Table S1 **the designed primers for qPCR**

|  |  |  |
| --- | --- | --- |
| Internal ID/gene | Primer Sequence | |
| Forward | Reverse |
| mRNAs |  |  |
| EVM0003971 | cGAATATGAGCCTGGAGAT | CGACCTTAGAATCCTTGT |
| EVM0004814 | GATTCTTCGCCGTTCAAG | ACATAAGGGTCTGGTATTCC |
| EVM0009373 | CTCATTGCTGGTGTTGTAT | GTATTACGGTCAAGGATAGAAC |
| EVM0008905 | GACGGACAAGTATGTAATGG | AATGGAAGGAAGTTGAACAG |
|  |  |  |
| EF1 | CGATACCTCCCTCCGCCCAG | ACAGGCGGAACGACCACAAC |

Table S2 the sequencing data and alignment statistics

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Samples** | **Clean reads** | **Clean bases** | **GC Content\*** | **%≥Q30Ψ** | **Mapped reads** |
| C-1 | 56,539,926 | 16,803,169,322 | 37.10% | 94.29% | 81,354,935 (71.94%) |
| C-2 | 58,566,590 | 17,455,882,080 | 37.23% | 94.56% | 85,057,246 (72.62%) |
| C-3 | 60,759,696 | 18,028,324,124 | 37.37% | 94.66% | 75,783,626 (62.36%) |
| Pre-C-1 | 21,365,220 | 6,395,062,008 | 37.54% | 94.11% | 35,882,293 (83.97%) |
| Pre-C-2 | 20,596,396 | 6,165,534,548 | 37.57% | 94.24% | 34,729,506 (84.31%) |
| Pre-C-3 | 21,521,034 | 6,447,217,940 | 37.37% | 93.94% | 36,143,008 (83.79%) |
| Post-C-1 | 22,055,956 | 6,606,661,946 | 36.81% | 94.13% | 36,498,667 (82.74%) |
| Post-C-2 | 20,455,959 | 6,128,162,266 | 36.45% | 93.73% | 33,753,277 (82.5%) |
| Post-C-3 | 22,409,737 | 6,710,299,490 | 36.78% | 94.48% | 37,116,052 (82.81%) |

\* GC content: GC content percentage of Clean Data, namely the percentage of Clean Data base G and C;  
**Ψ** %≥Q30: percentage of Clean Data which quality value is greater than or equal to Q30 (an error rate of 1 in 1000).

**Table S3** **Differential expression of selected genes putatively related to transcription factors (TF) during conidiation.**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Internal ID** | **FPKM\*** | | | **Log2(FC)** † | |  | **PHI** | **Annotation** |
| **Pre-C** | **C** | **Post-C** | **C vs. pre-C** | **C vs. post-C** |  |
| EVM0007139 | 0.25 | 5.57 | 2.88 | 3.89 | 1.21 |  | PHI:287 | GATA-4/5/6 TF |
| EVM0007072 | 16.24 | 41.74 | 23.84 | 1.39 | 1.07 |  | **/** | Histone-like TF |
| EVM0006849 | 44.03 | 101.27 | 57.09 | 1.23 | 1.09 |  | **/** | Transcription initiation factor TFIIA |
| Co \_242 | 0.00 | 18.18 | 2.89 | 7.70 | 2.82 |  | **/** | Homeobox phx1 TF |
| EVM0006123 | 0.92 | 4.69 | 0.97 | 2.33 | 2.35 |  | PHI:2128 | Homeobox phx1 TF |
| EVM0003245 | 0.00 | 2.34 | 0.13 | 6.15 | 3.79 |  | PHI:2039 | C2H2 finger domain TF |
| EVM0001087 | 1.34 | 5.91 | 1.52 | 2.09 | 2.12 |  | PHI:2039 | C2H2 finger domain TF |
| EVM0004983 | 0.06 | 2.99 | 0.31 | 4.95 | 3.40 |  | PHI:232 | STE-like TF |
| EVM0008462 | 1.93 | 18.15 | 5.54 | 3.19 | 1.90 |  | PHI:1405 | SteA TF |
| EVM0002148 | 0.11 | 2.13 | 0.24 | 3.90 | 3.18 |  | PHI:3315 | Activator of gluconeogenesis TF |
| EVM0007454 | 0.33 | 3.78 | 0.19 | 3.44 | 4.45 |  | PHI:1921 | RNA polymerase II-specific TF |
| EVM0000062 | 12.39 | 25.68 | 11.54 | 1.09 | 1.43 |  | PHI:2930 | Cutinase TF |
| EVM0010146 | 0.13 | 1.47 | 0.32 | 3.10 | 2.23 |  |  | Fungal specific TF |
| EVM0000205 | 18.17 | 41.06 | 15.94 | 1.22 | 1.63 |  | PHI:1742 | Fungal specific TF |
| EVM0003677 | 9.24 | 111.30 | 38.21 | 3.56 | 1.80 |  | PHI:2565 | Heat shock TF |
| EVM0008905 | 38.21 | 269.52 | 11.23 | 2.83 | 4.76 |  | PHI:2406 | Heat shock TF |
| Co \_1230 | 1.00 | 4.90 | 0.65 | 2.16 | 2.96 |  | **/** | Pcc1 TF |
| EVM0008509 | 28.60 | 61.05 | 19.28 | 1.13 | 1.93 |  | **/** | e(y)2 TF |
| EVM0006858 | 21.95 | 71.91 | 36.99 | 1.74 | 1.22 |  | **/** | Transcription initiation factor TFIID |
| EVM0002806 | 13.05 | 34.55 | 11.79 | 1.44 | 1.82 |  | PHI:1295 | Asexual reproduction regulation TF |
| EVM0000750 | 98.92 | 204.70 | 46.81 | 1.10 | 2.36 |  | PHI:3808 | CREB family TF |

\* The transcript level is expressed as fragments per kilobase per million mapped reads (FPKM).

† FC is the fold change (FC) of DEGs based on a FC of ≥ 2 and an FDR of < 0.01.

