Supplementary information for:

Deciphering interactions between the marine dinoflagellate *Prorocentrum lima* and the fungus *Aspergillus pseudoglaucus*

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Table S1. Fungal strains isolated from *Prorocentrum lima* PL4V.

Isolated fungal strain	Medium for isolation	Time before fungal colony first observation
MMS1589 *Aspergillus pseudoglaucus*	Dextrose Casein	21 days
MMS1591 *Aspergillus* sp.	Dextrose Casein	29 days
MMS1593 *Penicillium* sp.	Malt Extract	27 days
MMS1594 *Aspergillus* sp.	Dextrose Casein	27 days
MMS1596 *Penicillium* sp.	Malt Extract	34 days

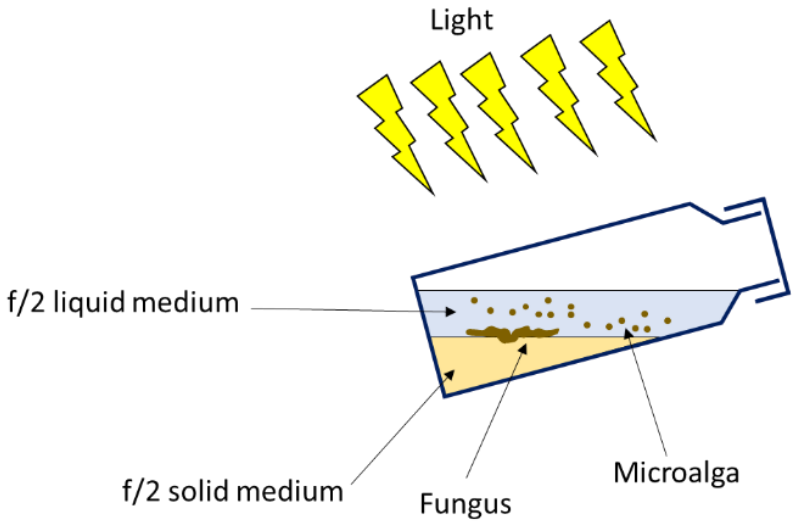


Figure S1. Scheme of the microscale environment designed for this study.

