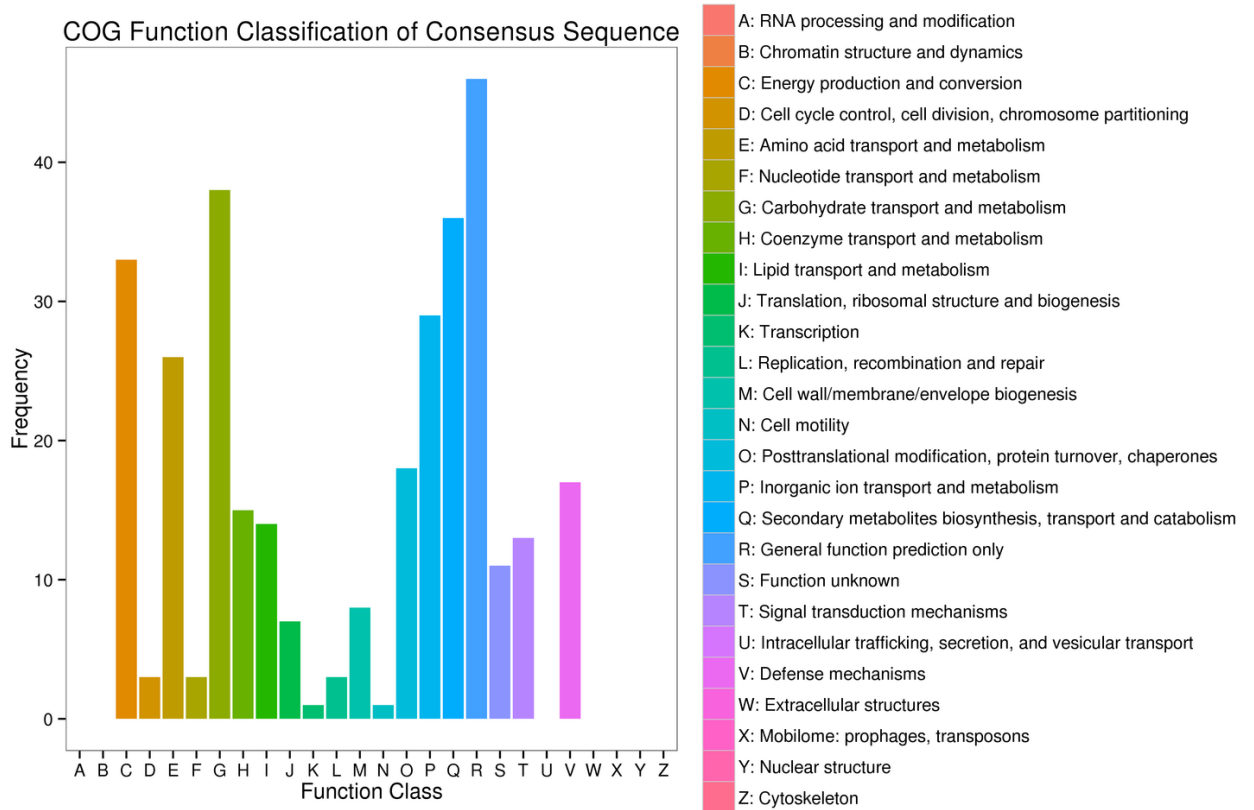
**Fig. S3** Gene ontology annotation of differentially expressed genes and all genes