Table S4 The DEGs associated with the main GO terms

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Internal ID** | **FPKM\*** | | | **Log2(FC)** † | |  | **Pfam annotation** |
| **Pre-C** | **C** | **Post-C** | **C vs. pre-C** | **C vs. post-C** |  |
| Biological Process:carbohydrate metabolic process (GO:0005975) | | | | | | | |
| EVM0003314\* | 0.30 | 21.02 | 0.00 | 5.88 | 9.51 |  | Glycosyl hydrolases family 16 |
| EVM0005673\* | 0.77 | 2.40 | 0.06 | 1.62 | 5.33 |  | Glycosyl hydrolases family 31 |
| EVM0009297 | 25.90 | 59.04 | 16.88 | 1.23 | 2.07 |  | Glycogen debranching enzyme |
| EVM0009626 | 31.33 | 65.56 | 20.27 | 1.11 | 1.96 |  | Glycogen debranching enzyme |
| EVM0000365\* | 10.12 | 47.79 | 0.87 | 2.27 | 5.99 |  | Glycosyl hydrolases family 16 |
| EVM0001373\* | 10.45 | 48.78 | 0.90 | 2.25 | 5.97 |  | Glycosyl hydrolases family 16 |
| EVM0008569 | 22.33 | 49.64 | 27.33 | 1.18 | 1.12 |  | Ribulose-phosphate 3 epimerase family |
| EVM0007041 | 76.64 | 161.17 | 57.15 | 1.11 | 1.76 |  | Ribulose-phosphate 3 epimerase family |
| EVM0008158\* | 0.00 | 1.55 | 0.07 | 6.09 | 4.10 |  | Glycosyl hydrolases family 18 |
| EVM0004064\* | 3.64 | 133.52 | 22.28 | 5.14 | 2.81 |  | Glycosyl hydrolases family 18 |
| EVM0001249\* | 6.24 | 148.22 | 24.14 | 4.48 | 2.84 |  | Glycosyl hydrolases family 18 |
| EVM0004020 | 1.58 | 206.41 | 17.19 | 6.98 | 3.82 |  | Glycosyl hydrolases family 18 |
| EVM0004131\* | 8.18 | 131.74 | 23.17 | 3.99 | 2.74 |  | Glycosyl hydrolases family 18 |
| Biological Process: transport (GO:0006810) | | | | | | | |
| EVM0004058 | 5.71 | 11.80 | 5.54 | 1.08 | 1.36 |  | ABC transporter |
| EVM0002255 | 0.02 | 3.49 | 0.42 | 5.89 | 2.85 |  | Major intrinsic protein |
| EVM0006467 | 0.04 | 5.42 | 0.12 | 4.52 | 5.47 |  | Sugar (and other) transporter |
| EVM0007330 | 2.86 | 54.35 | 4.28 | 4.26 | 3.92 |  | Sulfate permease family; STAS domain |
| EVM0006243 | 1.22 | 10.98 | 1.37 | 3.14 | 3.23 |  | Sulfate permease family |
| EVM0009518 | 12.87 | 35.39 | 12.83 | 1.47 | 1.68 |  | Sulfate permease family |
| EVM0009164 | 7.66 | 21.62 | 12.07 | 1.53 | 1.10 |  | STAS domain |
| EVM0002273 | 4.98 | 55.02 | 17.55 | 3.46 | 1.92 |  | Sodium/hydrogen exchanger family |
| EVM0004950 | 23.24 | 65.43 | 33.45 | 1.53 | 1.24 |  | Mitochondrial carrier |
| EVM0003315 | 7.42 | 16.96 | 6.98 | 1.18 | 1.50 |  | Mitochondrial carrier |
| EVM0000187 | 9.02 | 20.94 | 8.40 | 1.26 | 1.59 |  | ABC transporter |
| EVM0003819 | 10.66 | 20.92 | 11.24 | 1.01 | 1.17 |  | Nucleoside transporter |
| Biological Process: cellular process (GO:0009987) | | | | | | | |
| EVM0006180 | 0.21 | 7.20 | 1.11 | 4.70 | 2.91 |  | Glucanosyltransferase; X8 domain |
| EVM0007333 | 0.14 | 2.54 | 0.44 | 3.80 | 2.66 |  | Glucanosyltransferase; X8 domain |
| EVM0004067 | 86.45 | 544.69 | 301.14 | 2.67 | 1.12 |  | Cellulase (glycosyl hydrolase family 5) |
| EVM0010061 | 3.07 | 6.70 | 1.20 | 1.16 | 2.68 |  | Protein tyrosine kinase |
| EVM0008877 | 8.02 | 16.60 | 3.22 | 1.09 | 2.61 |  | Protein tyrosine kinase |
| Co \_2537 | 2.56 | 5.06 | 3.09 | 1.02 | 1.68 |  | Response regulator receiver domain |
| EVM0002403 | 3.76 | 20.76 | 10.86 | 2.48 | 1.21 |  | Lipase (class 3) |
| EVM0001310 | 6.53 | 15.93 | 6.64 | 1.28 | 1.51 |  | Dolichol phosphate-mannose biosynthesis regulatory protein (DPM2) |
| EVM0006252 | 0.00 | 5.03 | 0.97 | 7.84 | 2.50 |  | Protein tyrosine kinase; Kinase-like |
| EVM0004435 | 4.02 | 24.39 | 7.19 | 2.61 | 2.02 |  | Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD |
| EVM0003992 | 3.91 | 23.47 | 6.92 | 2.59 | 2.02 |  | Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD |
| EVM0003677 | 9.24 | 111.30 | 38.21 | 3.56 | 1.80 |  | HSF-type DNA-binding |
| EVM0002806 | 13.05 | 34.55 | 11.79 | 1.44 | 1.82 |  | Cell pattern formation-associated |
| EVM0003907 | 0.03 | 3.64 | 0.03 | 3.66 | 5.64 |  | Peptidase inhibitor I9 |
| EVM0001805 | 1.07 | 2.90 | 0.15 | 1.44 | 4.24 |  | Peptidase inhibitor I9 |
| Cellular Component: membrane (GO:0016020) | | | | | | | |
| EVM0004514 | 47.08 | 91.44 | 40.78 | 1.01 | 1.44 |  | Glucanosyltransferase; X8 domain |
| EVM0002472 | 2.21 | 9.34 | 1.72 | 2.11 | 2.71 |  | 1,3-beta-glucan synthase |
| EVM0003159 | 0.75 | 7.38 | 0.34 | 3.23 | 4.44 |  | -- |
| EVM0000484 | 2.27 | 9.24 | 1.73 | 2.06 | 2.68 |  | 1,3-beta-glucan synthase |
| EVM0004224 | 2.86 | 10.57 | 2.08 | 1.93 | 2.61 |  | 1,3-beta-glucan synthase |
| EVM0001764 | 6.32 | 21.13 | 4.13 | 1.78 | 2.62 |  | 1,3-beta-glucan synthase |
| EVM0005934 | 0.01 | 1.64 | 0.06 | 5.13 | 4.43 |  | Fibronectin type II domain |
| EVM0004067 | 86.45 | 544.69 | 301.14 | 2.67 | 1.12 |  | Cellulase |
| EVM0010219 | 126.01 | 321.21 | 52.74 | 1.38 | 2.87 |  | Fatty acid hydroxylase superfamily |
| EVM0003064 | 35.03 | 189.63 | 16.33 | 2.47 | 3.80 |  | ABC transporter |
| EVM0004058 | 5.71 | 11.80 | 5.54 | 1.08 | 1.36 |  | ABC transporter |
| EVM0000865 | 0.02 | 1.09 | 0.01 | 5.23 | 6.10 |  | E1-E2 ATPase |
| EVM0001785 | 0.02 | 1.12 | 0.01 | 5.10 | 6.13 |  | E1-E2 ATPase |
| EVM0001357 | 1.69 | 7.84 | 0.42 | 2.22 | 4.40 |  | E1-E2 ATPase |
| EVM0005475 | 23.17 | 766.40 | 1.97 | 5.06 | 8.74 |  | NADH-ubiquinone reductase complex 1 MLRQ subunit |
| EVM0006467 | 0.04 | 5.42 | 0.12 | 4.52 | 5.47 |  | Major Facilitator Superfamily |
| EVM0010232 | 11.82 | 36.07 | 3.93 | 1.65 | 3.45 |  | Sugar (and other) transporter |
| EVM0004950 | 23.24 | 65.43 | 33.45 | 1.53 | 1.24 |  | Mitochondrial carrier protein |
| EVM0004653 | 50.58 | 124.17 | 52.37 | 1.28 | 1.47 |  | Mitochondrial carrier protein |
| EVM0003315 | 7.42 | 16.96 | 6.98 | 1.18 | 1.50 |  | Mitochondrial carrier protein |
| EVM0004218 | 2.40 | 11.34 | 3.28 | 2.17 | 1.98 |  | Heavy-metal-associated domain |
| EVM0005466 | 28.92 | 90.54 | 17.56 | 1.69 | 2.64 |  | EamA-like transporter family |
| EVM0006025 | 11.59 | 27.57 | 5.91 | 1.29 | 2.49 |  | EamA-like transporter family |
| EVM0000187 | 9.02 | 20.94 | 8.40 | 1.26 | 1.59 |  | ABC transporter |
| EVM0005299 | 69.05 | 137.92 | 39.23 | 1.01 | 2.08 |  | Cytochrome c oxidase subunit VIc |
| EVM0002609 | 3.71 | 22.25 | 7.96 | 2.61 | 1.75 |  | Glycosyl hydrolase family 47 |
| EVM0003938 | 19.16 | 94.08 | 24.69 | 2.30 | 2.17 |  | NADH-ubiquinone oxidoreductase MWFE subunit |
| Cellular Component: cytosol (GO:0005829) | | | | | | | |
| EVM0001685 | 0.23 | 10.18 | 0.19 | 5.06 | 5.52 |  | Ubiquitin-conjugating enzyme |