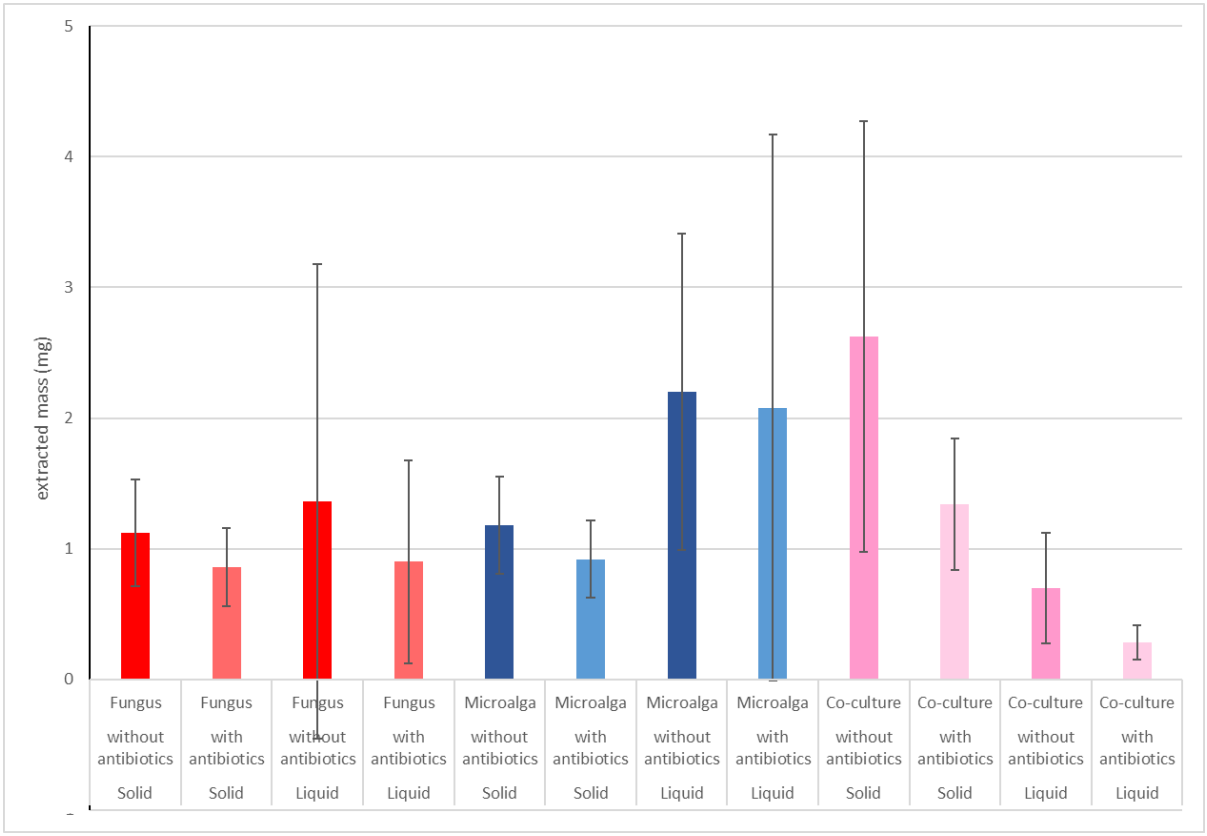


Figure S2. Amount of extract (with standard deviation) obtained in each culture conditions.

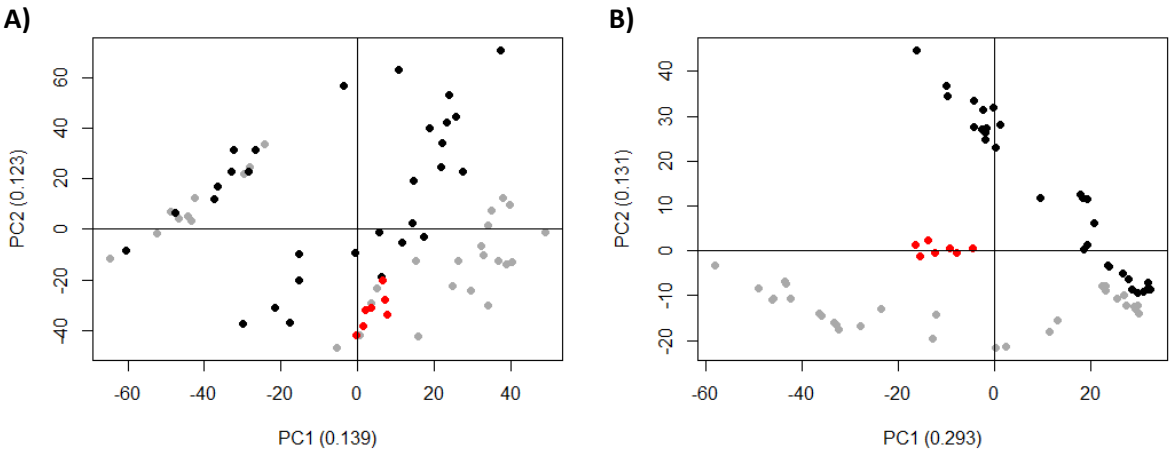


Figure S3. Principal component analysis (log transformed data with pareto scaling) using peaks detected in the LC-HRMS profiles in positive **(A)** negative **(B)** ionisation modes. QC samples, supernatant extract and solid phase extract are highlighted in red, black and grey, respectively.

