



Introducing COFUN: The first transcription factor knockout collection of filamentous fungal pathogens



Genome-wide knockout (KO) libraries have been used to great effect to establish an in depth understanding of microbial functional genomics.

COFUN aims to generate knockout mutants for all of the coding genes in the human pathogen *Aspergillus fumigatus*.

The first of these libraries consists of >400 transcription factor null mutants in the form of a panel, and is now available from NCPF.

The libraries can be used:

- to rapidly identify key genetic factors associated with your research interests
- validate the outputs from other genome-wide analysis
- identify mechanisms of drug resistance and tolerance
- to perform rapid quantitative parallel fitness analysis

Libraries of kinase and phosphatase knockout mutants will be made available soon.

www.phe-culturecollections.org.uk/COFUN

Contact us:

Culture Collections
Public Health England
Porton Down Salisbury
SP4 0JG
UK

Enquiries:

Tel: +44 (0)1980 612947
Email: CultureCollections.BusinessE@phe.gov.uk
Web: www.phe-culturecollections.org.uk/ncpf
Twitter: @TheNCPF