

Table S4. Sequenced transcript details regarding the core regulators of conidiation (*brlA*, *abaA*, *wetA*) and spore viability providing trehalose biosynthase (*tpsA*).

Gene	ORF length (bp)	Gene length (bp) ^a	Transcript length (bp) ^b	Number of exons (introns)	Residue identity (%) with <i>A. nidulans</i> ortholog ^c
<i>brlA</i>	NA	NA	NA	NA	75 ^d
<i>abaA</i>	2391	2491	5745 ^e	3 (2)	62
<i>wetA</i>	1632	1632	2700	-	61
<i>tpsA</i>	1542	1759	2435	5 (4)	90

^a based on the genomic region of strain NIH2624 between 5' and 3' of the corresponding gene

^b derived from the corresponding sequenced transcript of strain MUCL 38669, including sequenced up- and downstream regions with upstream introns if present

^c obtained by BLASTP analysis

^d the ID % is based on *brlA* annotation of strain NIH2624

^e sequenced transcript covers also ATEG_02626 gene of NIH2624 annotation
NA; not available for strain MUCL 38669