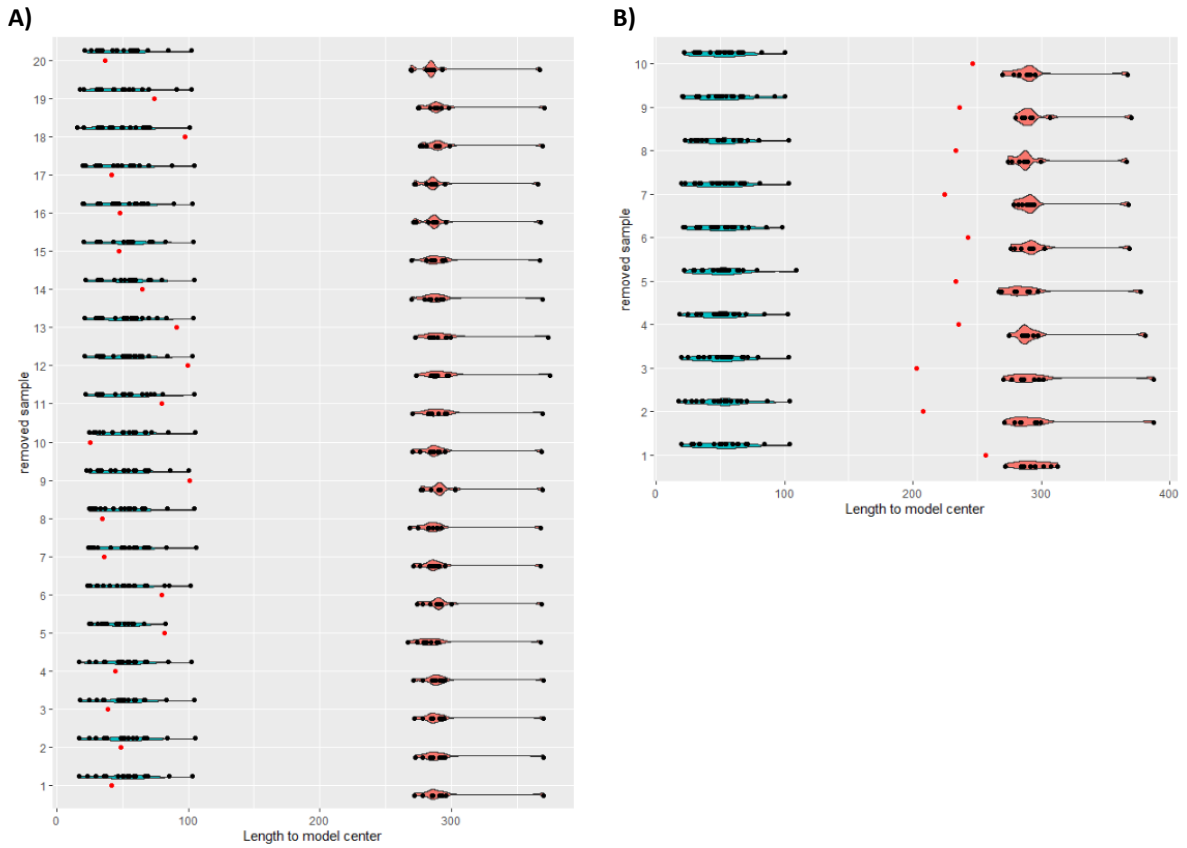


Figure S4. Validation of the POChEMon mixing model, using leave-one-out strategy, removing either a monoculture sample **(A**) or a co-culture sample (**B**). Sample distribution was represented as a violin plot (in blue: the monoculture sample distribution; in red the co-culture sample distribution). The removed sample was plotted back (red dot) within the generated model to highlight that no misclassification was observed.

