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641 **Supplementary Fig. S1.** The parameter “Maximum Height” estimated from the respiration
642 curves as measured with the OmniLog phenotyping device and discretized and visualized as
643 heatmap using the `opm` package. Plates and substrates are rearranged according to their
644 overall similarity (as depicted using the row and column dendrograms). Ochre colour
645 indicates positive reaction; blue colour indicates negative reaction; white colour indicates
646 ambiguous reaction. Letters (A/B) indicate each replicate of experiment.

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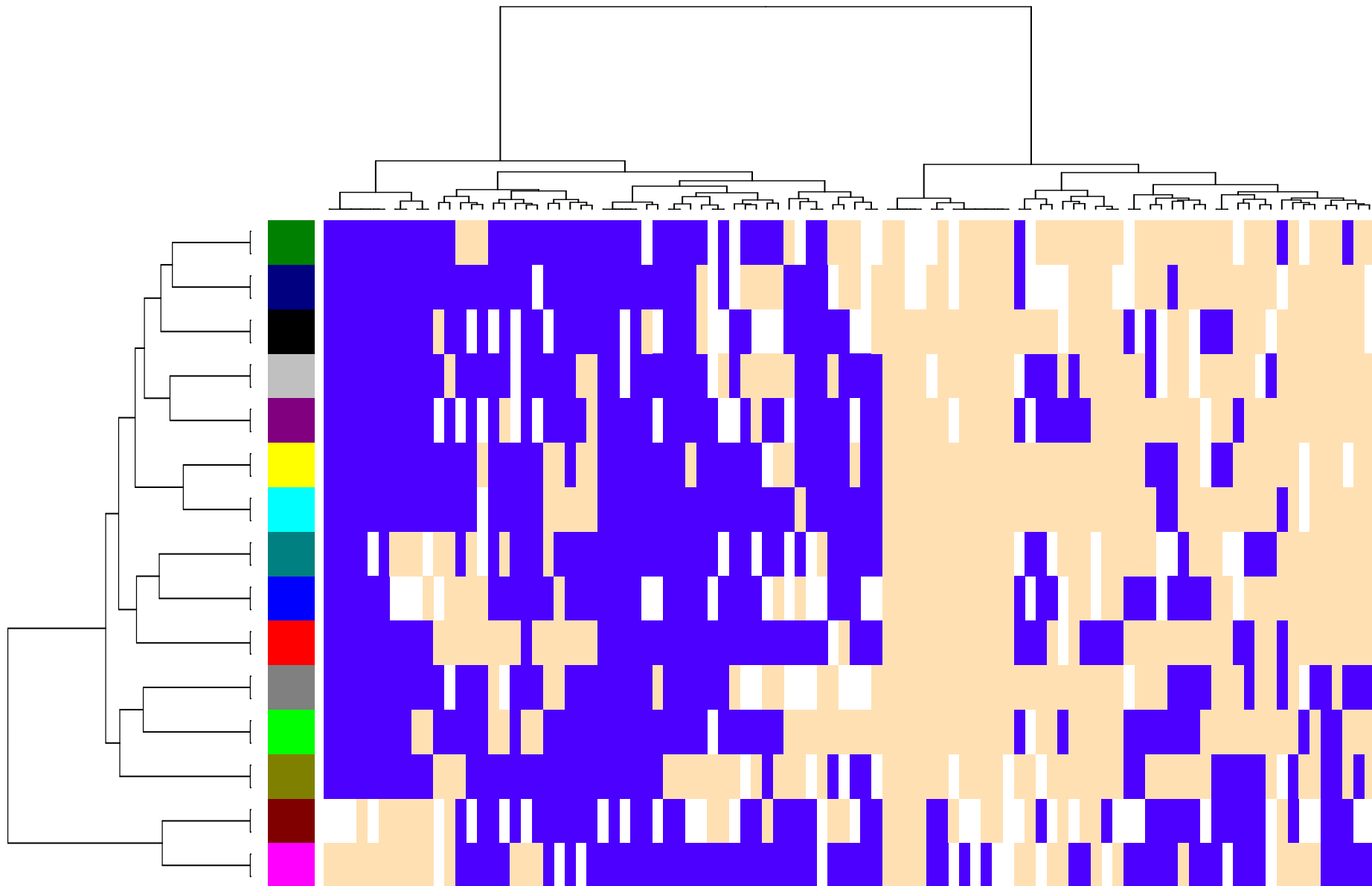