| Co\_1850 | 7.65 | 24.25 | 8.56 | 1.54 | 1.61 |  | LSM domain |
| EVM0005642 | 6.97 | 27.14 | 10.29 | 1.98 | 1.65 |  | LSM domain |
| EVM0002852 | 11.65 | 33.69 | 11.81 | 1.56 | 1.77 |  | Ubiquitin family |
| EVM0000395 | 72.33 | 192.18 | 69.85 | 1.44 | 1.73 |  | Ubiquitin family |
| EVM0010225 | 12.44 | 29.32 | 6.67 | 1.25 | 2.33 |  | U1 zinc finger |
| EVM0002141 | 7.76 | 15.95 | 4.99 | 1.07 | 1.93 |  | Cytidine and deoxycytidylate deaminase zinc-binding region |
| EVM0009693 | 2.90 | 18.26 | 3.28 | 2.54 | 2.62 |  | Uncharacterised protein family |
| EVM0005733 | 887.99 | 2628.51 | 612.76 | 1.60 | 2.36 |  | Ribosomal L29 protein |
| EVM0006554 | 50.75 | 259.70 | 60.76 | 2.38 | 2.35 |  | Thioredoxin; AhpC/TSA family |
| EVM0002020 | 99.80 | 266.43 | 113.85 | 1.44 | 1.49 |  | Thioredoxin; AhpC/TSA family |
| EVM0002444 | 252.14 | 506.80 | 158.18 | 1.03 | 1.94 |  | Thioredoxin; AhpC/TSA family |
| EVM0003561 | 89.95 | 228.12 | 117.78 | 1.36 | 1.21 |  | EF-hand domain |
| EVM0004218 | 2.40 | 11.34 | 3.28 | 2.17 | 1.98 |  | Heavy-metal-associated domain |
| EVM0006741 | 4.89 | 11.72 | 5.87 | 1.25 | 1.23 |  | Urm1 (Ubiquitin related modifier) |
| EVM0000925 | 15.56 | 44.95 | 18.82 | 1.57 | 1.53 |  | Acyl transferase |
| EVM0001674 | 12.36 | 34.64 | 13.94 | 1.53 | 1.59 |  | Acyl transferase |
| EVM0001137 | 10.84 | 25.60 | 9.36 | 1.26 | 1.72 |  | Acyl transferase |
| Cellular Component: nucleus (GO:0005634) | | | | | | | |
| EVM0001685 | 0.23 | 10.18 | 0.19 | 5.06 | 5.52 |  | Ubiquitin-conjugating enzyme |
| EVM0002852 | 11.65 | 33.69 | 11.81 | 1.56 | 1.77 |  | Ubiquitin family |
| EVM0000395 | 72.33 | 192.18 | 69.85 | 1.44 | 1.73 |  | Ubiquitin family |
| EVM0009693 | 2.90 | 18.26 | 3.28 | 2.54 | 2.62 |  | Uncharacterised protein family |
| EVM0006554 | 50.75 | 259.70 | 60.76 | 2.38 | 2.35 |  | Thioredoxin |
| EVM0002020 | 99.80 | 266.43 | 113.85 | 1.44 | 1.49 |  | Thioredoxin |
| EVM0002444 | 252.14 | 506.80 | 158.18 | 1.03 | 1.94 |  | Thioredoxin |
| EVM0003561 | 89.95 | 228.12 | 117.78 | 1.36 | 1.21 |  | EF-hand domain |
| EVM0004218 | 2.40 | 11.34 | 3.28 | 2.17 | 1.98 |  | Heavy-metal-associated domain |
| EVM0010037 | 177.80 | 1749.36 | 115.71 | 3.31 | 4.18 |  | Acyl CoA binding protein |
| EVM0008569 | 22.33 | 49.64 | 27.33 | 1.18 | 1.12 |  | Ribulose-phosphate 3 epimerase |
| EVM0007041 | 76.64 | 161.17 | 57.15 | 1.11 | 1.76 |  | Ribulose-phosphate 3 epimerase |
| EVM0004983 | 0.06 | 2.99 | 0.31 | 4.95 | 3.40 |  | STE like transcription factor |
| EVM0002148 | 0.11 | 2.13 | 0.24 | 3.90 | 3.18 |  | Fungal Zn(2)-Cys(6) binuclear cluster domain |
| Molecular Function: hydrolase activity (GO:0016787) | | | | | | | |
| EVM0009290 | 5.10 | 251.35 | 26.34 | 5.64 | 3.50 |  | Cellulase |
| EVM0007726 | 28.46 | 63.04 | 8.57 | 1.19 | 3.13 |  | Glycosyl hydrolase family |
| EVM0004067 | 86.45 | 544.69 | 301.14 | 2.67 | 1.12 |  | Cellulase) |
| EVM0003971 | 42.26 | 105.31 | 50.33 | 1.36 | 1.34 |  | Beta-glucan synthesis-associated protein (SKN1) |
| Co\_1182 | 0.00 | 0.47 | 0.11 | 6.18 | 2.22 |  | Platelet-activating factor acetylhydrolase |
| EVM0002220 | 1.39 | 6.54 | 1.47 | 2.26 | 2.41 |  | Amidohydrolase family |
| EVM0000082 | 0.02 | 0.65 | 0.00 | 4.10 | 6.64 |  | Subtilase family |
| EVM0001805 | 1.07 | 2.90 | 0.15 | 1.44 | 4.24 |  | Subtilase family |
| EVM0008226 | 9.05 | 53.10 | 1.22 | 2.57 | 5.63 |  | Trypsin |
| EVM0005001 | 21.39 | 88.68 | 1.10 | 2.08 | 6.55 |  | Trypsin |
| EVM0009772 | 2.42 | 5.80 | 0.08 | 1.27 | 5.66 |  | Trypsin |
| EVM0001721 | 48.83 | 147.41 | 19.30 | 1.63 | 3.20 |  | Trypsin |
| EVM0000789 | 0.02 | 2.06 | 0.01 | 5.13 | 6.18 |  | Glycosyl hydrolases family 18 |
| EVM0000088 | 0.47 | 10.13 | 0.64 | 4.38 | 4.18 |  | Glycosyl hydrolases family 18 |
| EVM0007380 | 0.00 | 1.05 | 0.01 | 5.72 | 5.23 |  | Glycosyl hydrolases family 18 |
| EVM0000612 | 0.46 | 8.30 | 0.60 | 4.13 | 4.00 |  | Glycosyl hydrolases family 18 |
| EVM0008574 | 0.11 | 0.87 | 0.27 | 2.72 | 1.88 |  | Glycosyl hydrolases family 18 |
| EVM0006427 | 0.11 | 0.84 | 0.32 | 2.68 | 1.63 |  | Glycosyl hydrolases family 18 |
| EVM0003563 | 0.11 | 0.84 | 0.25 | 2.64 | 1.89 |  | Glycosyl hydrolases family 18 |
| Molecular Function: catalytic activity (GO:0003824) | | | | | | | |
| EVM0006541 | 0.06 | 220.04 | 63.88 | 9.69 | 2.04 |  | Polysaccharide deacetylase |
| EVM0008805 | 0.00 | 10.70 | 0.00 | 8.66 | 9.19 |  | Glycosyl hydrolases family 16 |
| EVM0008271 | 0.00 | 9.93 | 0.00 | 8.44 | 8.98 |  | Glycosyl hydrolases family 16 |
| EVM0004224 | 2.86 | 10.57 | 2.08 | 1.93 | 2.61 |  | 1,3-beta-glucan synthase |
| EVM0000444 | 0.88 | 28.13 | 1.34 | 5.02 | 4.65 |  | Chitin synthase |
| EVM0006157 | 0.01 | 6.72 | 0.74 | 5.96 | 3.32 |  | Pyridoxal-dependent decarboxylase |
| EVM0009297 | 25.90 | 59.04 | 16.88 | 1.23 | 2.07 |  | Glycogen debranching enzyme |
| EVM0009626 | 31.33 | 65.56 | 20.27 | 1.11 | 1.96 |  | Glycogen debranching enzyme |
| EVM0003949 | 0.92 | 6.97 | 2.76 | 2.80 | 1.56 |  | HD domain |
| EVM0003025 | 10.15 | 24.96 | 14.34 | 1.31 | 1.05 |  | AMP-binding enzyme |
| Co\_102 | 0.03 | 4.79 | 0.04 | 6.32 | 6.31 |  | Eukaryotic aspartyl protease |
| EVM0007192 | 43.88 | 125.58 | 33.11 | 1.56 | 2.17 |  | Aminotransferase class I and II |
| EVM0007255 | 6.16 | 17.73 | 7.03 | 1.55 | 1.60 |  | Glycerophosphoryl diester phosphodiesterase family |
| EVM0004087 | 7.96 | 49.50 | 7.38 | 2.57 | 2.99 |  | Aminotransferase class I and II |
| Molecular Function: serine-type peptidase activity (GO:0008236) | | | | | | | |
| EVM0007218 | 0.00 | 6.15 | 0.01 | 7.49 | 7.29 |  | Subtilase family |
| EVM0000403 | 0.67 | 25.11 | 1.45 | 3.77 | 3.65 |  | Subtilase family |
| EVM0005632 | 0.41 | 10.97 | 1.22 | 3.70 | 2.98 |  | Subtilase family |
| EVM0004644 | 147.47 | 970.44 | 12.14 | 2.74 | 6.57 |  | Subtilase family |
| EVM0008109 | 0.06 | 14.77 | 0.12 | 6.93 | 4.37 |  | Trypsin |
| EVM0006838 | 4.46 | 290.36 | 7.64 | 5.96 | 5.43 |  | Trypsin |
| EVM0008156 | 0.47 | 36.30 | 3.51 | 5.95 | 3.56 |  | Trypsin |
| EVM0007680 | 0.16 | 8.65 | 0.04 | 5.14 | 6.88 |  | Trypsin |
| EVM0006920 | 10.03 | 255.93 | 10.92 | 4.64 | 4.76 |  | Trypsin |
| Co\_2766 | 2.87 | 42.32 | 0.45 | 3.87 | 6.62 |  | Trypsin |
| EVM0009083 | 5.02 | 36.42 | 0.99 | 2.87 | 5.41 |  | Trypsin |
| EVM0003166 | 6.32 | 27.37 | 6.54 | 2.15 | 2.33 |  | Trypsin |