during dimorphic transition

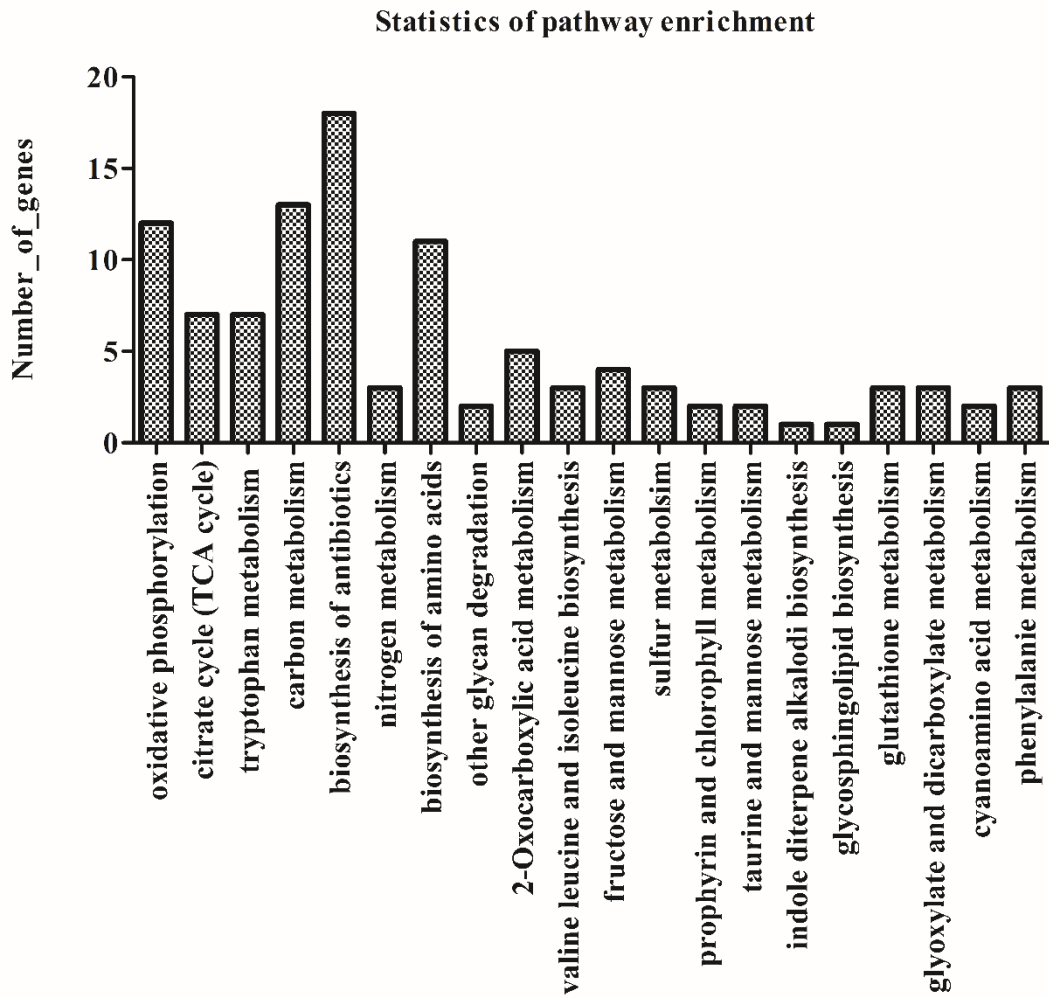


**Fig. S4** Clusters of orthologous groups classifications of consensus sequence during

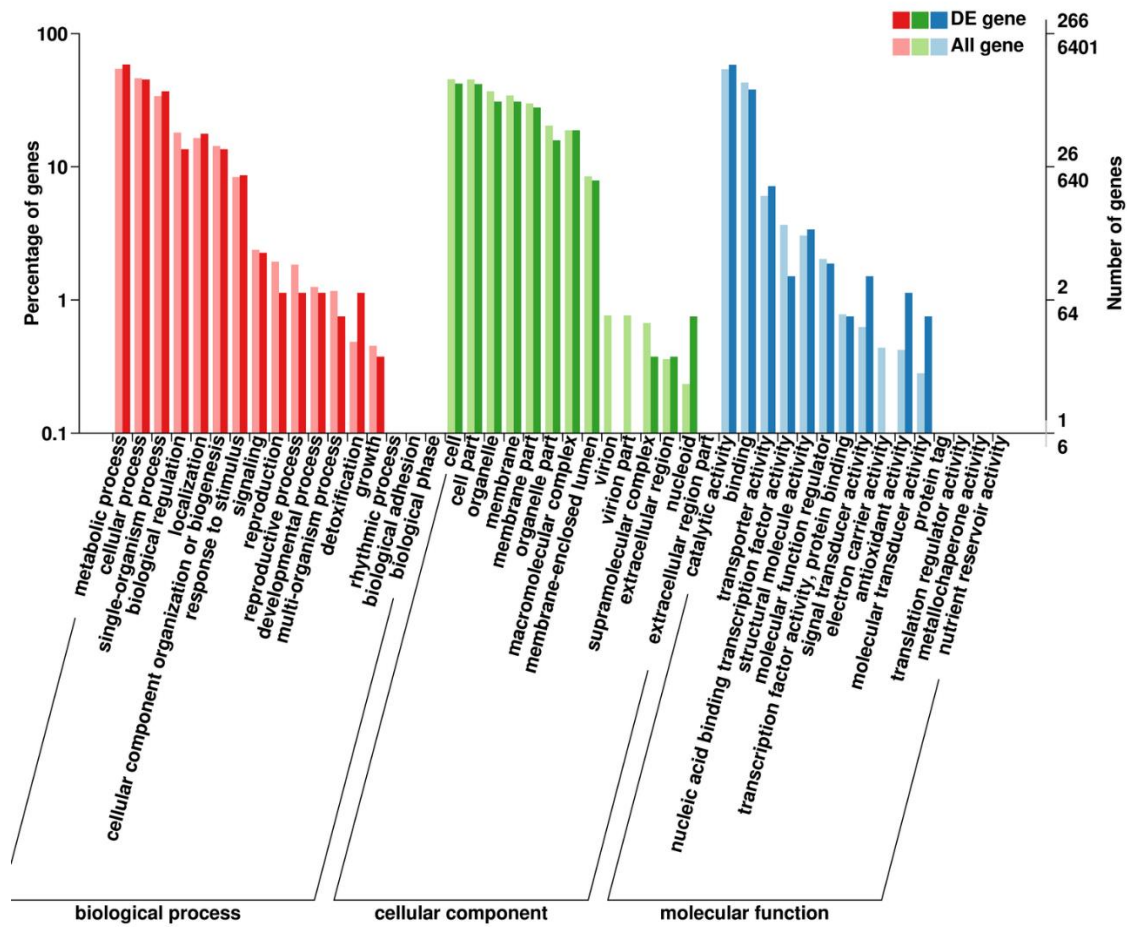