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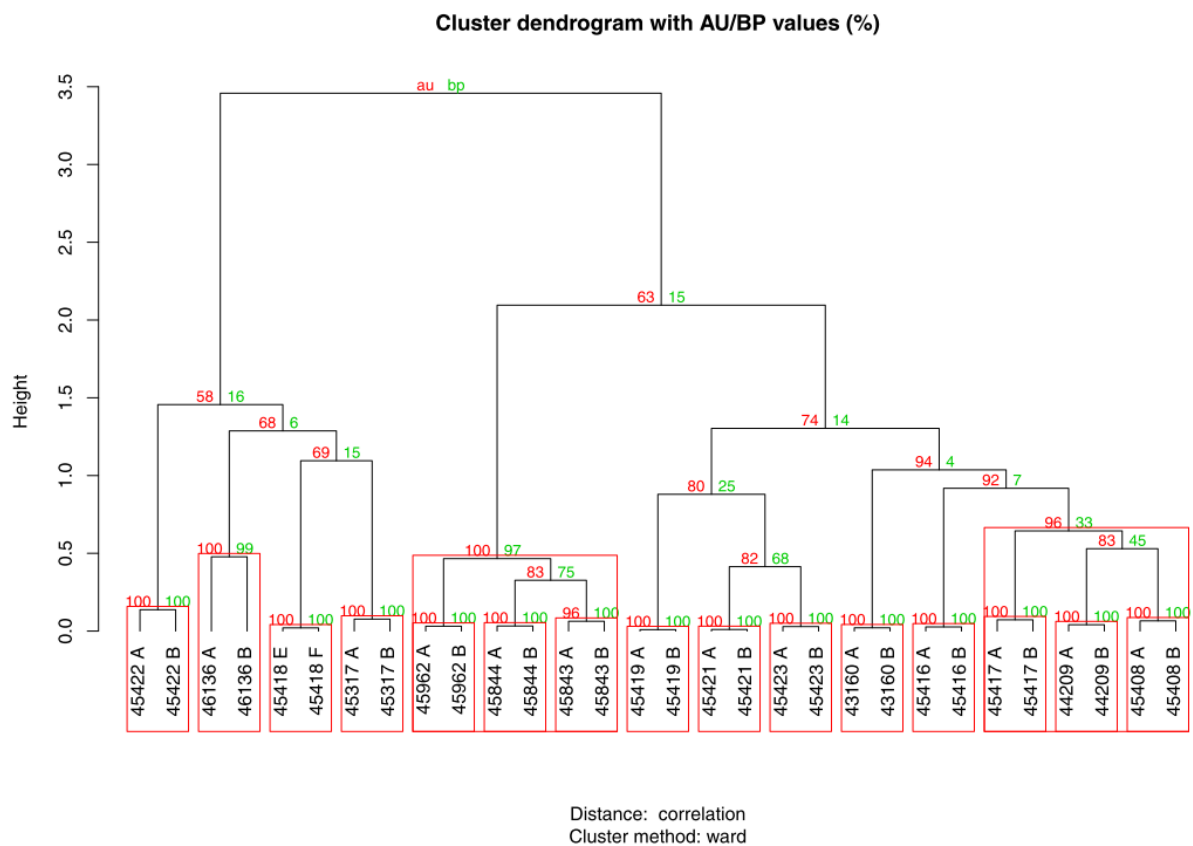
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DSM 45844^T B
 DSM 45844^T A
 DSM 45843^T B
 DSM 45843^T A
 DSM 45408^T B
 DSM 45408^T A
 DSM 45416^T B
 DSM 45416^T A
Strain G18^T A
Strain G18^T B
 DSM 45423^T B
 DSM 45423^T A
 DSM 45421^T B
 DSM 45421^T A
 DSM 43160^T B
 DSM 43160^T A
 DSM 45417^T B
 DSM 45417^T A
 DSM 45419^T B
 DSM 45419^T A
 DSM 45862^T B
 DSM 45862^T A
 DSM 45418^T F
 DSM 45418^T E
 DSM 45317^T B
 DSM 45317^T A
 DSM 46136^T B
 DSM 46136^T A
 DSM 45422^T B
 DSM 45422^T A

