**Supplementary Materials**

**Table SI.** NCBI Accession number of the genes used in phylogenetic analyses**.**

| Species | *tubß* | *cam* | *rpb2* | ITS |
|---|---|---|---|---|
| *Aspergillus creber* | JN853980 | JN854043 | JN853832 | JQ301889 |
| *A. puulaauensis* | JN853979 | JN854034 | JN853823 | JQ301893 |
| *A. tennesseensis* | JN853976 | JN854017 | JN853806 | JQ301895 |
| *A.cvjetkovicii* | EF652264 | EF652352 | EF652176 | EF652440 |
| *A. jensenii* | JN854007 | JN854046 | JN853835 | JQ301892 |
| *A. venenatus* | JN854003 | JN854014 | JN853803 | JQ301896 |
| *A. versicolor* | EF652266 | EF652354 | EF652178 | EF652442 |
| *A. fructus* | EF652273 | EF652361 | EF652185 | EF652449 |
| *A. tabacinus* | EF652302 | EF652390 | EF652214 | EF652478 |
| *A. amoenus* | JN853946 | JN854035 | JN853824 | EF652480 |
| *A. austroafricanus* | JN853963 | JN854025 | JN853814 | JQ301891 |
| *A. protuberus* | EF652284 | EF652372 | EF652196 | EF652460 |
| *A. subversicolor* | JN853970 | JN854010 | JN853799 | JQ301894 |
| *A. multicolor* | EF652301 | EF652389 | EF652213 | EF652477 |
| *A. nidulans* | EF652251 | EF652339 | EF652163 | EF652427 |
| *A. sydowii* NRRL 250 Reference | EF652274 | EF652362 | EF652186 | EF652450 |
| *A. sydowii* CBS59365 | EF428373 | EU443971 | NA | AB267812 |
| *A. sydowii* NRRL 5585 | JN853936 | JN854039 | JN853828 | NA |
| *A. sydowii* NRRL 4768 | JN853935 | EF652385 | EF652209 | EF652473 |
| *A. sydowii* NRRL 254 | EF652275 | EF652363 | EF652187 | EF652451 |
| *A. sydowii* PW3168 | LC000553 | LC000566 | LC000579 | AB987908 |
| *A. sydowii* PW3048 | LC000545 | LC000558 | LC000571 | AB987900 |
| *A. sydowii* AC4807 | KJ413350 | NA | KJ476438 | KJ413376 |
| *A. sydowii* PW3037 | LC000544 | LC000557 | LC000570 | AB987899 |

**Table S2.** Parameters for Maximum likelihood trees using PhyML-SMS

| Loci | Substitution model | Log-likelihood | Discrete gamma model | Number of categories | Gamma shape parameter | G-Blocks? |
|---|---|---|---|---|---|---|
| *tubß* | HKY85 | -1198.70048 | Yes | 4 | 0.331 | Yes |
| *cam* | TN93 | -2613.55927 | | | 0.35 | No |
| *rpb2* | TN93 | -3494.24192 | | | 0.215 | No |
| Concatenated alignment based on 4 loci (*tubß*, *cam*, *rpb2* and ITS) | TN93 | -10563.49438 | | | 0.685 | - |

**Table S3.** Primer and PCR conditions used in this study.

| Gene/Marker | Primer name | Sequence | Length (nt) | Tm(°C) | Th(°C) | Conc. (nM) | Purpose |
|---|---|---|---|---|---|---|---|
| *ITS* | ITS1 | TCCGTAGGTGAACCTGCGG | 19 | 63 | 55 | 200 | Phylogeny marker |
| | ITS4 | TCCTCCGCTTATTGATATGC | 20 | 54 | | 200 | |
| *rpb2* | RPB2-5F | GAYGAYMGWGATCAYTTYGG | 20 | 47-61 | 55 | 200 | Phylogeny marker |
| | RPB2-7CR | CCCATRGCTTGYTTRCCCAT | 20 | 55-65 | | 200 | |
| *benA* | Bt2a | GGTAACCAAATCGGTGCTGCTTTC | 24 | 62 | 55 | 200 | Phylogeny marker |
| | Bt2b | ACCCTCAGTGTAGTGACCCTTGGC | 24 | 66 | | 200 | |
| *cam* | CMD5 | CCGAGTACAAGGARGCCTTC | 20 | 58-61 | 55 | 200 | Phylogeny marker |
| | CMD6 | CCGATRGAGGTCATRACGTGG | 21 | 57-64 | | 200 | |
| *sarA* | Fw_qPCR_sar1 | GTTGCGATCCTTTCTCCTACC | 21 | 56 | 63 | 500 | qPCR reference gene |
| | Rv_qPCR_sar1 | ACAATTCCGCTAACTTCAGGG | 21 | 56 | | 500 | |
| *cox5* | Fw_qPCR_cox5 | TCTCTGTCGGCGTTTTCTAC | 20 | 55 | 63 | 700 | qPCR reference gene |
| | Rv_qPCR_cox5 | AGAGCGTATTCGTTGGTAGC | 20 | 56 | | 700 | |
| *sih1* | Fw_qPCR_sih1 | CGTCGATGCTGATGTTCTTAAC | 22 | 55 | 63 | 700 | qPCR |
| | Rv_qPCR_sih1 | ACGGGAATGCAAGGGATG | 18 | 56 | | 700 | |
| *sih2* | Fw_qPCR_sih2 | TGTCGGAAACACTGGTAACAG | 21 | 56 | 65 | 500 | qPCR |
| | Rv_qPCR_sih2 | GTGACCTCGTTACAGCAAGAG | 21 | 56 | | 500 | |
| *sih4* | Fw_qPCR_sih4 | GAGGAAACCCAAGAGTACGAC | 21 | 55 | 63 | 700 | qPCR |
| | Rv_qPCR_sih4 | TGTTGCCTCCGATAAGGTTG | 20 | 56 | | 700 | |
| *hog1* | Fw_qPCR_hog1 | TCGAGGTAGACATCTGGAGTG | 21 | 56 | 63 | 700 | qPCR |
| | Rv_qPCR_hog1 | ACTGGTTAACGTGGTCTTTCC | 21 | 56 | | 700 | |
| *sih4* | Fw_sih4 | ATAGAATTCGAGCAGAAACTCATC-> TCTGAAGAGGATCTGATCGAAGGT-> CGTATGCCTTCCTCCGAGCAGGCC | 72 | 79 | 58 | 200 | *sih4* cds cloning – Forward primer includes a c-myc tag and a Factor Xa cleavage site |
| | Rv_sih4 | ATTCTAGATTACTCCTCGGCCTCCTCGGTCT | 31 | 72 | | 200 | |