dimorphic transition



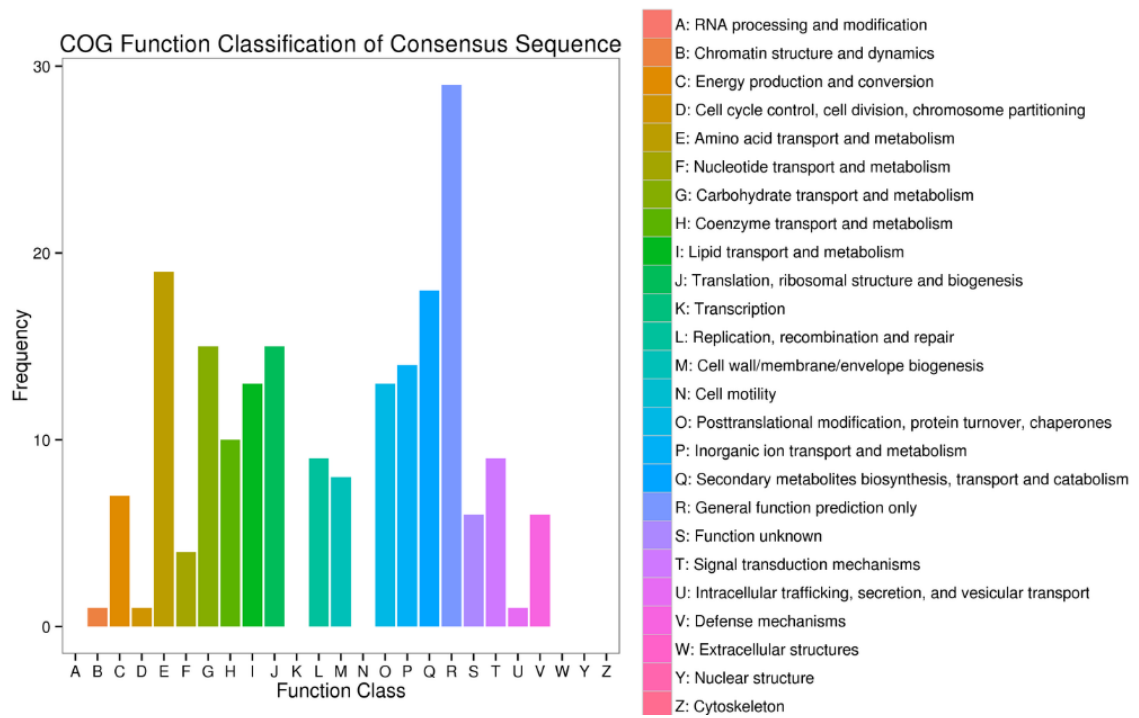
**Fig. S5** Kyoto Encyclopedia of Genes and Genomes enrichment pathways of differentially expressed genes during dimorphic transition