\* The transcript level is expressed in fragments per kilobase per million fragments (FPKM) values. S: mycelia at sporulating stage; Pre-S: mycelia before sporulating stage; Post-S: mycelia after sporulating stage.

† FC is the fold change of differentially expressed genes between the three libraries of S, Pre-S and Post-S. There are genes expressing with significant difference (a fold change ≥ 2 and a false discovery rate < 0.001).

\* Secretory proteins were screened based on their structures using the signal peptide that was predicted by SignalP v5.0 ([www.cbs.dtu.dk/services/signalp](http://www.cbs.dtu.dk/services/signalp)) and without a membrane spanning domain. Pfam – protein family database (El-Gebali et al. 2019

Table S5 The DEGs associated with the main KEGG pathway

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Internal ID** | **FPKM\*** | | | **Log2(FC)** † | |  | **Pfam annotation** |
| **Pre-C** | **C** | **Post-C** | **C vs. pre-C** | **C vs. post-C** |  |
| Oxidative phosphorylation (ko00190) | | | | | | | |
| EVM0009508 | 19.49 | 101.99 | 24.80 | 2.40 | 2.30 |  | ATP synthase subunit H |
| EVM0004390 | 11.36 | 41.00 | 12.96 | 1.86 | 1.91 |  | Vacuolar (H+)-ATPase G subunit |
| EVM0000869 | 11.09 | 39.75 | 12.80 | 1.85 | 1.88 |  | Vacuolar (H+)-ATPase G subunit |
| EVM0000557 | 85.43 | 262.37 | 75.67 | 1.65 | 2.05 |  | Vacuolar (H+)-ATPase G subunit |
| EVM0005475 | 23.17 | 766.40 | 1.97 | 5.06 | 8.74 |  | NADH-ubiquinone reductase complex 1 |
| EVM0007673 | 82.11 | 222.07 | 41.72 | 1.45 | 2.65 |  | NADH-ubiquinone oxidoreductase B18 |
| EVM0004399 | 40.00 | 104.82 | 37.18 | 1.39 | 1.73 |  | NADH:ubiquinone oxidoreductase, |
| EVM0001245 | 45.65 | 241.07 | 37.97 | 2.42 | 2.92 |  | Cytochrome oxidase c subunit VIb |
| EVM0008584 | 20.72 | 62.39 | 11.85 | 1.61 | 2.64 |  | Cytochrome c oxidase subunit VIIc |
| EVM0004161 | 50.11 | 185.06 | 101.63 | 1.87 | 1.11 |  | Cytochrome oxidase assembly protein |
| EVM0006582 | 254.08 | 559.04 | 183.56 | 1.17 | 1.88 |  | Cytochrome c oxidase subunit VIa |
| EVM0005299 | 69.05 | 137.92 | 39.23 | 1.01 | 2.08 |  | Cytochrome c oxidase subunit VIc |
| EVM0008956 | 8.39 | 39.48 | 8.45 | 2.20 | 2.44 |  | Ubiquinol-cytochrome C reductase hinge protein |
| EVM0007884 | 9.44 | 36.04 | 10.39 | 1.93 | 2.04 |  | Ubiquinol-cytochrome C reductase hinge protein |
| EVM0008409 | 9.62 | 34.39 | 10.52 | 1.81 | 1.93 |  | Ubiquinol-cytochrome C reductase hinge protein |
| EVM0002948 | 16.20 | 66.97 | 14.73 | 2.02 | 2.41 |  | Ubiquinol-cytochrome C reductase |
| EVM0003754 | 11.42 | 47.32 | 10.64 | 1.99 | 2.35 |  | Ubiquinol-cytochrome C reductase |
| EVM0009982 | 11.29 | 26.73 | 13.52 | 1.25 | 1.22 |  | Ubiquinol-cytochrome-c reductase complex subunit (QCR10) |
| EVM0005826 | 37.87 | 139.64 | 36.72 | 1.89 | 2.19 |  | ATP synthase complex subunit h |
| EVM0008514 | 58.16 | 164.13 | 46.60 | 1.52 | 2.07 |  | ATP synthase complex subunit h |
| EVM0000544 | 63.03 | 231.60 | 29.49 | 1.88 | 3.20 |  | Mitochondrial ATP synthase epsilon chain |
| EVM0001330 | 39.78 | 120.09 | 32.18 | 1.61 | 2.15 |  | Mitochondrial ribosomal protein L51 / S25 / CI-B8 domain |
| EVM0005601 | 42.32 | 109.17 | 29.39 | 1.37 | 2.13 |  | ATP synthase E chain |
| **Amino sugar and nucleotide sugar metabolism (ko00520)** | | | | | | | |
| EVM0000444 | 0.88 | 28.13 | 1.34 | 5.02 | 4.65 |  | Chitin synthase |
| EVM0004669 | 3.74 | 36.43 | 11.22 | 3.31 | 1.97 |  | Chitin synthase |
| EVM0001244 | 48.91 | 588.98 | 30.89 | 3.63 | 4.52 |  | Glycosyl hydrolase family 20 |
| EVM0005566 | 74.65 | 342.19 | 19.81 | 2.23 | 4.37 |  | Glycosyl hydrolase family 20 |
| EVM0007277 | 20.04 | 42.44 | 11.52 | 1.12 | 2.14 |  | Acetyltransferase (GNAT) family |
| EVM0008158 | 0.00 | 1.55 | 0.07 | 6.09 | 4.10 |  | Glycosyl hydrolases family 18 |
| EVM0000789 | 0.02 | 2.06 | 0.01 | 5.13 | 6.18 |  | Glycosyl hydrolases family 18 |
| EVM0007628 | 1.09 | 27.49 | 0.76 | 4.65 | 5.38 |  | Glycosyl hydrolases family 18 |
| EVM0000088 | 0.47 | 10.13 | 0.64 | 4.38 | 4.18 |  | Glycosyl hydrolases family 18 |
| EVM0007380 | 0.00 | 1.05 | 0.01 | 5.72 | 5.23 |  | Glycosyl hydrolases family 18 |
| EVM0004064 | 3.64 | 133.52 | 22.28 | 5.14 | 2.81 |  | Glycosyl hydrolases family 18 |
| EVM0001249 | 6.24 | 148.22 | 24.14 | 4.48 | 2.84 |  | Glycosyl hydrolases family 18 |
| EVM0004020 | 1.58 | 206.41 | 17.19 | 6.98 | 3.82 |  | Glycosyl hydrolases family 18 |
| EVM0004131 | 8.18 | 131.74 | 23.17 | 3.99 | 2.74 |  | Glycosyl hydrolases family 18 |
| EVM0002377 | 3.67 | 21.22 | 3.63 | 2.56 | 2.81 |  | Glycosyl hydrolases family 18 |
| EVM0000612 | 0.46 | 8.30 | 0.60 | 4.13 | 4.00 |  | Glycosyl hydrolases family 18 |
| EVM0008574 | 0.11 | 0.87 | 0.27 | 2.72 | 1.88 |  | Glycosyl hydrolases family 18 |
| EVM0006427 | 0.11 | 0.84 | 0.32 | 2.68 | 1.63 |  | Glycosyl hydrolases family 18 |
| EVM0003563 | 0.11 | 0.84 | 0.25 | 2.64 | 1.89 |  | Glycosyl hydrolases family 18 |
| EVM0005693 | 69.41 | 186.04 | 94.25 | 1.45 | 1.25 |  | GDP-mannose 4,6 dehydratase |
| **MAPK signaling pathway - yeast (ko04011)** | | | | | | | |
| EVM0008074 | 0.21 | 1.79 | 0.08 | 2.84 | 4.10 |  | 1,3-beta-glucan synthase component |
| EVM0002472 | 2.21 | 9.34 | 1.72 | 2.11 | 2.71 |  | 1,3-beta-glucan synthase component |
| EVM0003159 | 0.75 | 7.38 | 0.34 | 3.23 | 4.44 |  | 1,3-beta-glucan synthase component |
| EVM0007566 | 4.93 | 23.19 | 3.05 | 2.26 | 3.18 |  | 1,3-beta-glucan synthase component |
| EVM0000484 | 2.27 | 9.24 | 1.73 | 2.06 | 2.68 |  | 1,3-beta-glucan synthase component |
| EVM0004224 | 2.86 | 10.57 | 2.08 | 1.93 | 2.61 |  | 1,3-beta-glucan synthase component |
| EVM0001764 | 6.32 | 21.13 | 4.13 | 1.78 | 2.62 |  | 1,3-beta-glucan synthase component |
| EVM0005361 | 18.15 | 309.79 | 148.14 | 4.10 | 1.32 |  | Catalase-related immune-responsive |
| EVM0009987 | 4.35 | 71.98 | 34.28 | 4.02 | 1.33 |  | Catalase-related immune-responsive |
| EVM0007860 | 6.31 | 102.14 | 50.99 | 3.99 | 1.26 |  | Catalase-related immune-responsive |
| EVM0001653 | 22.96 | 61.12 | 33.62 | 1.45 | 1.13 |  | Variant SH3 domain |
| EVM0004983 | 0.06 | 2.99 | 0.31 | 4.95 | 3.40 |  | STE like transcription factor |
| EVM0001126 | 5.85 | 71.98 | 23.78 | 3.62 | 1.86 |  | GGL domain |
| EVM0008649 | 126.30 | 916.02 | 323.30 | 2.89 | 1.77 |  | GGL domain |
| EVM0000750 | 98.92 | 204.70 | 46.81 | 1.10 | 2.36 |  | bZIP transcription factor |
| **Ribosome (ko03010)** | | | | | | | |
| EVM0000242 | 815.77 | 2264.82 | 654.09 | 1.51 | 2.06 |  | S25 ribosomal protein |
| EVM0002937 | 950.39 | 3871.05 | 526.06 | 2.05 | 3.14 |  | Ribosomal protein S28e |
| EVM0005588 | 1245.76 | 3090.38 | 851.98 | 1.34 | 2.13 |  | Ribosomal protein S27 |
| EVM0009766 | 3.72 | 12.37 | 5.28 | 1.69 | 1.46 |  | Ribosomal protein L36 |
| EVM0009938 | 4.64 | 13.08 | 6.88 | 1.46 | 1.16 |  | Ribosomal protein L34 |
| EVM0003011 | 1717.35 | 7151.17 | 1263.06 | 2.09 | 2.77 |  | Ribosomal protein L44 |
| Co\_61 | 110.67 | 363.52 | 56.75 | 1.74 | 2.93 |  | Ribosomal L38e protein family |
| EVM0005733 | 887.99 | 2628.51 | 612.76 | 1.60 | 2.36 |  | Ribosomal L29 protein |
| Co\_2197 | 79.87 | 185.90 | 47.97 | 1.25 | 2.22 |  | Ribosomal L39 protein |
| Co\_3023 | 210.28 | 485.31 | 155.24 | 1.24 | 1.91 |  | Ribosomal L38e protein family |
| EVM0008541 | 286.98 | 658.84 | 211.23 | 1.23 | 1.91 |  | Ribosomal L38e protein family |
| EVM0001436 | 2710.86 | 6189.85 | 1919.84 | 1.23 | 1.96 |  | Ribosomal protein L32 |
| EVM0007727 | 124.99 | 359.92 | 71.21 | 1.56 | 2.60 |  | Ribosomal protein S27a |
| EVM0002763 | 750.10 | 1656.68 | 494.70 | 1.17 | 2.01 |  | Ribosomal protein S27a |

\* The transcript level is expressed in fragments per kilobase per million fragments (FPKM) values. S: mycelia at sporulating stage; Pre-S: mycelia before sporulating stage; Post-S: mycelia after sporulating stage.

† FC is the fold change of differentially expressed genes between the three libraries of S, Pre-S and Post-S. There are genes expressing with significant difference (a fold change ≥ 2 and a false discovery rate < 0.001).

**Table S6** **Differential expression of selected genes related to** **cell wall/membrane/envelope biogenesis during conidiation.**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Internal ID** | **FPKM\*** | | |  | **Log2(FC)** † | |  | **PHI** |
| **Pre-C** | **C** | **Post-C** |  | **C vs. pre-C** | **C vs. post-C** |  |
| **1,3-beta-glucan synthase** | | |  |  |  |  |  |  |
| EVM0008074 | 0.21 | 1.79 | 0.08 |  | 2.84 | 4.10 |  | PHI:2533 |
| EVM0002472 | 2.21 | 9.34 | 1.72 |  | 2.11 | 2.71 |  | PHI:2533 |
| EVM0003159 | 0.75 | 7.38 | 0.34 |  | 3.23 | 4.44 |  | PHI:2533 |
| EVM0007566 | 4.93 | 23.19 | 3.05 |  | 2.26 | 3.18 |  | PHI:2533 |
| EVM0000484 | 2.27 | 9.24 | 1.73 |  | 2.06 | 2.68 |  | PHI:2533 |
| EVM0004224 | 2.86 | 10.57 | 2.08 |  | 1.93 | 2.61 |  | PHI:2533 |
| EVM0001764 | 6.32 | 21.13 | 4.13 |  | 1.78 | 2.62 |  | PHI:2533 |
| EVM0003971 | 42.26 | 105.31 | 50.33 |  | 1.36 | 1.34 |  | **/** |
| **Glucanosyltransferase** |  |  |  |  |  |  |  |  |
| EVM0006180 | 0.21 | 7.20 | 1.11 |  | 4.70 | 2.91 |  | PHI:33 |
| EVM0007333 | 0.14 | 2.54 | 0.44 |  | 3.80 | 2.66 |  | PHI:33 |
| EVM0004514 | 47.08 | 91.44 | 40.78 |  | 1.01 | 1.44 |  | PHI:33 |
| **Glycosyl hydrolase** |  |  |  |  |  |  |  |  |
| EVM0007001 | 4.14 | 54.19 | 23.03 |  | 3.73 | 1.51 |  | **/** |
| EVM0007042 | 32.83 | 87.13 | 11.42 |  | 1.45 | 3.19 |  | PHI:748 |
| EVM0007726 | 28.46 | 63.04 | 8.57 |  | 1.19 | 3.13 |  | PHI:748 |
| EVM0005673 | 0.77 | 2.40 | 0.06 |  | 1.62 | 5.33 |  | PHI:1071 |
| EVM0003793 | 0.10 | 1.22 | 0.03 |  | 3.10 | 4.73 |  | **/** |
| **Chitin synthase/chitinase** | |  |  |  |  |  |  |  |
| EVM0000444 | 0.88 | 28.13 | 1.34 |  | 5.02 | 4.65 |  | PHI:3048 |
| EVM0004669 | 3.74 | 36.43 | 11.22 |  | 3.31 | 1.97 |  | PHI:3050 |
| EVM0008158 | 0.00 | 1.55 | 0.07 |  | 6.09 | 4.10 |  | PHI:2388 |
| EVM0000789 | 0.02 | 2.06 | 0.01 |  | 5.13 | 6.18 |  | PHI:2388 |
| EVM0007628 | 1.09 | 27.49 | 0.76 |  | 4.65 | 5.38 |  | PHI:2388 |
| EVM0000088 | 0.47 | 10.13 | 0.64 |  | 4.38 | 4.18 |  | PHI:2388 |
| **Cellulase** |  |  |  |  |  |  |  |  |
| EVM0009290 | 5.10 | 251.35 | 26.34 |  | 5.64 | 3.50 |  | PHI:323 |
| EVM0004067 | 86.45 | 544.69 | 301.14 |  | 2.67 | 1.12 |  | PHI:323 |
| **Ergosterol** |  |  |  |  |  |  |  |  |
| EVM0010219 | 126.01 | 321.21 | 52.74 |  | 1.38 | 2.87 |  | PHI:3035 |
| **Mannan biosynthesis/mannoprotein assembly** | | | |  |  |  |  |  |
| EVM0006408 | 0.47 | 277.15 | 40.64 |  | 8.94 | 2.98 |  | **/** |
| EVM0003767 | 0.95 | 5.10 | 2.14 |  | 2.35 | 1.48 |  | PHI:2482 |

\* The transcript level is expressed as fragments per kilobase per million mapped reads (FPKM).

