

Table S3. Genome characteristics and found Benchmarking Universal Single-Copy Orthologues (BUSCO) genes of the assembled *Aspergillus niger* strain CBS 554.65.

Genome	<i>A. niger</i> CBS 554.65
Assembly size (bp)	40,425,233
G+C content (%)	49.57
Scaffolds (≥ 0 bp)	17
Scaffolds (≥ 1000 bp)	17
Largest scaffold (bp)	6,394,477
N50 (bp)	4,067,305
L50 (scaffolds)	4
N's per 100 kbp	0.00
Complete BUSCO (%)	100.00
Partial BUSCO (%)	0.00

Table S4. Masked repetitive elements found with RepeatMasker v4.0.9 and tRNA genes found by tRNAscan-SE v1.3.1. *Most repeats that were fragmented by insertions or deletions have been counted as one element.

Masked element	Number of elements*	Length occupied in bp	Percentage of sequence
SINEs	16	1,147	-
LINEs	127	8,842	0.02%
LTR elements	4	281	-
DNA elements	52	3,841	0.01%
Small RNA	338	163,900	0.41%
Simple repeats	9,791	401,723	0.99%
Low complexity	1,694	90,392	0.22%
tRNA	277	23,237	0.06%