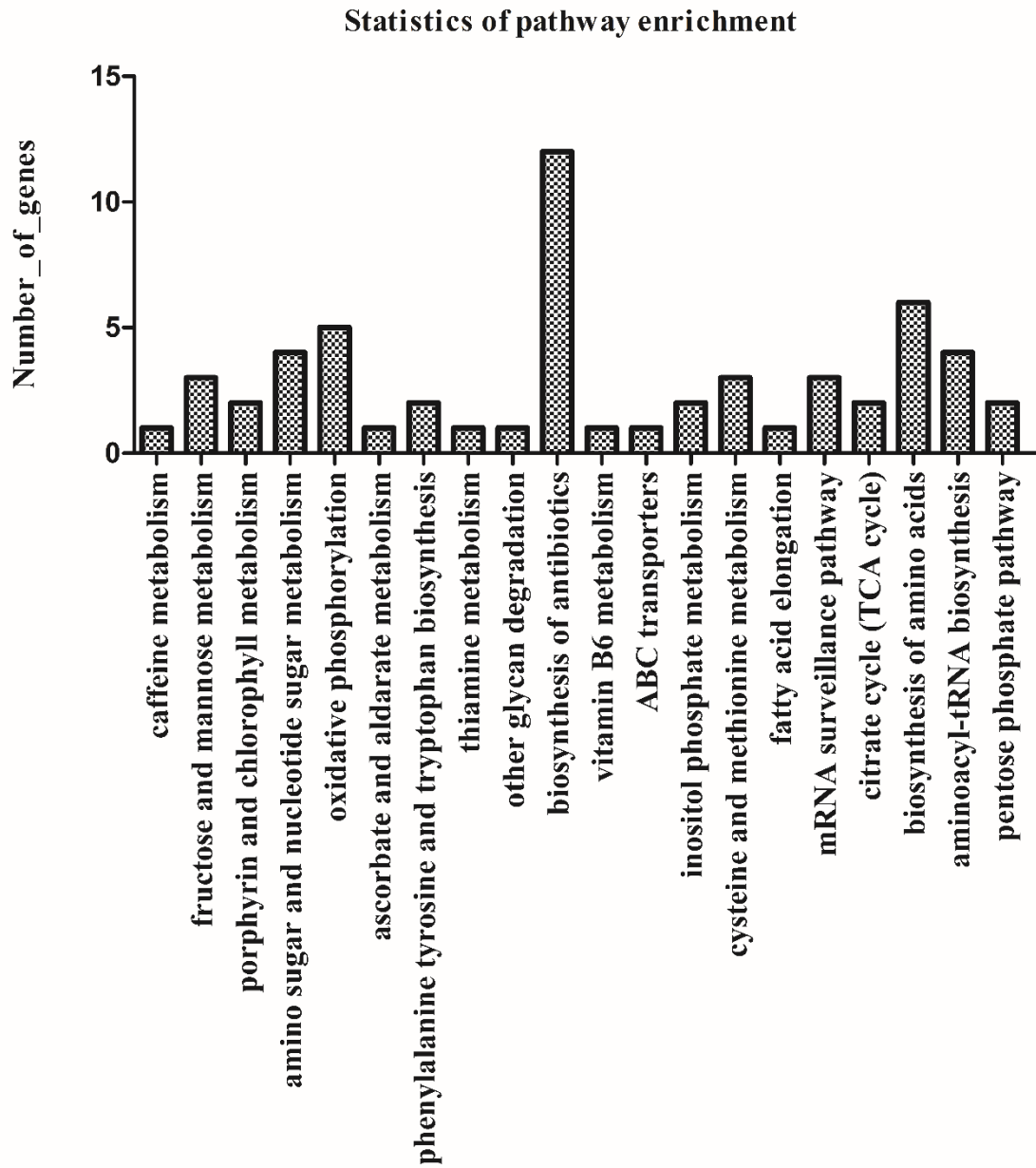
**Fig. S6** Gene ontology annotation of differentially expressed genes and all genes during microsclerotium development