† FC is the fold change (FC) of DEGs based on a FC of ≥ 2 and an FDR of < 0.01.

Table S7 The DEGs associated with PHI database\*

|  |  |
| --- | --- |
| DEG ID | PHI |
| EVM0001654 | PHI:432|FGL1|AAQ23181|5518|Fusarium\_graminearum|Reduced\_virulence |
| EVM0003421 | AKT7|PHI:4194|V5XZS6|5599|Alternaria\_alternata|increased\_virulence\_(Hypervirulence) |
| EVM0006252 | PHI:1221|FGSG\_03146|I1RJM9|5518|Gibberella\_zeae\_(related:\_Fusarium\_graminearum)|Lethal |
| EVM0004341 | PHI:2117|SPM1|P58371|148305|Magnaporthe\_oryzae\_(related:\_Magnaporthe\_grisea)|Reduced\_virulence |
| EVM0004394 | AKT7|PHI:4194|V5XZS6|5599|Alternaria\_alternata|increased\_virulence\_(Hypervirulence) |
| EVM0007784 | PHI:432|FGL1|AAQ23181|5518|Fusarium\_graminearum|Reduced\_virulence |
| EVM0007218 | PHI:2117|SPM1|P58371|148305|Magnaporthe\_oryzae\_(related:\_Magnaporthe\_grisea)|Reduced\_virulence |
| EVM0009119 | PHI:652|GIP1|AAL11720|67593|Phytophthora\_sojae|Effector\_(plant\_avirulence\_determinant) |
| EVM0004379 | AKT7|PHI:4194|V5XZS6|5599|Alternaria\_alternata|increased\_virulence\_(Hypervirulence) |
| EVM0004020 | PHI:144|CHT42|AAC05829|29875|Trichoderma\_virens|Reduced\_virulence |
| EVM0008109 | PHI:653|GIP2|AAL11721|67593|Phytophthora\_sojae|Effector\_(plant\_avirulence\_determinant) |
| EVM0008303 | PHI:2321|SidI|Q4WR83|746128|Aspergillus\_fumigatus|Reduced\_virulence |
| EVM0009549 | AKT7|PHI:4194|V5XZS6|5599|Alternaria\_alternata|increased\_virulence\_(Hypervirulence) |
| EVM0002185 | AKT7|PHI:4194|V5XZS6|5599|Alternaria\_alternata|increased\_virulence\_(Hypervirulence) |
| EVM0000830 | PHI:1180|(Sc\_Sat4)|I1RS32|5518|Gibberella\_zeae\_(related:\_Fusarium\_graminearum)|Reduced\_virulence |
| EVM0003125 | PHI:2042|ABC3|Q3Y5V5|148305|Magnaporthe\_oryzae\_(related:\_Magnaporthe\_grisea)|Loss\_of\_pathogenicity |
| EVM0002496 | PHI:652|GIP1|AAL11720|67593|Phytophthora\_sojae|Effector\_(plant\_avirulence\_determinant) |
| EVM0009502 | PHI:438|BcBOT1\_(related:\_CND5)|AAQ16576|40559|Botrytis\_cinerea|Reduced\_virulence |
| EVM0004492 | PHI:397|LAC2|AAV64894|5207|Cryptococcus\_neoformans|Unaffected\_pathogenicity |
| EVM0008865 | PHI:429|ClPLS1|CAD43407|290576|Colletotrichum\_lindemuthianum|Loss\_of\_pathogenicity |
| EVM0001751 | PHI:2117|SPM1|P58371|148305|Magnaporthe\_oryzae\_(related:\_Magnaporthe\_grisea)|Reduced\_virulence |
| EVM0003245 | PHI:2039|Con7p|Q069J4|148305|Magnaporthe\_oryzae\_(related:\_Magnaporthe\_grisea)|Loss\_of\_pathogenicity |
| EVM0008158 | PHI:2388|Chi2|0|5530|Metarhizium\_anisopliae|Mixed\_outcome |
| EVM0006838 | PHI:652|GIP1|AAL11720|67593|Phytophthora\_sojae|Effector\_(plant\_avirulence\_determinant) |
| EVM0006157 | PHI:177|ODC|CAB56523|13684|Stagonospora\_nodorum|Reduced\_virulence |
| EVM0008156 | PHI:652|GIP1|AAL11720|67593|Phytophthora\_sojae|Effector\_(plant\_avirulence\_determinant) |
| EVM0000614 | PHI:697|ugt51E1|AAM81358|5022|Leptosphaeria\_maculans|Unaffected\_pathogenicity |
| EVM0001824 | PHI:1161|MgMfs1|A4ZGP3|54734|Mycosphaerella\_graminicola\_(related:\_Zymoseptoria\_triticii)|Chemistry\_target |
| EVM0007380 | PHI:144|CHT42|AAC05829|29875|Trichoderma\_virens|Reduced\_virulence |
| EVM0009290 | PHI:323|VFGLU1|AAO63562|93591|Verticillium\_fungicola|Reduced\_virulence |
| EVM0004016 | PHI:511|CaNAG4|EAK93098|5476|Candida\_albicans|Reduced\_virulence |
| EVM0008454 | PHI:1541|GzFlbD|I1RE42|5518|Gibberella\_zeae\_(related:\_Fusarium\_graminearum)|Unaffected\_pathogenicity |
| EVM0000952 | PHI:777|MGG\_00883|EDK02450|318829|Magnaporthe\_oryzae|Loss\_of\_pathogenicity |
| EVM0002960 | AKT7|PHI:4194|V5XZS6|5599|Alternaria\_alternata|increased\_virulence\_(Hypervirulence) |
| EVM0007590 | PHI:2021|Pac2|MGG\_06564|5270|Ustilago\_maydis|Reduced\_virulence |
| EVM0005882 | Ktr1|PHI:3095|J5JDI1|176275|Beauveria\_bassiana|unaffected\_pathogenicity\_ |
| EVM0001943 | PHI:577|NoxB|BAE72682|35717|Epichloe\_festucae|Wild-type\_mutualism |
| EVM0000865 | PHI:440|PMR1|CAB87245|5476|Candida\_albicans|Reduced\_virulence |
| EVM0007554 | PHI:2117|SPM1|P58371|148305|Magnaporthe\_oryzae\_(related:\_Magnaporthe\_grisea)|Reduced\_virulence |
| EVM0004064 | PHI:144|CHT42|AAC05829|29875|Trichoderma\_virens|Reduced\_virulence |
| EVM0007680 | PHI:653|GIP2|AAL11721|67593|Phytophthora\_sojae|Effector\_(plant\_avirulence\_determinant) |
| EVM0000789 | PHI:2388|Chi2|0|5530|Metarhizium\_anisopliae|Mixed\_outcome |
| EVM0001785 | PHI:440|PMR1|CAB87245|5476|Candida\_albicans|Reduced\_virulence |
| EVM0000444 | CSMA|PHI:3048|Q4X0H6|746128|Aspergillus\_fumigatus|mixed\_outcome\_ |
| EVM0004983 | PHI:232|STE12a|AAG49739|5207|Cryptococcus\_neoformans|Reduced\_virulence |
| EVM0005502 | PHI:1511|GzHOME009|I1RXF3|5518|Gibberella\_zeae\_(related:\_Fusarium\_graminearum)|Reduced\_virulence |
| EVM0007786 | PHI:1221|FGSG\_03146|I1RJM9|5518|Gibberella\_zeae\_(related:\_Fusarium\_graminearum)|Lethal |
| EVM0003715 | PHI:2357|CYP52X1|E2EAF6|475271|Beauveria\_bassiana|Reduced\_virulence |
| EVM0009373 | PHI:652|GIP1|AAL11720|67593|Phytophthora\_sojae|Effector\_(plant\_avirulence\_determinant) |
| EVM0006180 | PHI:33|PHR1|AAA68196|5476|Candida\_albicans|Reduced\_virulence |
| EVM0007628 | PHI:2388|Chi2|0|5530|Metarhizium\_anisopliae|Mixed\_outcome |
| EVM0006920 | PHI:653|GIP2|AAL11721|67593|Phytophthora\_sojae|Effector\_(plant\_avirulence\_determinant) |
| EVM0006467 | PHI:2968|Hxs1|J9VQA5|5207|Cryptococcus\_neoformans|Reduced\_virulence |
| EVM0001249 | PHI:144|CHT42|AAC05829|29875|Trichoderma\_virens|Reduced\_virulence |
| EVM0001327 | AKT7|PHI:4194|V5XZS6|5599|Alternaria\_alternata|increased\_virulence\_(Hypervirulence) |
| EVM0004130 | PHI:1434|GzC2H103|I1S8Y5|5518|Gibberella\_zeae\_(related:\_Fusarium\_graminearum)|Unaffected\_pathogenicity |
| EVM0000088 | PHI:2388|Chi2|0|5530|Metarhizium\_anisopliae|Mixed\_outcome |
| EVM0008112 | PHI:2839|RED1|Q8NJQ2|5016|Cochliobolus\_heterostrophus|Reduced\_virulence |
| EVM0000612 | PHI:144|CHT42|AAC05829|29875|Trichoderma\_virens|Reduced\_virulence |
| EVM0003018 | PHI:2839|RED1|Q8NJQ2|5016|Cochliobolus\_heterostrophus|Reduced\_virulence |
| EVM0005361 | PHI:106|CAT1|AAC39448|5476|Candida\_albicans|Reduced\_virulence |
| EVM0007723 | PHI:104|CaMNT1|CAA67930|5476|Candida\_albicans|Reduced\_virulence |
| EVM0009987 | PHI:106|CAT1|AAC39448|5476|Candida\_albicans|Reduced\_virulence |
| EVM0004131 | PHI:144|CHT42|AAC05829|29875|Trichoderma\_virens|Reduced\_virulence |
| EVM0007860 | PHI:106|CAT1|AAC39448|5476|Candida\_albicans|Reduced\_virulence |
| EVM0001410 | PHI:1310|GzbHLH011|I1RQC1|5518|Gibberella\_zeae\_(related:\_Fusarium\_graminearum)|Unaffected\_pathogenicity |
| EVM0010093 | PHI:432|FGL1|AAQ23181|5518|Fusarium\_graminearum|Reduced\_virulence |
| EVM0002148 | conx1|PHI:3315|G4MT41|318829|Magnaporthe\_oryzae|reduced\_virulence\_ |
| EVM0007672 | PHI:2839|RED1|Q8NJQ2|5016|Cochliobolus\_heterostrophus|Reduced\_virulence |
| EVM0007139 | PHI:287|CLNR1|AAN65464|290576|Colletotrichum\_lindemuthianum|Loss\_of\_pathogenicity |
| EVM0007333 | PHI:33|PHR1|AAA68196|5476|Candida\_albicans|Reduced\_virulence |
| EVM0000403 | PHI:2117|SPM1|P58371|148305|Magnaporthe\_oryzae\_(related:\_Magnaporthe\_grisea)|Reduced\_virulence |
| EVM0007619 | PHI:2117|SPM1|P58371|148305|Magnaporthe\_oryzae\_(related:\_Magnaporthe\_grisea)|Reduced\_virulence |