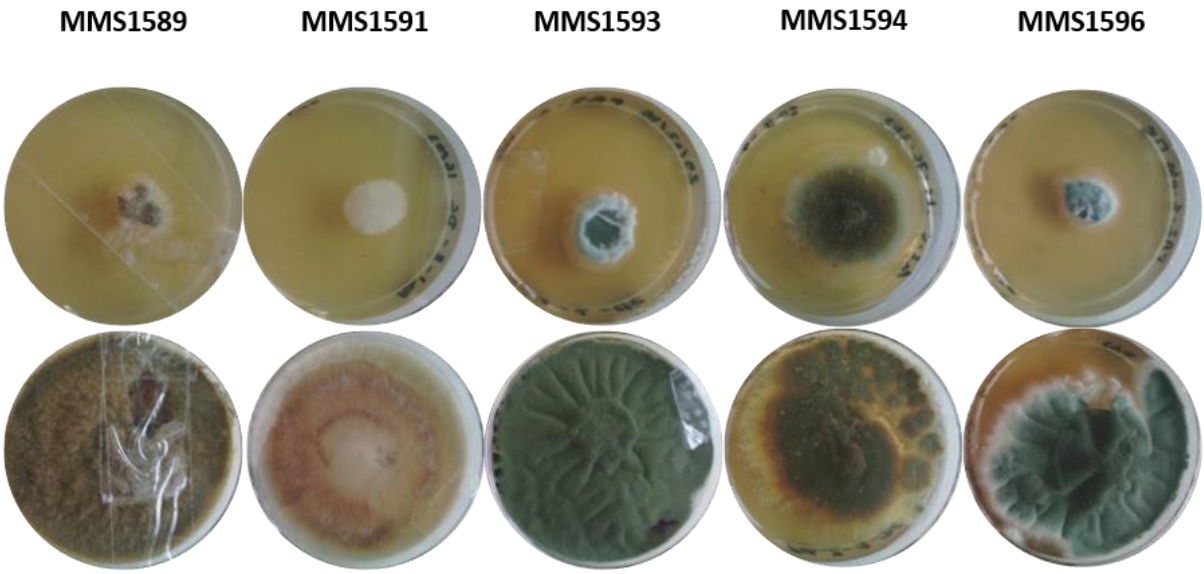


Figure S5. Morphology of fungal strains isolated from *Prorocentrum lima* PL4V after 3 days (top) after 10 days (bottom). The growth was performed in 5-cm Petri dishes.

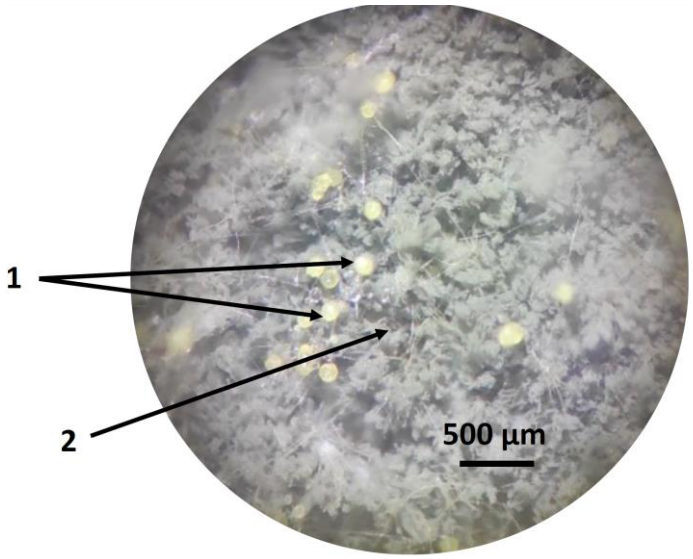
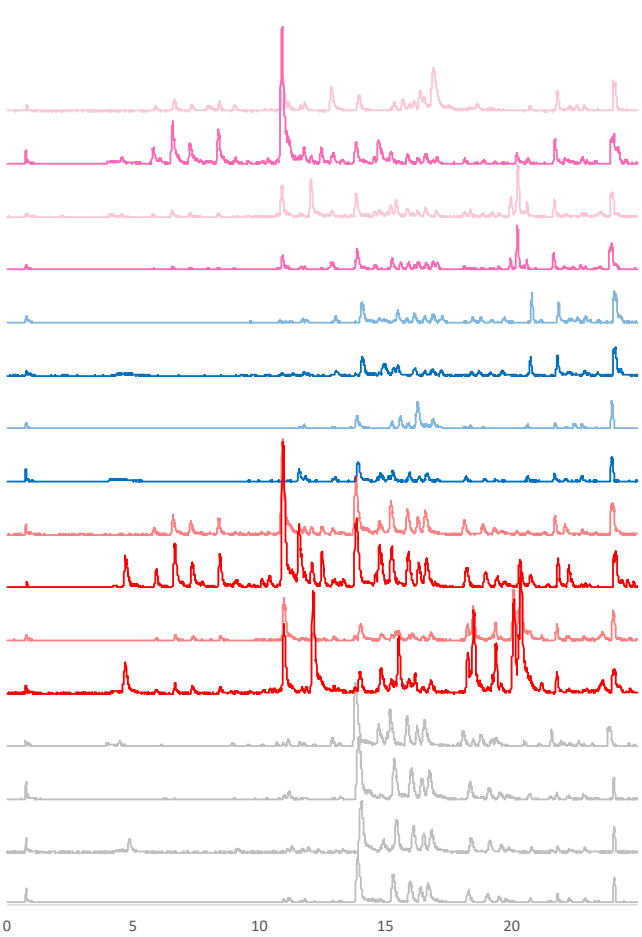
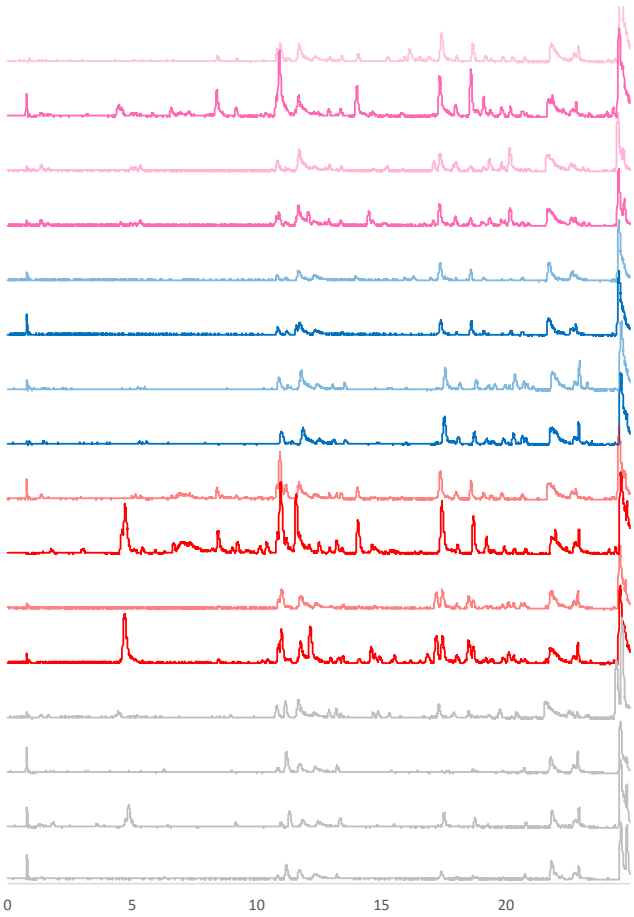