**Fig. S7** Clusters of orthologous groups classifications of consensus sequence during  
microsclerotium development

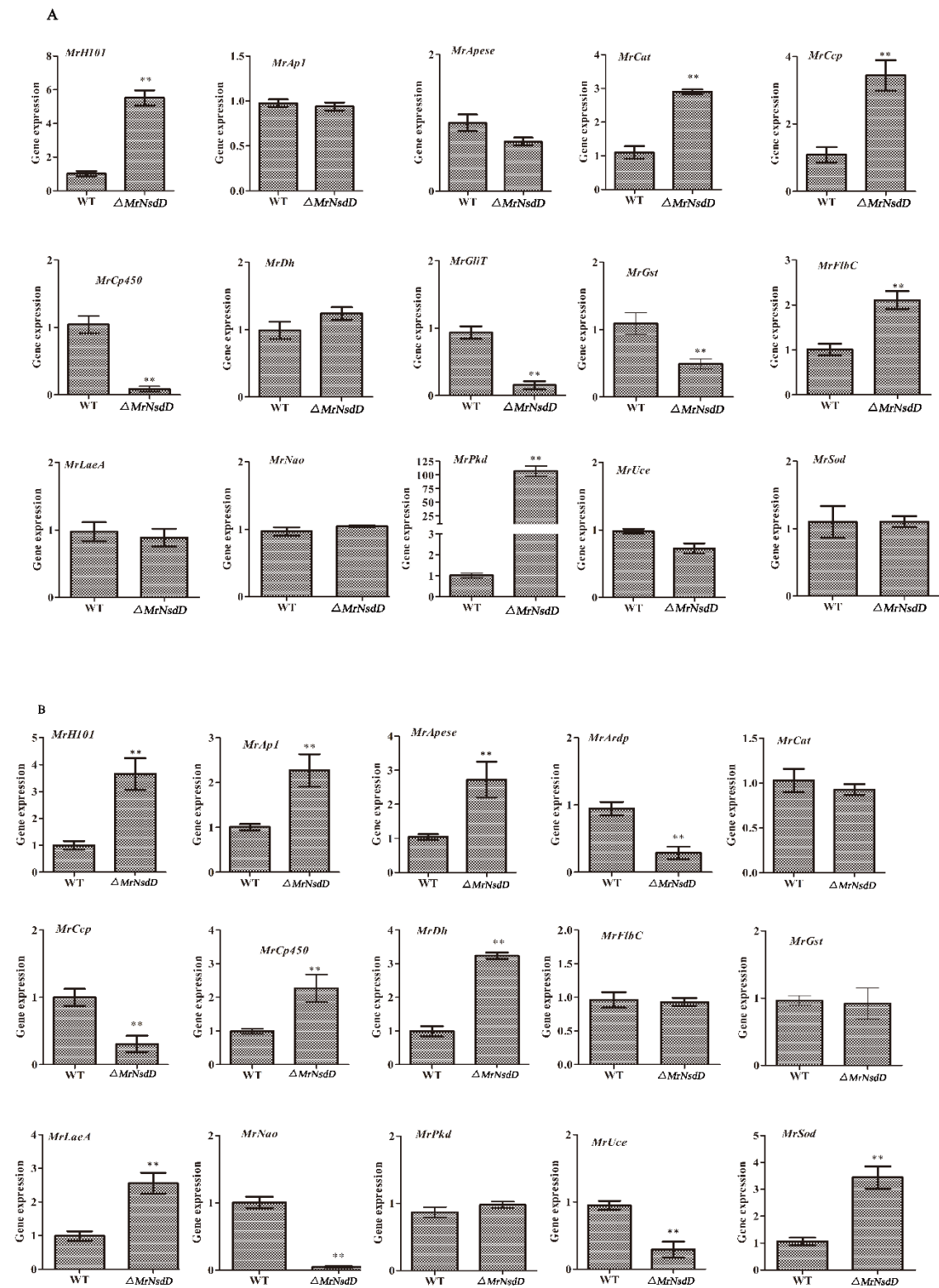


**Fig. S8** Kyoto Encyclopedia of Genes and Genomes enrichment pathways of differentially expressed genes during microsclerotium development