| EVM0005600 | PHI:2920|FET3-1|E3QRA4|31870|Colletotrichum\_graminicola|Reduced\_virulence |
| EVM0004577 | PHI:383|SOD5|EAL00626|5476|Candida\_albicans|Loss\_of\_pathogenicity |
| EVM0005632 | PHI:2117|SPM1|P58371|148305|Magnaporthe\_oryzae\_(related:\_Magnaporthe\_grisea)|Reduced\_virulence |
| EVM0006099 | PHI:213|CPA1|AAF69795|5207|Cryptococcus\_neoformans|Reduced\_virulence |
| EVM0003907 | PHI:2117|SPM1|P58371|148305|Magnaporthe\_oryzae\_(related:\_Magnaporthe\_grisea)|Reduced\_virulence |
| EVM0001001 | PHI:652|GIP1|AAL11720|67593|Phytophthora\_sojae|Effector\_(plant\_avirulence\_determinant) |
| EVM0003677 | PHI:2565|Q5APJ0|Q5APJ0|5476|Candida\_albicans|Reduced\_virulence |
| EVM0003126 | PHI:1161|MgMfs1|A4ZGP3|54734|Mycosphaerella\_graminicola\_(related:\_Zymoseptoria\_triticii)|Chemistry\_target |
| EVM0009891 | PHI:674|Can2|AAZ30051|178876|Cryptococcus\_neoformans|Increased\_virulence\_(Hypervirulence) |
| EVM0001772 | PHI:2839|RED1|Q8NJQ2|5016|Cochliobolus\_heterostrophus|Reduced\_virulence |
| EVM0009087 | PHI:2128|MoHox1|MGG\_04853|148305|Magnaporthe\_oryzae\_(related:\_Magnaporthe\_grisea)|reduced\_virulence |
| EVM0006347 | PHI:2844|BRM2|O93802|5599|Alternaria\_alternata|Unaffected\_pathogenicity |
| EVM0005592 | AKT7|PHI:4194|V5XZS6|5599|Alternaria\_alternata|increased\_virulence\_(Hypervirulence) |
| EVM0002733 | PHI:2844|BRM2|O93802|5599|Alternaria\_alternata|Unaffected\_pathogenicity |
| EVM0000479 | PHI:419|CSH1|AAP93915|5476|Candida\_albicans|Reduced\_virulence |
| EVM0007454 | PHI:1921|GzZC236|I1RCH8|5518|Gibberella\_zeae\_(related:\_Fusarium\_graminearum)|Reduced\_virulence |
| EVM0002401 | PHI:2100|Spf1|MGG\_12005|148305|Magnaporthe\_oryzae\_(related:\_Magnaporthe\_grisea)|Mixed\_outcome |
| EVM0001521 | PHI:1511|GzHOME009|I1RXF3|5518|Gibberella\_zeae\_(related:\_Fusarium\_graminearum)|Reduced\_virulence |
| EVM0004669 | CHSF|PHI:3050|Q4WC58|746128|Aspergillus\_fumigatus|mixed\_outcome\_ |
| EVM0004891 | PHI:432|FGL1|AAQ23181|5518|Fusarium\_graminearum|Reduced\_virulence |
| EVM0003159 | PHI:2533|FKS1|Q4WLT4|746128|Aspergillus\_fumigatus|Lethal |
| EVM0008462 | PHI:1405|GzC2H069|I1RWW2|5518|Gibberella\_zeae\_(related:\_Fusarium\_graminearum)|Unaffected\_pathogenicity |
| EVM0001555 | PHI:881|MGG\_04556|EDJ96020|318829|Magnaporthe\_oryzae|Reduced\_virulence |
| EVM0003299 | PHI:578|NoxR|BAF36501|35717|Epichloe\_festucae|Enhanced\_antagonism |
| EVM0004556 | PHI:2266|Ptr2|0|13684|Phaeosphaeria\_nodorum\_(related:\_Stagonospora\_nodorum)|Unaffected\_pathogenicity |
| EVM0008074 | PHI:2533|FKS1|Q4WLT4|746128|Aspergillus\_fumigatus|Lethal |
| EVM0004814 | PHI:2534|ERG11A|Q4WNT5|746128|Aspergillus\_fumigatus|Mixed\_outcome |
| EVM0008905 | PHI:2406|MoSKN7|G4N7Y2|148305|Magnaporthe\_oryzae\_(related:\_Magnaporthe\_grisea)|Unaffected\_pathogenicity |
| EVM0006845 | PHI:2086|Moatg24|MGG\_03638|148305|Magnaporthe\_oryzae\_(related:\_Magnaporthe\_grisea)|Unaffected\_pathogenicity |
| EVM0003041 | PHI:2158|MoCMK1|EU\_984498|148305|Magnaporthe\_oryzae\_(related:\_Magnaporthe\_grisea)|Reduced\_virulence |
| EVM0010231 | PHI:511|CaNAG4|EAK93098|5476|Candida\_albicans|Reduced\_virulence |
| EVM0004644 | PHI:2117|SPM1|P58371|148305|Magnaporthe\_oryzae\_(related:\_Magnaporthe\_grisea)|Reduced\_virulence |
| EVM0003276 | PHI:2042|ABC3|Q3Y5V5|148305|Magnaporthe\_oryzae\_(related:\_Magnaporthe\_grisea)|Loss\_of\_pathogenicity |
| EVM0004948 | PHI:2293|cycA|B0XTA5|746128|Aspergillus\_fumigatus|Reduced\_virulence |
| EVM0008574 | PHI:144|CHT42|AAC05829|29875|Trichoderma\_virens|Reduced\_virulence |
| EVM0005176 | PHI:2293|cycA|B0XTA5|746128|Aspergillus\_fumigatus|Reduced\_virulence |
| EVM0002621 | PHI:881|MGG\_04556|EDJ96020|318829|Magnaporthe\_oryzae|Reduced\_virulence |
| EVM0006427 | PHI:144|CHT42|AAC05829|29875|Trichoderma\_virens|Reduced\_virulence |
| EVM0004067 | PHI:323|VFGLU1|AAO63562|93591|Verticillium\_fungicola|Reduced\_virulence |
| EVM0003563 | PHI:144|CHT42|AAC05829|29875|Trichoderma\_virens|Reduced\_virulence |
| EVM0001189 | PHI:267|MLT1|AAD51594|5476|Candida\_albicans|Reduced\_virulence |
| EVM0003856 | PHI:1564|GzOB004|Q4IPZ1|5518|Gibberella\_zeae\_(related:\_Fusarium\_graminearum)|Unaffected\_pathogenicity |
| EVM0004435 | PHI:249|CYP1|AAG13968|318829|Magnaporthe\_oryzae|Reduced\_virulence |
| EVM0002609 | PHI:2488|Man1|G4ND25|148305|Magnaporthe\_oryzae\_(related:\_Magnaporthe\_grisea)|Unaffected\_pathogenicity |
| EVM0003992 | PHI:249|CYP1|AAG13968|318829|Magnaporthe\_oryzae|Reduced\_virulence |
| EVM0008226 | PHI:653|GIP2|AAL11721|67593|Phytophthora\_sojae|Effector\_(plant\_avirulence\_determinant) |
| EVM0006512 | C14DM|PHI:3258|Q4QGX0|5664|Leishmania\_major|reduced\_virulence\_ |
| EVM0002377 | PHI:144|CHT42|AAC05829|29875|Trichoderma\_virens|Reduced\_virulence |
| EVM0000213 | PHI:1506|GzHOME001|I1RC01|5518|Gibberella\_zeae\_(related:\_Fusarium\_graminearum)|Unaffected\_pathogenicity |
| EVM0002403 | PHI:2081|Moatg15|MGG\_12828|148305|Magnaporthe\_oryzae\_(related:\_Magnaporthe\_grisea)|Loss\_of\_pathogenicity |
| EVM0003064 | PHI:267|MLT1|AAD51594|5476|Candida\_albicans|Reduced\_virulence |
| EVM0008611 | PHI:397|LAC2|AAV64894|5207|Cryptococcus\_neoformans|Unaffected\_pathogenicity |
| EVM0000693 | GGT|PHI:3146|O25743|210|Helicobacter\_pylori|unaffected\_pathogenicity\_ |
| EVM0008849 | PHI:2117|SPM1|P58371|148305|Magnaporthe\_oryzae\_(related:\_Magnaporthe\_grisea)|Reduced\_virulence |
| EVM0001903 | PHI:432|FGL1|AAQ23181|5518|Fusarium\_graminearum|Reduced\_virulence |
| EVM0006554 | PHI:2644|thioredoxin\_1|P0AA28|90371|Salmonella\_enterica\_serovar\_Typhimurium|Reduced\_virulence |
| EVM0001722 | PHI:432|FGL1|AAQ23181|5518|Fusarium\_graminearum|Reduced\_virulence |
| EVM0003767 | PHI:2482|AlHK1|Q09JB7|160389|Alternaria\_longipes|Increased\_virulence\_(Hypervirulence) |
| EVM0006123 | PHI:2128|MoHox1|MGG\_04853|148305|Magnaporthe\_oryzae\_(related:\_Magnaporthe\_grisea)|reduced\_virulence |
| EVM0007566 | PHI:2533|FKS1|Q4WLT4|746128|Aspergillus\_fumigatus|Lethal |
| EVM0002356 | PHI:1494|MAT1-1-3|I1RX41|5518|Gibberella\_zeae\_(related:\_Fusarium\_graminearum)|Unaffected\_pathogenicity |
| EVM0003636 | PHI:811|MGG\_10510|EDK06580|318829|Magnaporthe\_oryzae|Reduced\_virulence |
| EVM0008542 | PHI:2545|TIF35|Q4X1I3|746128|Aspergillus\_fumigatus|Mixed\_outcome |
| EVM0001357 | PHI:440|PMR1|CAB87245|5476|Candida\_albicans|Reduced\_virulence |
| EVM0003013 | PHI:2128|MoHox1|MGG\_04853|148305|Magnaporthe\_oryzae\_(related:\_Magnaporthe\_grisea)|reduced\_virulence |
| EVM0008015 | PHI:1161|MgMfs1|A4ZGP3|54734|Mycosphaerella\_graminicola\_(related:\_Zymoseptoria\_triticii)|Chemistry\_target |
| EVM0009816 | PHI:2510|msdS/AfmsdC|Q6PWQ1|746128|Aspergillus\_fumigatus|Unaffected\_pathogenicity |
| EVM0003166 | PHI:652|GIP1|AAL11720|67593|Phytophthora\_sojae|Effector\_(plant\_avirulence\_determinant) |
| EVM0009054 | ssp|PHI:3418|Q5DPX0|29385|Staphylococcus\_saprophyticus|mixed\_outcome\_ |
| EVM0003445 | PHI:1052|PHL1|ACB38886|135779|Cercospora\_zeae-maydis|Unaffected\_pathogenicity |
| EVM0002682 | PHI:2400|Fgp2|I1S215|5518|Gibberella\_zeae\_(related:\_Fusarium\_graminearum)|Unaffected\_pathogenicity |
| EVM0002472 | PHI:2533|FKS1|Q4WLT4|746128|Aspergillus\_fumigatus|Lethal |
| EVM0001087 | PHI:2039|Con7p|Q069J4|148305|Magnaporthe\_oryzae\_(related:\_Magnaporthe\_grisea)|Loss\_of\_pathogenicity |
