

(B)

ATGTCCTCCAACGAACCCCATCTCTGCTTCCGCTCCTTCGAAGCCCTCAAGGCAGACAACGACCTCGTCGGGATAAACGACCCCATTGAC ŢŢġĂĂġĊŢġĊĊġĊĊĂŢĊĸĊĠĊĠŢĊŢĠġĠĊŤġŢġĂġĂĂĂĊĠĂĊġĂġĂĂĂĂĠĊĂĊĊġĊŢġŢŢĊĬĂĊĂĂĊĊĂĊĊġĊġĊġĊċĊĸŎġĠ TCGCATCCTCGGTGCACCGGCCTCACAAAGAAAGTCTCAGAACGATATGGTCGTCTGGCGCGTCATCTGGCTCTTCCTCCAACG ададаттстӐдасаладатостобото собталадттоссоссодатоссобссадодото то собто TGAAGGCGAĊCAGATCGACĊTCACGAAGCTTCCGGTACCĊATGGTCCACÅAGTCTGATGĠCGGGGCTTAĊATCCAGACG GGC CCCCCGACGGCAAGTGGACGAACTGGTCCATTGCGCGTGCCATGGTGCATGATAAGAA <u>GAGCCCCAĞCATATCTGGČAGATCCACCĂGATGTGGAAĞAAGGAAAACĊĞCGATGTCCČCTGGGTTCTĂĞCGTTCGGCĞTCCCCC</u> CTATCATGGCGTCCAGCATGCCGATTC <u>ας σατάς σα αταττητης στης ς τος σα ας τος σα στο στος τος σα σα σα στο τος ας σα ας σα σα σα σα σα σα σα σα σ</u> <u>ϲϛΑΤGA</u>GCΤČGTGCGGCAAÂ<u>CTTACCGA</u>ŢĞAŖAC<u>GCATAČAATGA</u>T<u>CGGČTCCCTTGCCĞCTGCTG</u>AGAŤČCGCAAŖATČT<u>GTC</u>AGAAŖĞC<u>Ŗ</u>A 1,140 1,150 1,160 1,170 1,180 1 TGCCGGAAAATCGGCGACCTCATTTTTCAATCACAAAGCGGGATACACAATCCATC 210 1,220 1,230 1,240 1,250 1,260 1,270 1,270 1,280 1,290 GACATTGACGTTCACAACAATAAGGCTGTAATGTGGGGCGTTCAGCACGAGGTGCAAGCCTGGTGTGGACGAAGTGTTCTATGACGAC 1,400 1,410 1,420 1,430 1,440 1,450 1,450 1,460 1,460 1,470 1,480 A T G G A C A T C G G A G G A C G G G A A T T G G G A G G C T G C A G A T C C G G A G G C G T G A A T G T G C AATGGGAGAAA

(C)

A. niger_NRRL3 genome

A. nidulans FGSC A4 orignal prediction of AN3010 A. nidulans FGSC A4 corrected version of AN3010 A. nidulans AN3010 corrected A. niger cdcA Mutations 1 and 2 (deletion)

CDS

		· /				
	610	617	627	637	646	656
A. nidulans AN3010 corrected	GAAAACCGC	- GATGICCCC	W V L A	F G V	P - P A	A I M
A. niger cdcA	GAAGGCCGCAG	D V P	W A L A	F G V	PPA	A I M

Mutation 3 (insertion)

	1,13	6	1,1	46	1,156		1,166	1,17	;	1,186	
A. nidulans AN3010 corrected		R K		G GAC		F N		A G G G G A	Y T		C
A. niger cdcA	F R	AAGAGI K R	V V	GAGAC G D	GTCGTC V V	F - N		A G	Y T		C

	Mutation 4 (substitution)						
	46	1,456		1,466	1,476	1,486	1,500
A. nidulans AN3010 corrected	N G	S Y	P E		K S N	V L G	AATGGGAGAAA K W E K
A. niger cdcA	GATCIC D L	AAGCAG K Q	AAGG <mark>I</mark> O K V	L D	AACTGGAC	K M G	F S N *

Supplementary Figure 1. Exon/intron boundary analysis of Aspergillus nidulans cdcA (AN3010). A. RNAseq of A. nidulans was mapped against the A. nidulans FGSC A4 and revealed that the predicted exon/intron boundaries were incorrect. Based on the mapped reads, two genes are located in this region. On position 811.492 till 812.280 reads were mapped containing one intron, however no clear ORF was not found. RNAseg data was downloaded from the NCBI Sequence Read Archive (SRA) under the accession numbers SRR9166076 and SRR7500532. Data was analyzed with the galaxy data platform (https://usegalaxy.eu/). Quality of RNAseq data was determined by FastQC (http://www.bioinformatics.babraham.ac.uk/projects/ fastqc/) and reads were trimmed with Trimmomatic tool (http://www.usadellab.org/cms/index. php?page=trimmomatic). Reads were then mapped against the A. nidulans FGSC A4 genome with TopHat Gapped-read mapper, using 40 bp as minimum intron size. The A. nidulans and A. niger genomes were downloaded from JGI mycocosm (https://mycocosm.jgi.doe.gov/mycocosm/ home). Mapped reads were visualized with Jbrowse (Skinner et al., 2009). Forward reads are colored red and reverse reads are colored blue. B. Transcript sequence of AN3010 based on the intron exon boundaries of the mapped reads. The transcript contains several premature stops resulting in a truncated enzyme. C. AN3010 mapped against the cdcA from A. niger. In total four mutations were observed in the corrected AN3010 compared to *cdcA*. The first deletion results in non-sense mutation removing a serine while the second deletion results in a frame shift. The third mutations, an insertion of a thymine, also results in a frameshift. The fourth mutation is the substitution of a thymine to an adenine, replacing the stop codon with lysine.

Skinner, M. E., Uzilov, A. V., Stein, L. D., Mungall, C. J., and Holmes, I. H. (2009). JBrowse: a next-generation genome browser. Genome research, 19(9), 1630-1638.