**Fig. S9** Quantitative real-time-PCR (qPCR) of the WT and the  $\Delta MrNsdD$  mutant

during (A) dimorphic transition and (B) microsclerotium development

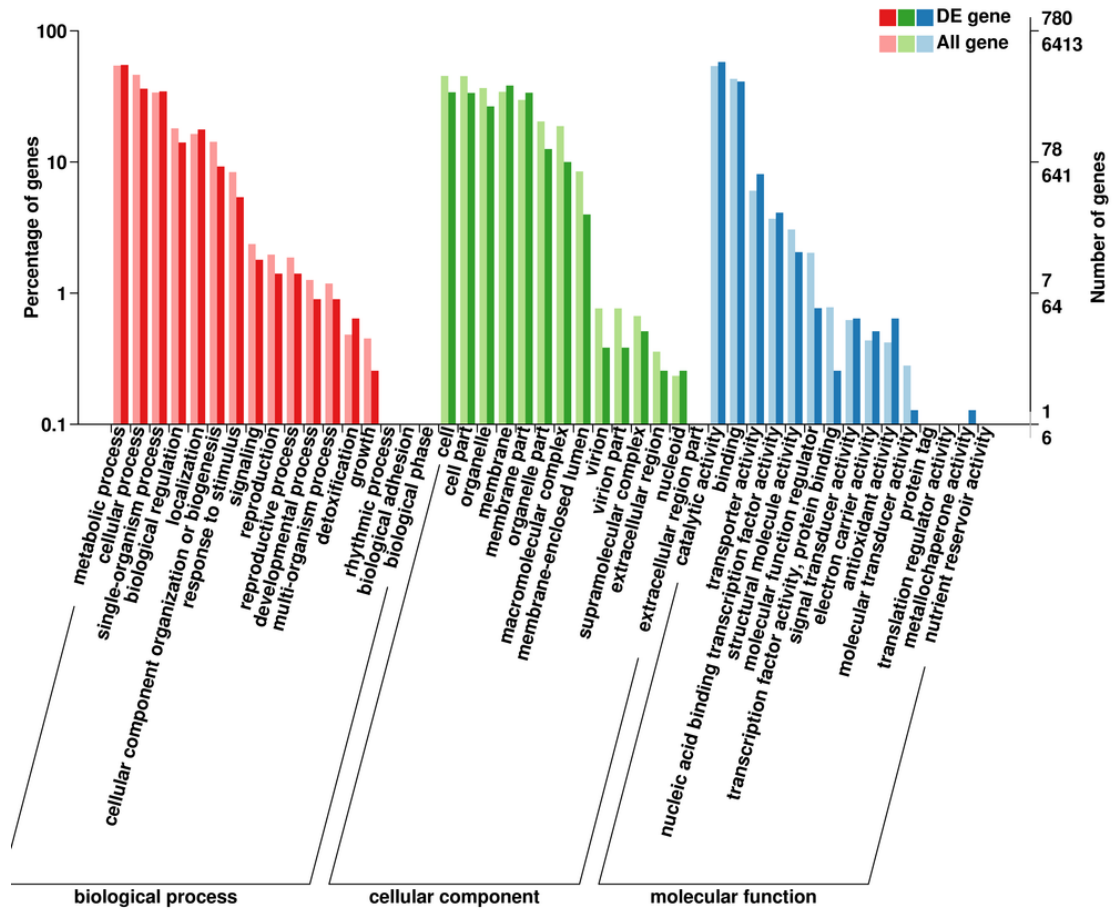


Error bars represent standard error. \*  $P < 0.05$ , \*\*  $P < 0.01$  compared with WT strain.