Abbreviations: **Tm** – Calculated Melting Temperature of primer, **Th** – Actual Annealing Temperature used in PCR, **Conc**. – Primer concentration in the assay.

**Figure S1.** Maximum likelihood phylograms based on their specific best substitution models. All the nodes with bootstrap support >50% are indicated at nodes with a circle. **Aspergillus sydowii* reference strain (Samson et al. 2014).

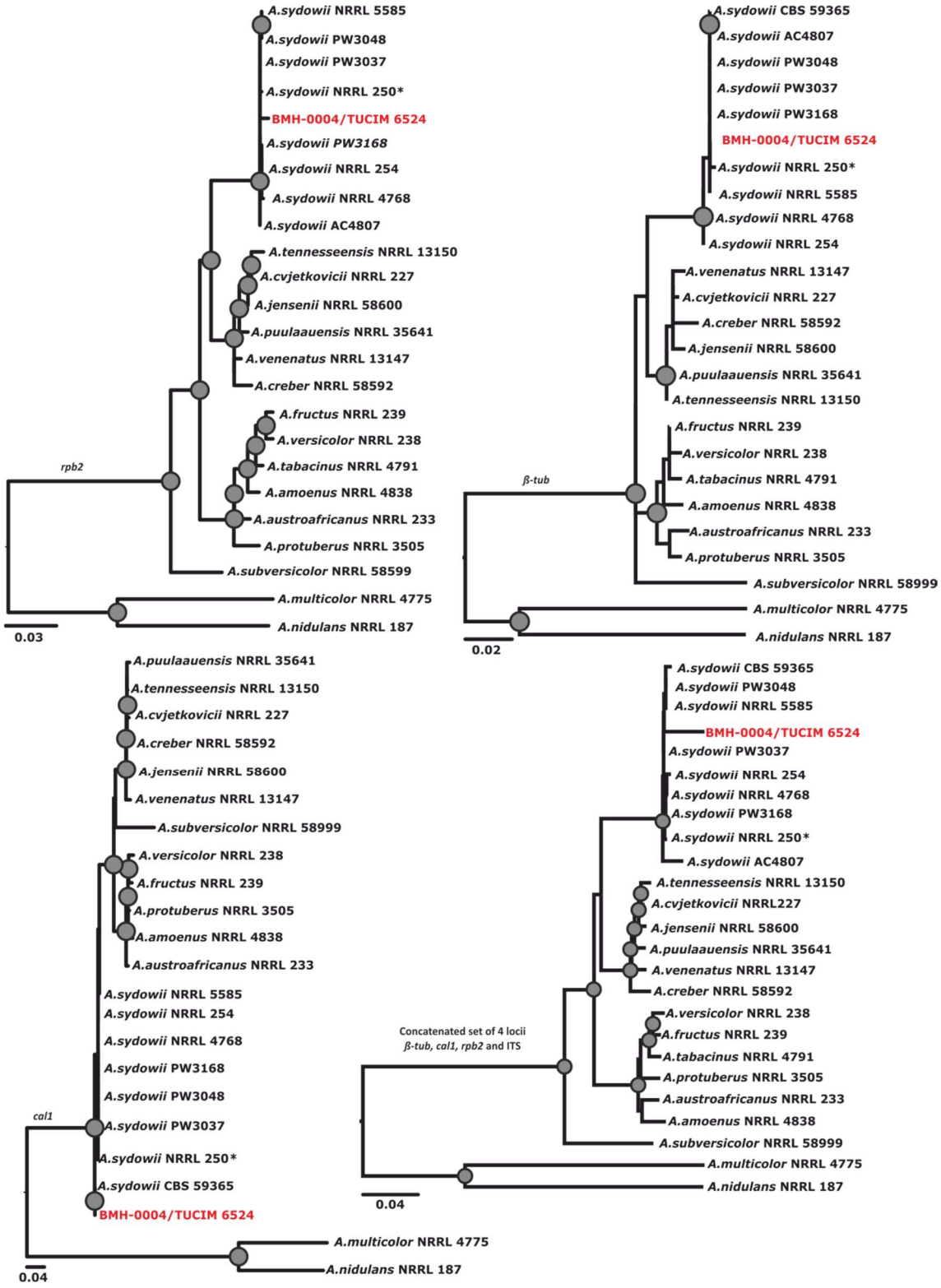

**Figure S2.** Effect of filtering out the transcripts with low read counts on gene expression profile and discrimination between experimental groups by unsupervised clustering (**a** and **b**) and on the identification of DE transcripts (**c**).