| EVM0005001 | Vsp|PHI:3018|B7VSJ8|212663|Vibrio\_splendidus|reduced\_virulence\_ |
| EVM0000484 | PHI:2533|FKS1|Q4WLT4|746128|Aspergillus\_fumigatus|Lethal |
| EVM0007607 | PHI:1816|GzZC131|I1RRS3|5518|Gibberella\_zeae\_(related:\_Fusarium\_graminearum)|Unaffected\_pathogenicity |
| EVM0006745 | PHI:2272|CpkB|A9Z1V6|13684|Phaeosphaeria\_nodorum\_(related:\_Stagonospora\_nodorum)|Unaffected\_pathogenicity |
| EVM0004713 | Pop1|PHI:3209|A4KTQ9|312341|Ceratocystis\_populicola|reduced\_virulence\_ |
| EVM0002111 | PHI:816|MGG\_04582|EDJ95999|318829|Magnaporthe\_oryzae|Reduced\_virulence |
| EVM0008189 | PHI:811|MGG\_10510|EDK06580|318829|Magnaporthe\_oryzae|Reduced\_virulence |
| EVM0004224 | PHI:2533|FKS1|Q4WLT4|746128|Aspergillus\_fumigatus|Lethal |
| EVM0007154 | PHI:1301|GzbHLH002|I1RB45|5518|Gibberella\_zeae\_(related:\_Fusarium\_graminearum)|Unaffected\_pathogenicity |
| EVM0004161 | PHI:503|COX15|AAB64668|4932|Saccharomyces\_cerevisiae|Reduced\_virulence |
| EVM0002963 | PHI:1301|GzbHLH002|I1RB45|5518|Gibberella\_zeae\_(related:\_Fusarium\_graminearum)|Unaffected\_pathogenicity |
| EVM0001554 | PHI:438|BcBOT1\_(related:\_CND5)|AAQ16576|40559|Botrytis\_cinerea|Reduced\_virulence |
| EVM0009437 | PHI:1343|GzC2H003|I1RAF0|5518|Gibberella\_zeae\_(related:\_Fusarium\_graminearum)|Reduced\_virulence |
| EVM0000556 | PHI:881|MGG\_04556|EDJ96020|318829|Magnaporthe\_oryzae|Reduced\_virulence |
| EVM0007007 | PHI:871|MGG\_12656|EDK01997|318829|Magnaporthe\_oryzae|Reduced\_virulence |
| EVM0001764 | PHI:2533|FKS1|Q4WLT4|746128|Aspergillus\_fumigatus|Lethal |
| EVM0006956 | PHI:373|PLD1|EAK93902|5476|Candida\_albicans|Reduced\_virulence |
| EVM0004888 | PHI:2349|VE1\_(VEA)\_(velvet)|G8CYZ6|5518|Gibberella\_zeae\_(related:\_Fusarium\_graminearum)|Reduced\_virulence |
| EVM0005411 | PHI:881|MGG\_04556|EDJ96020|318829|Magnaporthe\_oryzae|Reduced\_virulence |
| EVM0000067 | PHI:881|MGG\_04556|EDJ96020|318829|Magnaporthe\_oryzae|Reduced\_virulence |
| EVM0004407 | PHI:2519|LYS9|Q4WQ27|746128|Aspergillus\_fumigatus|Lethal |
| EVM0005673 | PHI:1071|Gas1|CAF05793|5270|Ustilago\_maydis|Loss\_of\_pathogenicity |
| EVM0008273 | PHI:1541|GzFlbD|I1RE42|5518|Gibberella\_zeae\_(related:\_Fusarium\_graminearum)|Unaffected\_pathogenicity |
| EVM0009965 | PHI:871|MGG\_12656|EDK01997|318829|Magnaporthe\_oryzae|Reduced\_virulence |
| EVM0000925 | PHI:96|FAS2|AAA34345|5476|Candida\_albicans|Loss\_of\_pathogenicity |
| EVM0003286 | PHI:2544|PAB1|Q4WK03|746128|Aspergillus\_fumigatus|Mixed\_outcome |
| EVM0004950 | PHI:2038|Mir1|MGG\_02370|148305|Magnaporthe\_oryzae\_(related:\_Magnaporthe\_grisea)|Unaffected\_pathogenicity |
| EVM0009621 | PHI:601|orf48|AAL20303|216597|Salmonella\_enterica|Unaffected\_pathogenicity |
| EVM0001674 | PHI:96|FAS2|AAA34345|5476|Candida\_albicans|Loss\_of\_pathogenicity |
| EVM0007332 | PHI:2601|Oligopeptidase\_B|Q94795|5693|Trypanosoma\_cruzi|Reduced\_virulence |
| EVM0001689 | PHI:1506|GzHOME001|I1RC01|5518|Gibberella\_zeae\_(related:\_Fusarium\_graminearum)|Unaffected\_pathogenicity |
| EVM0005693 | PHI:274|USX1|AAM22494|5207|Cryptococcus\_neoformans|Loss\_of\_pathogenicity |
| EVM0001653 | PHI:2222|Sho1|XP\_759303|5270|Ustilago\_maydis|Mixed\_outcome |
| EVM0007042 | PHI:748|um00446|Not\_available|5270|Ustilago\_maydis|Unaffected\_pathogenicity |
| EVM0002020 | PHI:2644|thioredoxin\_1|P0AA28|90371|Salmonella\_enterica\_serovar\_Typhimurium|Reduced\_virulence |
| EVM0001805 | PHI:2117|SPM1|P58371|148305|Magnaporthe\_oryzae\_(related:\_Magnaporthe\_grisea)|Reduced\_virulence |
| EVM0002806 | PHI:1295|FgStuA|I1S0A8|5518|Gibberella\_zeae\_(related:\_Fusarium\_graminearum)|Reduced\_virulence |
| EVM0006840 | PHI:2490|MCA|E9B636|5665|Leishmania\_mexicana|Mixed\_outcome |
| EVM0010219 | FgERG3A|PHI:3035|I1RFM2|5518|Fusarium\_graminearum|reduced\_virulence\_ |
| EVM0003076 | PHI:2976|CgOPT1|C6ZRH8|29905|Colletotrichum\_gloeosporioides\_f.\_sp.\_aeschynomenes|Reduced\_virulence |
| EVM0005568 | PHI:2008|HST1|EDJ98541|148305|Magnaporthe\_oryzae\_(related:\_Magnaporthe\_grisea)|Unaffected\_pathogenicity |
| EVM0003561 | PHI:2109|CNB|MGG\_06933|148305|Magnaporthe\_oryzae\_(related:\_Magnaporthe\_grisea)|Mixed\_outcome |
| EVM0001631 | PHI:871|MGG\_12656|EDK01997|318829|Magnaporthe\_oryzae|Reduced\_virulence |
| EVM0007761 | PHI:2510|msdS/AfmsdC|Q6PWQ1|746128|Aspergillus\_fumigatus|Unaffected\_pathogenicity |
| EVM0000122 | Pop1|PHI:3209|A4KTQ9|312341|Ceratocystis\_populicola|reduced\_virulence\_ |
| EVM0003025 | PHI:2321|SidI|Q4WR83|746128|Aspergillus\_fumigatus|Reduced\_virulence |
| EVM0008744 | PHI:1180|(Sc\_Sat4)|I1RS32|5518|Gibberella\_zeae\_(related:\_Fusarium\_graminearum)|Reduced\_virulence |
| EVM0004653 | PHI:2038|Mir1|MGG\_02370|148305|Magnaporthe\_oryzae\_(related:\_Magnaporthe\_grisea)|Unaffected\_pathogenicity |
| EVM0005770 | PHI:419|CSH1|AAP93915|5476|Candida\_albicans|Reduced\_virulence |
| EVM0009772 | PHI:652|GIP1|AAL11720|67593|Phytophthora\_sojae|Effector\_(plant\_avirulence\_determinant) |
| EVM0010134 | PHI:2544|PAB1|Q4WK03|746128|Aspergillus\_fumigatus|Mixed\_outcome |
| EVM0001137 | PHI:96|FAS2|AAA34345|5476|Candida\_albicans|Loss\_of\_pathogenicity |
| EVM0000187 | PHI:2042|ABC3|Q3Y5V5|148305|Magnaporthe\_oryzae\_(related:\_Magnaporthe\_grisea)|Loss\_of\_pathogenicity |
| EVM0004080 | Pop1|PHI:3209|A4KTQ9|312341|Ceratocystis\_populicola|reduced\_virulence\_ |
| EVM0004025 | PHI:871|MGG\_12656|EDK01997|318829|Magnaporthe\_oryzae|Reduced\_virulence |
| EVM0008974 | PHI:2552|NOP4|Q4WNM3|746128|Aspergillus\_fumigatus|Mixed\_outcome |
| EVM0000205 | PHI:1742|GzZC057|I1S7H5|5518|Gibberella\_zeae\_(related:\_Fusarium\_graminearum)|Unaffected\_pathogenicity |
| EVM0007726 | PHI:748|um00446|Not\_available|5270|Ustilago\_maydis|Unaffected\_pathogenicity |
| EVM0003315 | PHI:2038|Mir1|MGG\_02370|148305|Magnaporthe\_oryzae\_(related:\_Magnaporthe\_grisea)|Unaffected\_pathogenicity |
| EVM0010224 | PHI:2643|CFAS|A4HTK3|5671|Leishmania\_infantum|Reduced\_virulence |
| EVM0010061 | PHI:1255|FGSG\_07745|I1RQ67|5518|Gibberella\_zeae\_(related:\_Fusarium\_graminearum)|Unaffected\_pathogenicity |
| EVM0006879 | PHI:438|BcBOT1\_(related:\_CND5)|AAQ16576|40559|Botrytis\_cinerea|Reduced\_virulence |
| EVM0008470 | PHI:2158|MoCMK1|EU\_984498|148305|Magnaporthe\_oryzae\_(related:\_Magnaporthe\_grisea)|Reduced\_virulence |
| EVM0000351 | PHI:871|MGG\_12656|EDK01997|318829|Magnaporthe\_oryzae|Reduced\_virulence |
| EVM0007277 | PHI:174|GNA1|BAA36496|5476|Candida\_albicans|Reduced\_virulence |
| EVM0001968 | PHI:2510|msdS/AfmsdC|Q6PWQ1|746128|Aspergillus\_fumigatus|Unaffected\_pathogenicity |
| EVM0000750 | Atf1|PHI:3808|I1S0C0|5518|Fusarium\_graminearum\_(related:\_Gibberella\_zeae)|effector\_(plant\_avirulence\_determinant) |
| EVM0000062 | PHI:2930|ctf2|J9MFF7|59765|Fusarium\_oxysporum\_f.\_sp.\_Lycopersici|Reduced\_virulence |
| EVM0008877 | PHI:1255|FGSG\_07745|I1RQ67|5518|Gibberella\_zeae\_(related:\_Fusarium\_graminearum)|Unaffected\_pathogenicity |
| EVM0004058 | PHI:2042|ABC3|Q3Y5V5|148305|Magnaporthe\_oryzae\_(related:\_Magnaporthe\_grisea)|Loss\_of\_pathogenicity |
| EVM0002444 | PHI:2644|thioredoxin\_1|P0AA28|90371|Salmonella\_enterica\_serovar\_Typhimurium|Reduced\_virulence |
| EVM0004514 | PHI:33|PHR1|AAA68196|5476|Candida\_albicans|Reduced\_virulence |

