

Deletion of the *celA* gene in *Aspergillus nidulans* triggers overexpression of secondary metabolite biosynthetic genes

Gea Guerriero^{1,*}, Lucia Silvestrini², Sylvain Legay¹, Frank Maixner³, Michael Sulyok⁴, Jean-Francois Hausman¹, Joseph Strauss^{2,*}

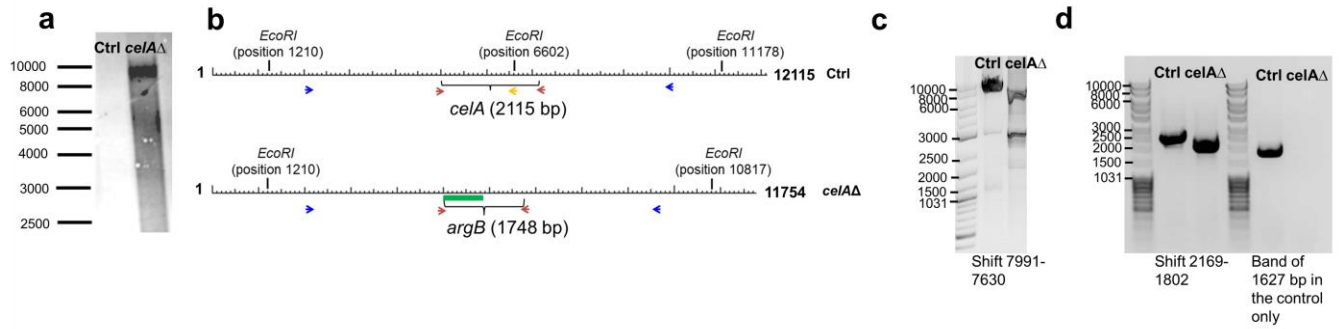
¹Luxembourg Institute of Science and Technology (LIST), Environmental Research and Innovation (ERIN) Department, Esch/Alzette, L-4362, Luxembourg.

²University of Natural Resources and Life Sciences Vienna (BOKU), Department of Applied Genetics and Cell Biology, Fungal Genetics and Genomics Unit, BOKU Campus Tulln/Donau, A-3430, Austria.

³European Academy of Bozen/Bolzano (EURAC), Institute for Mummies and the Iceman, Bolzano, 39100, Italy.

⁴University of Natural Resources and Life Sciences Vienna (BOKU), Department for Agrobiotechnology (IFA-Tulln), A-3430 Tulln, Austria.

*gea.guerriero@list.lu; joseph.strauss@boku.ac.at



Supplementary Figure 1. Molecular validation of *celAΔ*. a) Southern blotting (band size 9607 bp). b) *EcoRI* restriction map of the *celA* genomic region (+/- 5 kbps) with details of *celA* nested Fwd and *celA* nested Rev (in blue), *celA* diagnostic Fwd and *celA* diagnostic Rev (in red) and *celA* specific Rev (in yellow). The probe (815 bp) used for the Southern blotting (amplified with the primer pair *argchimera* Fwd and *arg* Southern Rev, Suppl. Information) is indicated in green. c) PCR on the control and *celAΔ* strain using primers *celA* nested Fwd and *celA* nested Rev. d) PCRs on the control and *celAΔ* strain using primers *celA* diagnostic Fwd and *celA* diagnostic Rev and *celA* diagnostic Fwd and *celA* specific Rev.