F10 (Nicotinic) E12 (Nicotinic) E11 (Quaridine Hydrochloride) D11 (1,2,3,4,6-Pentakis) B12 (6s, 8s) C11 (Fumaric Acid) C12 (D, L-Serine) D12 (Minoxidil) F12 (Tetrastichum Volskelii) D07 (D-Fructose 6-Phosphate) R06 (Gluconicamide) H09 (Sodium Formate) E08 (L-Aspartic Acid) E06 (L-Aspartic Acid) D04 (D-Glucose) F02 (D-Galactaric Acid) E10 (Nicotinic) F03 (D-Gluconic Acid) D03 (D-Asorbic) H02 (g-Amino-n-Butyric Acid) F09 (D-Saccharic Acid) G01 (D-Hydroxy-Phenylacetic Acid) E04 (L-Agmatine) F03 (L-Galactonic Acid-g-Lactone) D08 (D-Aspartic Acid) R08 (N-Acetyl-D-Galactosamine) R09 (M-Acetyl-D-Galactosamine) D06 (D-Glucose 6-Phosphate) B07 (N-Acetyl-D-Mannosamine) D09 (D-Serine) D09 (D-Serine) F07 (Malic Acid) E07 (L-Histidine) G05 (Citric Acid) B04 (p-Methyl-D-Glucosamine) A01 (Nigellein Core) B01 (D-Threonine) A02 (Nucleoside) B02 (D-Glucose) C09 (Inosine) A08 (D-Gentianose) E09 (L-Serine) C08 (D-Fucose) A12 (PM 5) E01 (Gellan) E00 (L-Alanine) B02 (d-Lactose) C05 (D-O-Methyl-D-Glucose) B08 (N-Acetyl-D-Glucosamine) F10 (Nicotinic) G04 (D-Glucose) A10 (Pheolic Core) A11 (PM 6) H07 (Phenolic Acid) A23 (D-Maltose) H91 (Invert-4) C03 (D-Fructose) C01 (D-Glucose) A07 (Sucrose) A02 (Quercetin) A04 (D-Threonine) B11 (6s, 8s) H12 (L-Aspartic Acid) G01 (Uridum Chloride) C14 (1,5-Sodium Lactate) H11 (Butyric Acid) E09 (L-Glutamic Acid) A08 (Turanose) G12 (Passarum Triterpene) A05 (D-Cellobiose) B10 (1s, 6s) D01 (D-Sorbitol) D02 (D-Mannitol) F08 (Quinic Acid) F04 (L-Ascorbic Acid) G04 (D-Malic Acid) G09 (Inosine) C09 (Inosine) C07 (D-Malic Acid) G04 (L-Lactic Acid) D05 (Glycerol) H02 (a-Hydroxy-Butyric Acid) B05 (D-Salicin) C08 (L-Rhamnose) H05 (a-Keto-Butyric Acid) G02 (Methyl-Phenylurea) D11 (Ribitose) H04 (p-Hydroxy-Butyric Acid) G03 (D-Glucose) G08 (L-Malic Acid) F04 (D-Gluconic Acid) F01 (Pectin) H08 (Acetic Acid) G02 (D-Mannose) C04 (D-Galactose)

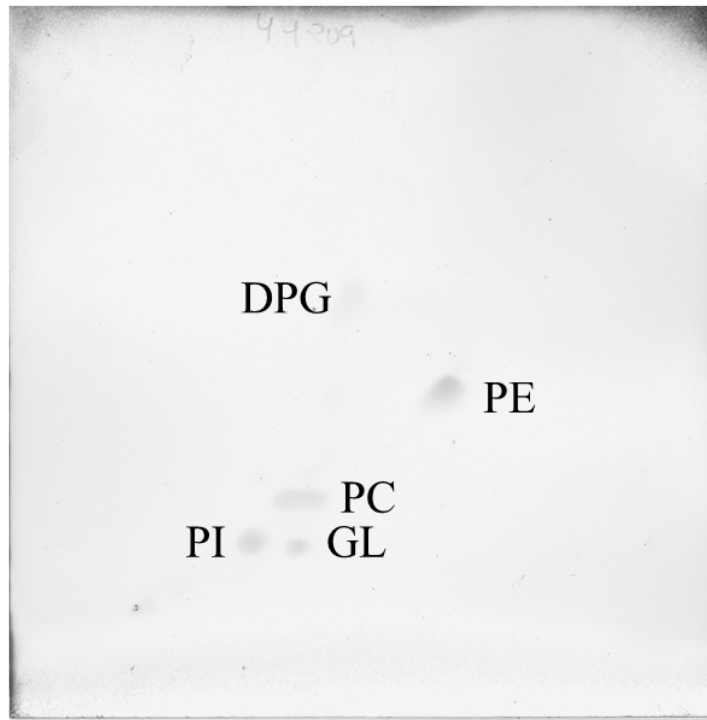
658 **Supplementary Fig. S2.** Phenotypic dendrogram based on the parameter “Maximun Height”
 659 estimated from the respiration curves as measured with the OmniLog phenotyping device
 660 using Ward algorithm for agglomerative hierarchical clustering and correlation coefficient as a
 661 distance metric using the `pvclust` package. Support values approximately unbiased (AU,
 662 left) and bootstrapping (BP, right) are shown above the branches. Well supported clusters are
 663 defined by red squares.