Figure S6. Morphology of *Aspergillus pseudoglaucus* MMS1589 (binocular view). Cleistothecia (**1**) and classic mycelium bearing conidiophores (**2**).



Culture	Antibiotics	Phase
Coculture	No	Supernatant
Coculture	Yes	Supernatant
Coculture	No	Solid phase
Coculture	Yes	Solid phase
Microalgae	No	Supernatant
Microalgae	Yes	Supernatant
Microalgae	No	Solid phase
Microalgae	Yes	Solid phase
Fungi	No	Supernatant
Fungi	Yes	Supernatant
Fungi	No	Solid phase
Fungi	Yes	Solid phase
Blank	Yes	Solid phase
Blank	No	Solid phase
Blank	Yes	Supernatant
Blank	No	Supernatant

Figure S7. LC-HRMS profiles in negative ionisation of extracts used for metabolomics (only one replicates is presented here). All extracts were profiled at 1 mg/ml concentration and chromatograms were all scaled (Y) to the same ion count intensity (inter-chromatogram Y-step corresponds to 84 000 counts).



Culture	Antibiotics	Phase
Coculture	No	Supernatant
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Microalgae	Yes	Supernatant
Microalgae	No	Solid phase
Microalgae	Yes	Solid phase
Fungi	No	Supernatant
Fungi	Yes	Supernatant
Fungi	No	Solid phase
Fungi	Yes	Solid phase
Blank	Yes	Solid phase
Blank	No	Solid phase
Blank	Yes	Supernatant
Blank	No	Supernatant

Figure S8. LC-HRMS profiles in positive ionisation of extracts used for metabolomics (only one replicates is presented here). All extracts were profiled at 1 mg/ml concentration and chromatograms were all scaled (Y) to the same ion count intensity (inter-chromatogram Y-step corresponds to 140 000 counts).