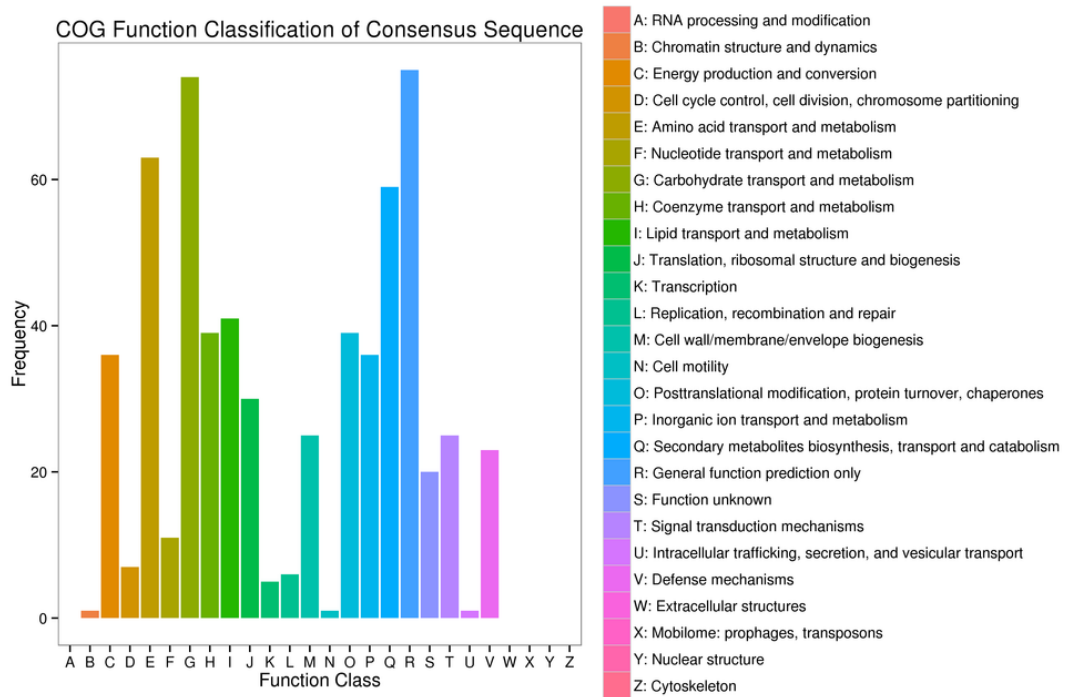


**Fig. S10** Gene ontology annotation of differentially expressed genes and all genes in two developmental stages (dimorphic transition vs microsclerotium development)