\*DEGs were significantly upregulated in both S vs. pre-S and S vs. post-S.

**T****able S8 Differential expression of selected genes related to secondary metabolite biosynthesis, transport, and catabolism during conidiation.**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Internal ID** | **FPKM\*** | | |  | **Log2(FC)** † | |  | **PHI** |
| **Pre-C** | **C** | **Post-C** |  | **C vs. pre-C** | **C vs. post-C** |  |
| **ABC transporter** | |  |  |  |  |  |  |  |
| EVM0003125 | 0.00 | 3.00 | 0.00 |  | 6.51 | 7.05 |  | PHI:2042 |
| EVM0004058 | 5.71 | 11.80 | 5.54 |  | 1.08 | 1.36 |  | PHI:2042 |
| EVM0000187 | 9.02 | 20.94 | 8.40 |  | 1.26 | 1.59 |  | PHI:2042 |
| EVM0003276 | 0.48 | 3.21 | 0.46 |  | 2.74 | 3.05 |  | PHI:2042 |
| EVM0003064 | 35.03 | 189.63 | 16.33 |  | 2.47 | 3.80 |  | PHI:267 |
| EVM0001189 | 34.69 | 210.88 | 36.30 |  | 2.64 | 2.80 |  | PHI:267 |
| **Alcohol dehydrogenase GroES-like** | | | |  |  |  |  |  |
| EVM0001555 | 0.21 | 2.13 | 0.03 |  | 3.10 | 5.26 |  | PHI:881 |
| EVM0002621 | 0.30 | 2.22 | 0.10 |  | 2.68 | 4.23 |  | PHI:881 |
| EVM0000556 | 0.49 | 1.78 | 0.06 |  | 1.80 | 4.61 |  | PHI:881 |
| EVM0000067 | 0.31 | 1.06 | 0.02 |  | 1.72 | 4.86 |  | PHI:881 |
| EVM0005411 | 1.27 | 4.32 | 0.44 |  | 1.72 | 3.31 |  | PHI:881 |
| **Cytochrome P450** | |  |  |  |  |  |  |  |
| EVM0003715 | 0.08 | 3.17 | 0.42 |  | 4.84 | 3.10 |  | PHI:2357 |
| EVM0002185 | 0.04 | 73.62 | 4.56 |  | 6.53 | 4.22 |  | PHI:4194 |
| EVM0006879 | 10.31 | 22.53 | 9.59 |  | 1.16 | 1.49 |  | PHI:438 |
| Co\_147 | 6.23 | 12.54 | 6.30 |  | 1.06 | 1.26 |  | / |
| EVM0009502 | 0.02 | 3.72 | 0.33 |  | 6.30 | 3.43 |  | PHI:438 |
| EVM0001327 | 0.03 | 1.65 | 0.17 |  | 4.48 | 3.19 |  | PHI:4194 |
| EVM0004394 | 0.04 | 14.15 | 2.03 |  | 7.69 | 3.01 |  | PHI:4194 |
| EVM0009549 | 0.08 | 10.82 | 3.89 |  | 6.73 | 1.73 |  | PHI:4194 |
| EVM0001554 | 18.15 | 64.35 | 27.86 |  | 1.86 | 1.48 |  | PHI:438 |
| Co\_423 | 0.03 | 1.76 | 0.14 |  | 4.97 | 3.49 |  | / |
| EVM0005592 | 0.28 | 3.49 | 0.52 |  | 3.46 | 2.88 |  | PHI:4194 |
| EVM0002960 | 0.27 | 13.76 | 6.94 |  | 5.49 | 1.25 |  | PHI:4194 |
| EVM0003421 | 0.00 | 12.09 | 0.08 |  | 8.77 | 6.96 |  | PHI:4194 |
| EVM0004379 | 0.00 | 3.30 | 0.24 |  | 7.10 | 3.77 |  | PHI:4194 |
| EVM0004814 | 14.66 | 103.77 | 31.34 |  | 2.84 | 1.98 |  | PHI:2534 |
| Co\_207 | 0.07 | 1.37 | 0.44 |  | 2.72 | 1.49 |  | / |
| **Multicopper oxidase** | |  |  |  |  |  |  |  |
| EVM0004492 | 0.13 | 14.31 | 0.52 |  | 6.28 | 4.77 |  | PHI:397 |
| EVM0008611 | 0.34 | 1.85 | 0.68 |  | 2.40 | 1.68 |  | PHI:397 |
| EVM0005600 | 0.53 | 7.57 | 0.41 |  | 3.73 | 4.37 |  | PHI:2920 |

\* The transcript level is expressed as fragments per kilobase per million mapped reads (FPKM).

† FC is the fold change (FC) of DEGs based on a FC of ≥ 2 and an FDR of < 0.01.

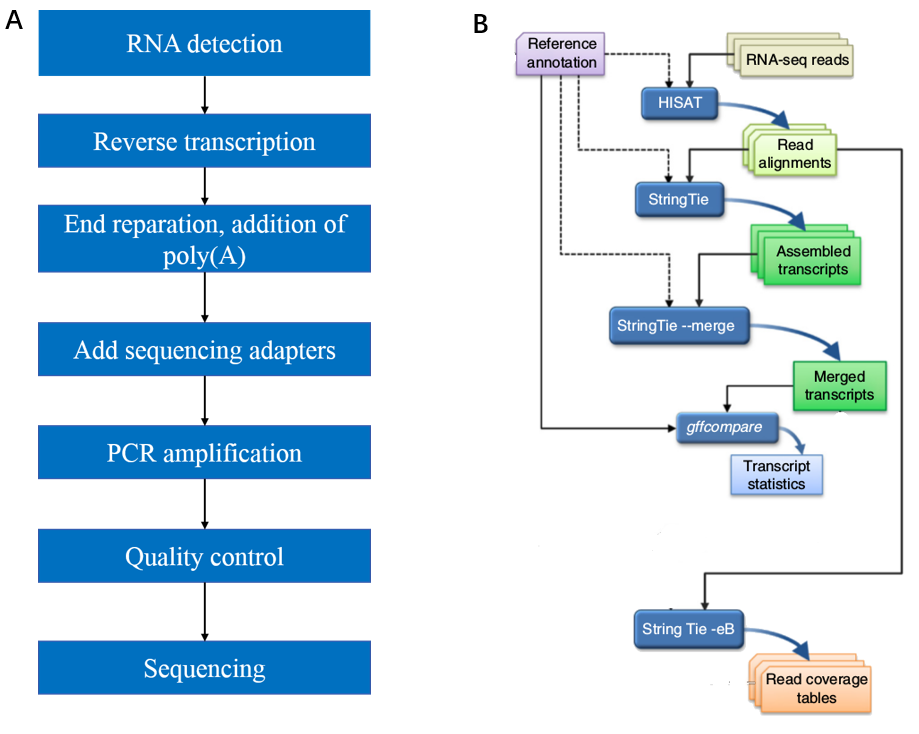


Fig S1 mRNA sequencing experimental pineline (A) and the workflow of transcript assembly and statistics (B).

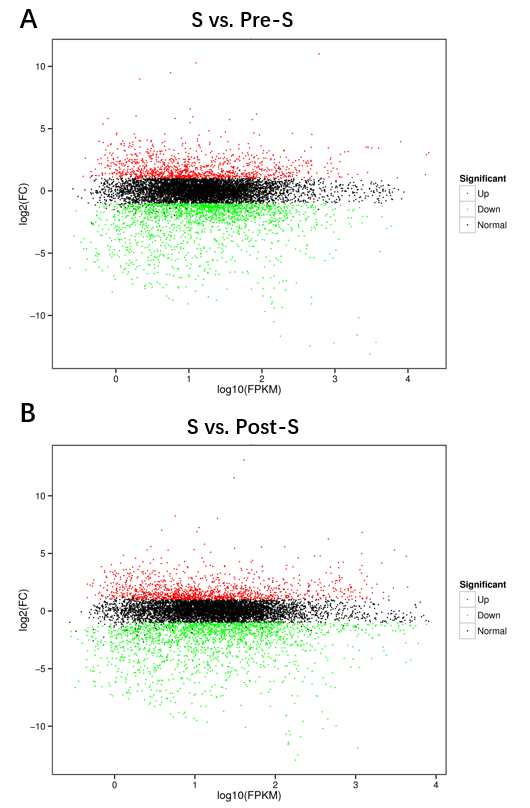


Figure S2 the MA plots of DEGs in C vs. Pre-C and C vs. Post-C.

Fig S3. Transcription factor families

