

Supplementary Material

Deciphering molecular determinants underlying *Penicillium digitatum* response to biological and chemical antifungal agents by Tandem Mass Tag (TMT)-based high-resolution LC-MS/MS

Lucía Citores^{1‡}, Mariangela Valletta^{2‡}, Vikram Pratap Singh², Paolo Vincenzo Pedone², Rosario Iglesias¹, José M. Ferreras¹, Angela Chambery^{§2*}, Rosita Russo^{§2*}

¹Department of Department of Biochemistry and Molecular Biology and Physiology, Faculty of Sciences, University of Valladolid, E-47011 Valladolid, Spain; lucia.citores@uva.es (L.C.); riglesia@bio.uva.es (R.I.); josemiguel.ferreras@uva.es (J.M.F.)

²Department of Environmental, Biological and Pharmaceutical Sciences and Technologies, University of Campania Luigi Vanvitelli, Caserta, Italy; mariangela.valletta@unicampania.it (M.V.); vikrampratap.singh@unicampania.it (V.P.S.); paolovincenzo.pedone@unicampania.it (P.V.P.); angela.chambery@unicampania.it (A.C.); rosita.russo@unicampania.it (R.R.)

*Correspondence: angela.chambery@unicampania.it; Tel.: +39 (0)823 274583; rosita.russo@unicampania.it; Tel.: +39 (0)823 274535;

‡ These authors share equal first authorship

§ These authors share equal senior authorship

Figure S1. Bar charts reporting the counts of peptide groups abundances versus CV% values for α -sarcin-, BE27- and TBZ - treated and untreated (CTR) *P. digitatum* samples.

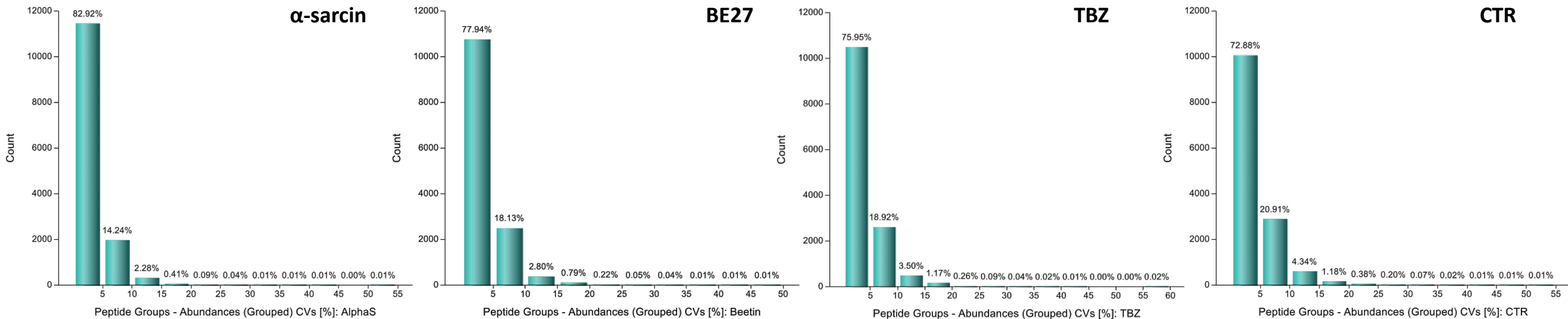


Figure S2. Volcano plots obtained from TMT-based quantitative proteomics analysis showing $-\text{Log}_{10}$ p-values versus Log_2 fold-change values of TBZ, BE27 and α -sarcin treatments in *P. digitatum* with respect to control (CTR). Plots are referred to unfiltered datasets. Identified proteins with no changes in their regulation levels are reported in grey. Up- and down-regulated proteins (fold change ≥ 1.5) are indicated in red and green, respectively.