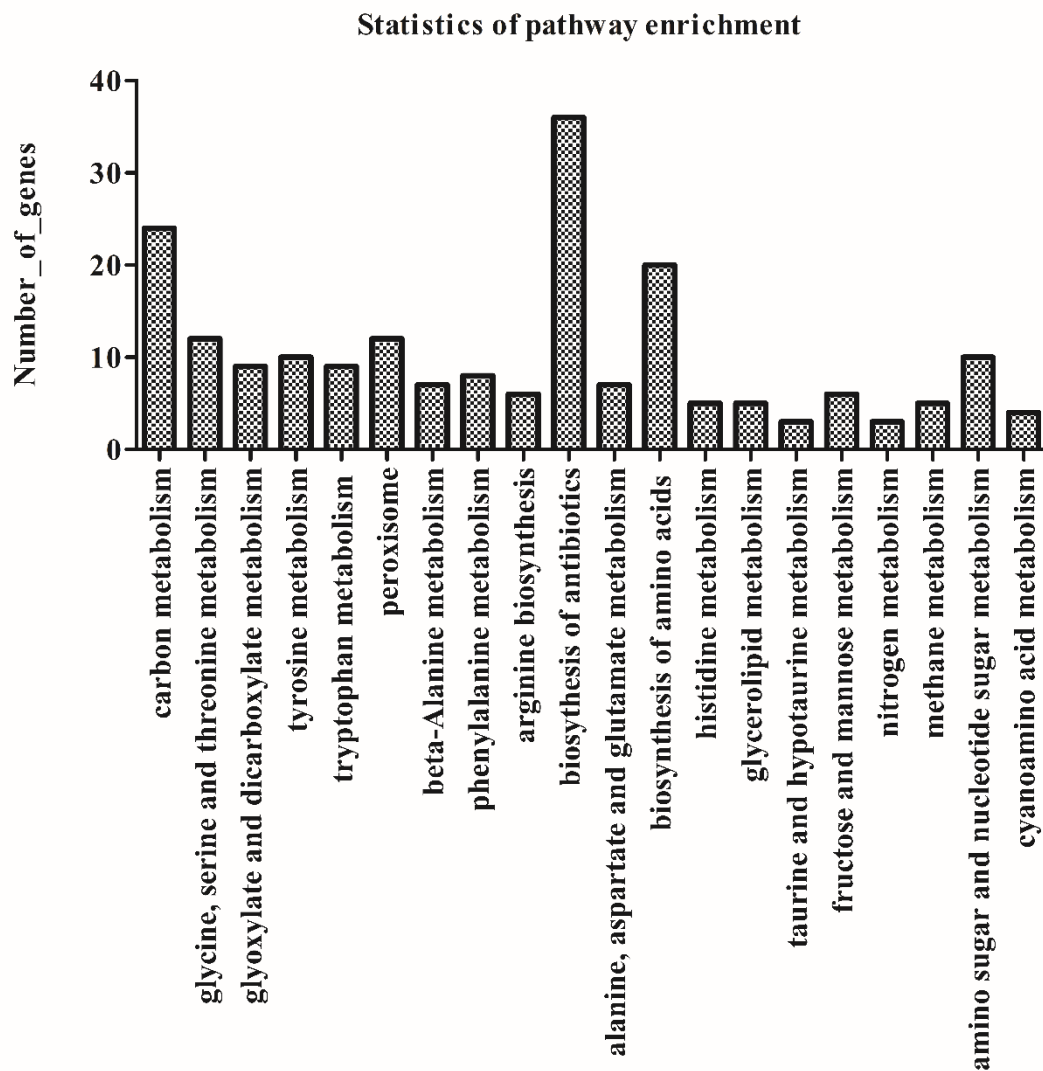
in the  $\Delta MrNsdd$  mutant



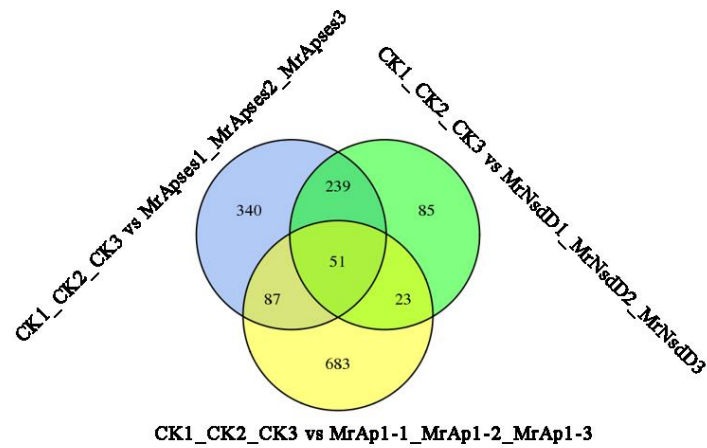
**Fig. S11** Clusters of orthologous groups classifications of consensus sequence in two developmental stages stage (dimorphic transition vs microsclerotium development) in the  $\Delta MrNsdd$  mutant



**Fig. S12** Kyoto Encyclopedia of Genes and Genomes enrichment pathways of consensus sequence in two developmental stages (dimorphic transition vs microsclerotium development) in the  $\Delta MrNsdD$  mutant



**Fig. S13** Venn diagram showing the number of shared differentially expressed genes in the three fungal transcription factors



The distribution of shared upregulated and downregulated genes in wild-type (WT),  $\Delta MrNsdD$ ,  $\Delta MrApses$ , and  $\Delta MrAp1$  mutants during microsclerotium development. CK1, CK2, and CK3 were three replicates of the WT strain. *MrNsdD1*, *MrNsdD2*, and *MrNsdD3* were three replicates of the  $\Delta MrNsdD$  mutant. *MrApses1*, *MrApses2*, and *MrApses3* were three replicates of the  $\Delta MrApses$  mutant. *MrAp1-1*, *MrAp1-2*, and *MrAp1-3* were three replicates of the  $\Delta MrAp1$  mutant.