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665 **Supplementary Fig. S3.** Polar lipids profile of *Geodermatophilus poikilotrophi* sp. nov.
 666 G18^T, after separation by two-dimensional TLC. Plate was sprayed with molybdophosphoric
 667 acid for detection of total polar lipid. DPG, diphosphadidylglycerol; PE,
 668 phosphatidylethanolamine; PC, phosphatidylcholine; PI, phosphatidylinositol; GL, unknown
 669 glycolipid.

***Geodermatophilus poikilotrophi* sp. nov. G18^T**



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673 **Supplementary R-code File. S4.** Exemplary code to fit the model and compute the

674 confidence intervals using the R package `lethal`.

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676 #####

677 `##Extraction of lethal doses`

678 `### Example code for the manuscript`

679 `## Geodermatophilus poikilotrophi` sp. nov., a multi-tolerant actinomycete

680 `## isolated from dolomitic marble`

```
681  ## by Maria del Carmen Montero-Calasanz, Benjamin Hofner, Markus Göker,
682  ## Manfred Rohde, Cathrin Spröer, Karima Hezbri, Maher Gtari,
683  ## Peter Schumann, Hans-Peter Klenk
684  ## Author of the code: Benjamin Hofner
685  #####
686  ## Install and load package
687  install.packages("lethal", repos = "http://r-forge.r-project.org",
688             type = "source")
689  library("lethal")
690  ## Run this only once as it takes some time; Thus if the results exist already,
691  ## skip this
692  if (!file.exists("lethal_dose_uv.Rda")) {
693      ## load UV radiation data, which is also part of the package lethal
694      data("geoderm.uv")
695      summary(geoderm.uv)
696      ## make sure that strain and replicate are factors
697      geoderm.uv$strain <- as.factor(geoderm.uv$strain)
```

```
698 geoderm.uv$replicate <- as.factor(geoderm.uv$replicate)

699 mod.uv <- LD(value ~ time, groups = "strain", experiment = "replicate",

700     dose_trafo = "sqrt", data = geoderm.uv,

701     family = negbin(theta = c(0.5, 10)))

702 ## Set seed to make results reproducible

703 ## (as we use bootstrap confidence intervals)

704 set.seed(0703)

705 ## On a linux machine one can easily use parallel programming by specifying

706 ## the numbers of cores to use with the additional argument "mc.cores", e.g.

707 ## confint(mod.uv, B1 = 20, B2 = 100, mc.cores = 10)

708 ci.uv <- confint(mod.uv)

709 ## to reproduce results from the paper, one must use mc.cores = 3

710 save("mod.uv", "ci.uv", file = "lethal_dose_uv.Rda")

711 } else {

712     load("lethal_dose_uv.Rda")

713 }

714 #####

715 ## Extract results
```

```
716  ## extract model and LDs

717  mod.uv

718  ## extract LDs only

719  LD(mod.uv)

720  ## extract confidence intervals (and LDs)

721  ci.uv

722  #####

723  ## Produce plots

724  ## simple graphic without CIs:

725  plot(mod.uv, xlab = "Time (min)", ylab = expression(c.f.u.ml^-1))

726  ## graphic with survival fractions and confidence intervals:

727  plot(ci.uv, xlab = "Time (min)", upper_ylab = expression(c.f.u.ml^-1),

728      mar = c(4, 9.3, 2, 2.5))

729  ## add labels

730  mtext(rep(c("LD10", "LD50"), 3), side = 4, at = c(0.8, 1.2, 1.8, 2.2, 2.8, 3.2),

731      cex = 0.75, las = 2)

732

733
```