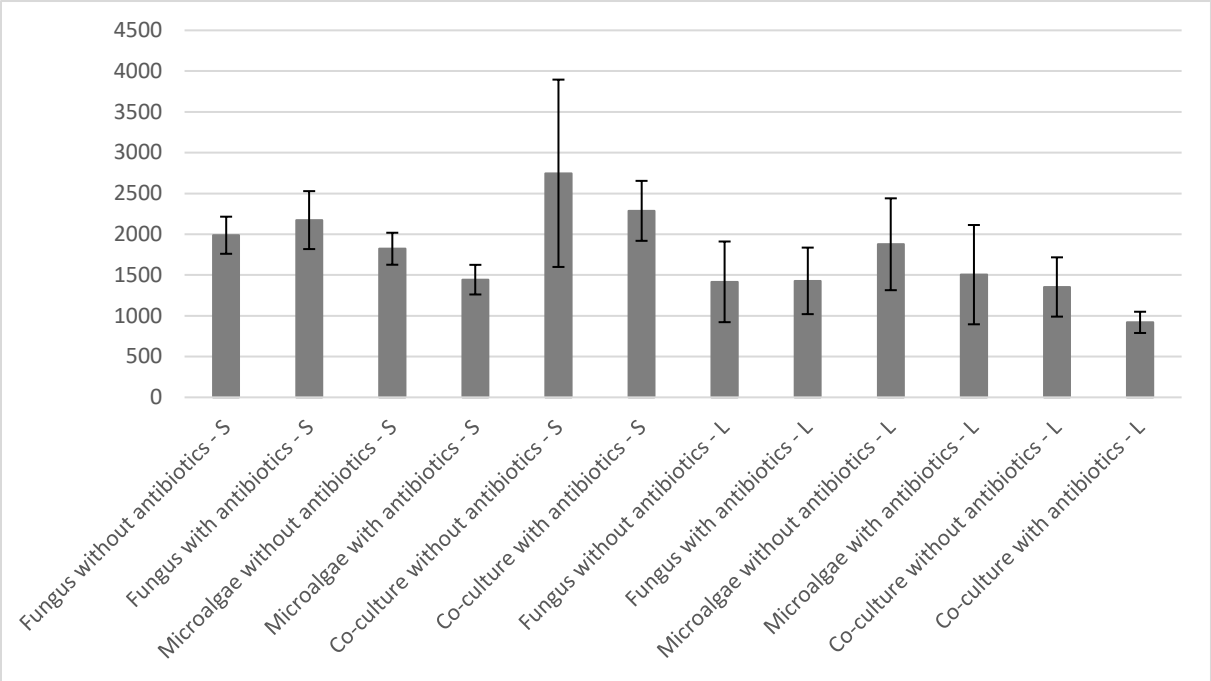

Figure S9. Number of detected features per conditions (mean +/- standard deviation), obtained with MZmine 2 processing of LC-HRMS data. S: solid phase extract, L: liquid extract.

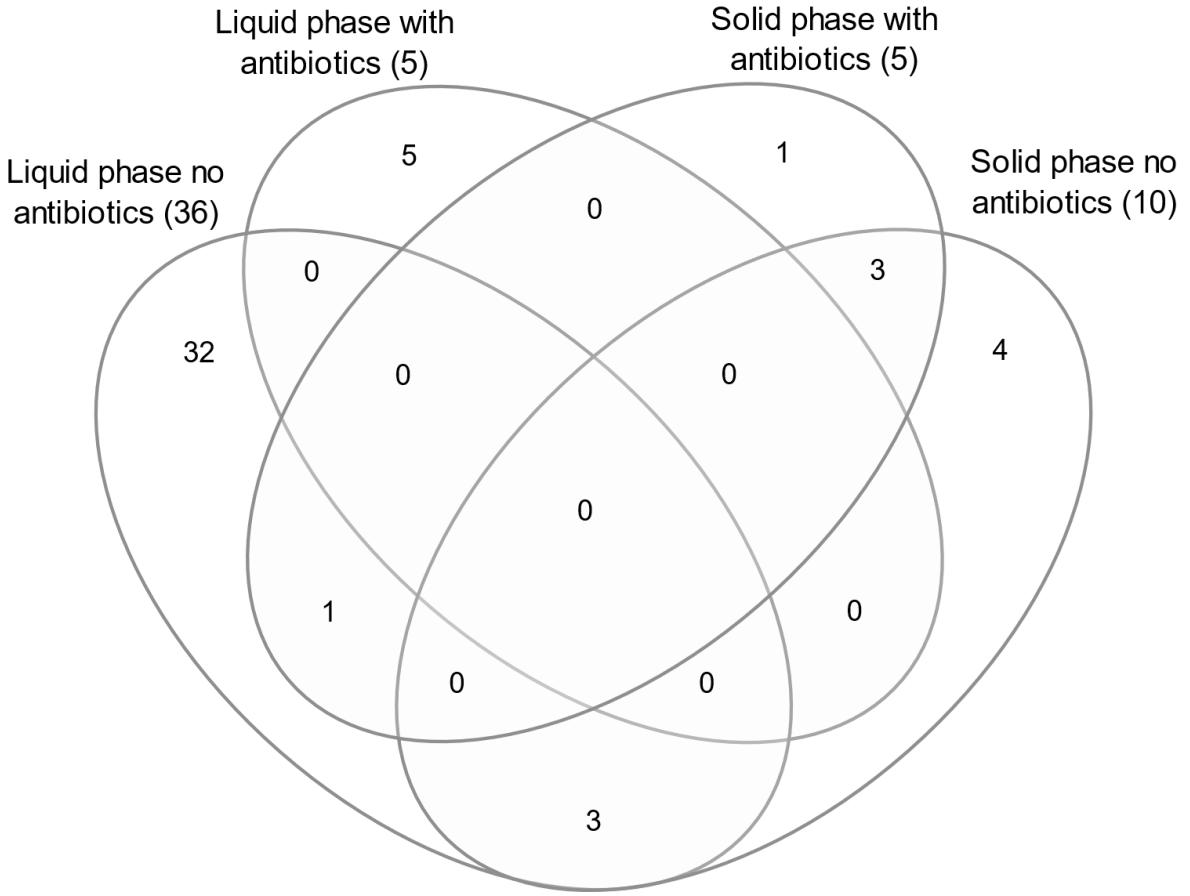

Figure S10. Venn Diagram [1] of feature distribution following origin (liquid or solid phase) and antibiotic (ATB) exposure using the selected top features according to the three different statistical treatments applied on the data matrix (highest significance in Student test, highest VIPs in the OPLS-DA, best SSrank values) and withdrawing of redundant selected features.

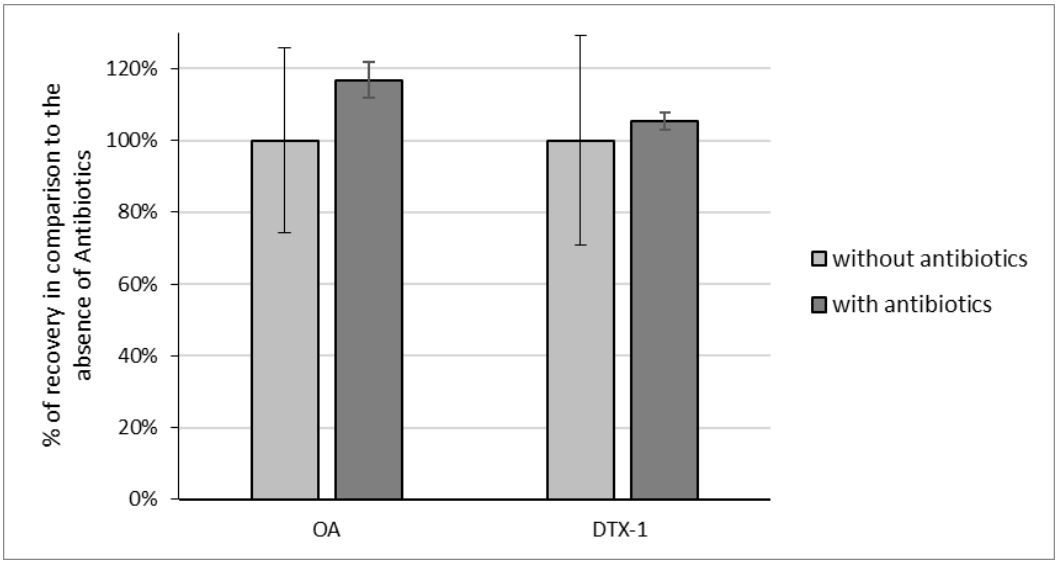

Figure S11. Recovery of okadaic acid (OA) and dinophysistoxin 1 (DTX-1) after addition to blank samples (with and without antibiotics) showing the absence of extraction bias due to the presence of the antibiotic cocktail.

References

1. Heberle H, Meirelles GV, da Silva FR, Telles GP, Minghim R. InteractiVenn: a web-based tool for the analysis of sets through Venn diagrams. *BMC Bioinformatics* 2015; **16**: 169.